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(57) Abstract

The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele–specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.

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BIALLELIC MARKERS

RELATED APPLICATIONS

    This application claims priority to U.S. provisional
application Serial No. 60/030,455, filed November 6, 1996,
5 the entire teachings of which are incorporated herein by
reference.

BACKGROUND OF THE INVENTION

    The genomes of all organisms undergo spontaneous
mutation in the course of their continuing evolution,
10 generating variant forms of progenitor sequences (Gusella,
Ann. Rev. Biochem. 55, 831-854 (1986)). The variant form
may confer an evolutionary advantage or disadvantage
relative to a progenitor form or may be neutral. In some
instances, a variant form confers a lethal disadvantage and
15 is not transmitted to subsequent generations of the
organism. In other instances, a variant form confers an
evolutionary advantage to the species and is eventually
incorporated into the DNA of many or most members of the
species and effectively becomes the progenitor form. In
20 many instances, both progenitor and variant form(s) survive
and co-exist in a species population. The coexistence of
multiple forms of a sequence gives rise to polymorphisms.
    Several different types of polymorphism have been
reported. A restriction fragment length polymorphism
25 (RFLP) Is a variation in DNA sequence that alters the
length of a restriction fragment (Botstein *et al.*, *Am. J.
Hum. Genet.* 32, 314-331 (1980)). The restriction fragment
length polymorphism may create or delete a restriction
site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic
analyses (see WO 90/13668; WO90/11369; Donis-Keller, *Cell*
51, 319-337 (1987); Lander *et al.*, *Genetics* 121, 85-99
(1989)). When a heritable trait can be linked to a

5   particular RFLP, the presence of the RFLP in an individual
can be used to predict the likelihood that the animal will
also exhibit the trait.

Other polymorphisms take the form of short tandem
repeats (STRs) that include tandem di-, tri- and tetra-

10 nucleotide repeated motifs. These tandem repeats are also
referred to as variable number tandem repeat (VNTR)
polymorphisms. VNTRs have been used in identity and
paternity analysis (US 5,075,217; Armour *et al.*, *FEBS Lett.*
307, 113-115 (1992); Horn *et al.*, WO 91/14003; Jeffreys, EP

15 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide
variations between individuals of the same species. Such
polymorphisms are far more frequent than RFLPs, STRs and
VNTRs. Some single nucleotide polymorphisms occur in

20 protein-coding sequences, in which case, one of the
polymorphic forms may give rise to the expression of a
defective or other variant protein and, potentially, a
genetic disease. Examples of genes, in which polymorphisms
within coding sequences give rise to genetic disease

25 include β-globin (sickle cell anemia) and CFTR (cystic
fibrosis). Other single nucleotide polymorphisms occur in
noncoding regions. Some of these polymorphisms may also
result in defective protein expression (e.g., as a result
of defective splicing). Other single nucleotide

30 polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same
manner as RFLPs and VNTRs, but offer several advantages.
Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the
genome than other forms of polymorphism. The greater
frequency and uniformity of single nucleotide polymorphisms
means that there is a greater probability that such a
5   polymorphism will be found in close proximity to a genetic
locus of interest than would be the case for other
polymorphisms. The different forms of characterized single
nucleotide polymorphisms are often easier to distinguish
than other types of polymorphism (e.g., by use of assays
10   employing allele-specific hybridization probes or primers).
       Only a small percentage of the total repository of
polymorphisms in humans and other organisms has been
identified. The limited number of polymorphisms identified
to date is due to the large amount of work required for
15   their detection by conventional methods. For example, a
conventional approach to identifying polymorphisms might be
to sequence the same stretch of DNA in a population of
individuals by dideoxy sequencing. In this type of
approach, the amount of work increases in proportion to
20   both the length of sequence and the number of individuals
in a population and becomes impractical for large stretches
of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a
5   polymorphic site. Complements of these segments are also included.   The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying
10 the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base .(Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These
15 oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table,
20 column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a
25 set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases
30 present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION
DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or
double-stranded. Oligonucleotides can be naturally
occurring or synthetic, but are typically prepared by
synthetic means. The oligonucleotides of the present
invention can comprise all of an oligonucleotide sequence
presented in column 7 of the Table or a segment of such an
oligonucleotide which includes a polymorphic site.
Oligonucleotides can be all of a nucleic acid segment as
represented in column 7 of the Table; a nucleic acid
sequence which comprises a nucleic acid segment represented
in column 7 of the Table and additional nucleic acids
(present at either or both ends of a nucleic acid segment
of column 7); or a portion (fragment) of a nucleic acid
segment represented in column 7 of the Table which includes
a polymorphic site. Preferred oligonucleotides of the
invention include segments of DNA, or their complements,
which include any one of the polymorphic sites shown in the
Table. The segments can be between 5 and 250 bases, and,
in specific embodiments, are between 5-10, 5-20, 10-20, 10-
50, 20-50 or 10-100 bases. The polymorphic site can occur
within any position of the segment. The segments can be
from any of the allelic forms of DNA shown in the Table.

Hybridization probes are oligonucleotides which bind in
a base-specific manner to a complementary strand of nucleic
acid. Such probes include peptide nucleic acids, as
described in Nielsen *et al.*, *Science* 254, 1497-1500 (1991).

As used herein, the term primer refers to a single-
stranded oligonucleotide which acts as a point of
initiation of template-directed DNA synthesis under
appropriate conditions (*e.g.*, in the presence of four
different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse
transcriptase) in an appropriate buffer and at a suitable
temperature. The appropriate length of a primer depends on
the intended use of the primer, but typically ranges from
5   15 to 30 nucleotides. Short primer molecules generally
require cooler temperatures to form sufficiently stable
hybrid complexes with the template. A primer need not
reflect the exact sequence of the template, but must be
sufficiently complementary to hybridize with a template.
10   The term primer site refers to the area of the target DNA
to which a primer hybridizes. The term primer pair refers
to a set of primers including a 5' (upstream) primer that
hybridizes with the 5' end of the DNA sequence to be
amplified and a 3' (downstream) primer that hybridizes with
15   the complement of the 3' end of the sequence to be
amplified.

       As used herein, linkage describes the tendency of
genes, alleles, loci or genetic markers to be inherited
together as a result of their location on the same
20   chromosome. It can be measured by percent recombination
between the two genes, alleles, loci or genetic markers.

       As used herein, polymorphism refers to the occurrence
of two or more genetically determined alternative sequences
or alleles in a population. A polymorphic marker or site
25   is the locus at which divergence occurs. Preferred markers
have at least two alleles, each occurring at frequency of
greater than 1%, and more preferably greater than 10% or
20% of a selected population. A polymorphic locus may be
as small as one base pair. Polymorphic markers include
30   restriction fragment length polymorphisms, variable number
of tandem repeats (VNTR's), hypervariable regions,
minisatellites, dinucleotide repeats, trinucleotide
repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified
allelic form is arbitrarily designated as the reference
form and other allelic forms are designated as alternative
or variant alleles. The allelic form occurring most
5 frequently in a selected population is sometimes referred
to as the wildtype form. Diploid organisms may be
homozygous or heterozygous for allelic forms. A diallelic
or biallelic polymorphism has two forms. A triallelic
polymorphism has three forms.
10   A single nucleotide polymorphism occurs at a
polymorphic site occupied by a single nucleotide, which is
the site of variation between allelic sequences. -The site
is usually preceded by and followed by highly conserved
sequences of the allele (e.g., sequences that vary in less
15 than 1/100 or 1/1000 members of the populations).
       A single nucleotide polymorphism usually arises due to
substitution of one nucleotide for another at the
polymorphic site. A transition is the replacement of one
purine by another purine or one pyrimidine by another
20 pyrimidine. A transversion is the replacement of a purine
by a pyrimidine or vice versa. Single nucleotide
polymorphisms can also arise from a deletion of a
nucleotide or an insertion of a nucleotide relative to a
reference allele. Typically the polymorphic site is
25 occupied by a base other than the reference base. For
example, where the reference allele contains the base "T"
at the polymorphic site, the altered allele can contain a
"C", "G" or "A" at the polymorphic site.
       Hybridizations are usually performed under stringent
30 conditions, for example, at a salt concentration of no more
than 1 M and a temperature of at least 25°C. For example,
conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM
EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe
hybridizations. Equivalent conditions can be determined by
varying one or more of the parameters given as an example,
as known in the art, while maintaining a similar degree of
5   identity or similarity between the target nucleotide
sequence and the primer or probe used.
     The term "isolated" is used herein to indicate that the
material in question exists in a physical milieu distinct
from that in which it occurs in nature. For example, an
10   isolated nucleic acid of the invention may be substantially
isolated with respect to the complex cellular milieu in
which it naturally occurs. In some instances, the isolated
material will form part of a composition (for example, a
crude extract containing other substances), buffer system
15   or reagent mix. In other circumstance, the material may be
purified to essential homogeneity, for example as
determined by PAGE or column chromatography such as HPLC.
Preferably, an isolated nucleic acid comprises at least
about 50, 80 or 90 percent (on a molar basis) of all
20   macromolecular species present.

I.   Novel Polymorphisms of the Invention
     The novel polymorphisms of the invention are listed in
the Table. The first column of the Table lists the names
assigned to the fragments in which the polymorphisms occur.
25   The fragments are all human genomic fragments. The
sequence of one allelic form of each of the fragments
(arbitrarily referred to as the prototypical or reference
form) has been previously published. These sequences are
listed at http://www-genome.wi.mit.edu/ (all STS's
30   (sequence tag sites)); http://shgc.stanford.edu (Stanford
STS's); and http://ww.tigr.org/ (TIGR STS's). The Web
sites also list primers for amplification of the fragments,

and the genomic location of fragments. Some fragments are
expressed sequence tags, and some are random genomic
fragments. All information in the websites concerning the
fragments listed in the Table is incorporated by reference
5   in its entirety for all purposes.

The second column lists the position in the fragment in
which a polymorphic site has been found. Positions are
numbered consecutively with the first base of the fragment
sequence as listed in one of the above databases being
10   assigned the number one. The third column lists the base
occupying the polymorphic site in the sequence in the data
base. This base is arbitrarily designated the reference or
prototypical form, but it is not necessarily the most
frequently occurring form. The fourth column in the Table
15   lists the alternative base(s) at the polymorphic site. The
fifth column of the Table lists a 5' (upstream or forward)
primer that hybridizes with the 5' end of the DNA sequence
to be amplified. The sixth column of the Table lists a 3'
(downstream or reverse) primer that hybridizes with the
20   complement of the 3' end of the sequence to be amplified.
The seventh column of the Table lists a number of bases of
sequence on either side of the polymorphic site in each
fragment. The indicated sequences can be either DNA or
RNA. In the latter, the T's shown in the Table are
25   replaced by U's. The base occupying the polymorphic site
is indicated in EUPAC-IUB ambiguity code.

II.   Analysis of Polymorphisms
A.   Preparation of Samples
Polymorphisms are detected in a target nucleic acid
30   from an individual being analyzed. For assay of genomic
DNA, virtually any biological sample (other than pure red
blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine,
fecal material, sweat, buccal, skin and hair. For assay of
cDNA or mRNA, the tissue sample must be obtained from an
organ in which the target nucleic acid is expressed. For
5   example, if the target nucleic acid is a cytochrome P450,
the liver is a suitable source.
        Many of the methods described below require
amplification of DNA from target samples. This can be
accomplished by e.g., PCR. *See generally PCR Technology:*
10   *Principles and Applications for DNA Amplification* (ed. H.A.
Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A*
Guide to Methods and Applications (eds. Innis, et al.,
Academic Press, San Diego, CA, 1990); Mattila *et al.,*
Nucleic Acids Res. 19, 4967 (1991); Eckert *et al., PCR*
15   *Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson
et al., IRL Press, Oxford); and U.S. Patent 4,683,202.
        Other suitable amplification methods include the ligase
chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560
(1989), Landegren *et al., Science* 241, 1077 (1988),
20   transcription amplification (Kwoh *et al., Proc. Natl. Acad.*
Sci. USA 86, 1173 (1989)), and self-sustained sequence
replication (Guatelli *et al., Proc. Nat. Acad. Sci. USA,*
87, 1874 (1990)) and nucleic acid based sequence
amplification (NASBA). The latter two amplification
25   methods involve isothermal reactions based on isothermal
transcription, which produce both single stranded RNA
(ssRNA) and double stranded DNA (dsDNA) as the
amplification products in a ratio of about 30 or 100 to 1,
respectively.

30   B. Detection of Polymorphisms in Target DNA
        There are two distinct types of analysis of target DNA
for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is
carried out to identify polymorphic sites not previously
characterized (i.e., to identify new polymorphisms). This
analysis compares target sequences in different individuals
5   to identify points of variation, i.e., polymorphic sites.
By analyzing groups of individuals representing the
greatest ethnic diversity among humans and greatest breed
and species variety in plants and animals, patterns
characteristic of the most common alleles/haplotypes of the
10   locus can be identified, and the frequencies of such
alleles/haplotypes in the population can be determined.
Additional allelic frequencies can be determined for
subpopulations characterized by criteria such as geography,
race, or gender. The de novo identification of
15   polymorphisms of the invention is described in the Examples
section. The second type of analysis determines which
form(s) of a characterized (known) polymorphism are present
in individuals under test. There are a variety of suitable
procedures, which are discussed in turn.

20   1. Allele-Specific Probes
The design and use of allele-specific probes for
analyzing polymorphisms is described by e.g., Saiki et al.,
Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki,
WO 89/11548. Allele-specific probes can be designed that
25   hybridize to a segment of target DNA from one individual
but do not hybridize to the corresponding segment from
another individual due to the presence of different
polymorphic forms in the respective segments from the two
individuals. Hybridization conditions should be
30   sufficiently stringent that there is a significant
difference in hybridization intensity between alleles, and
preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are
designed to hybridize to a segment of target DNA such that
the polymorphic site aligns with a central position (e.g.,
in a 15-mer at the 7 position; in a 16-mer, at either the 8
or 9 position) of the probe. This design of probe achieves
good discrimination in hybridization between different
allelic forms.

     Allele-specific probes are often used in pairs, one
member of a pair showing a perfect match to a reference
form of a target sequence and the other member showing a
perfect match to a variant form. Several pairs of probes
can then be immobilized on the same support for
simultaneous analysis of multiple polymorphisms within the
same target sequence.

2. Tiling Arrays

     The polymorphisms can also be identified by
hybridization to nucleic acid arrays, some examples of
which are described in WO 95/11995. One form of such
arrays is described in the Examples section in connection
with de novo identification of polymorphisms. The same
array or a different array can be used for analysis of
characterized polymorphisms. WO 95/11995 also describes
subarrays that are optimized for detection of a variant
form of a precharacterized polymorphism. Such a subarray
contains probes designed to be complementary to a second
reference sequence, which is an allelic variant of the
first reference sequence. The second group of probes is
designed by the same principles as described in the
Examples, except that the probes exhibit complementarity to
the second reference sequence. The inclusion of a second
group (or further groups) can be particularly useful for
analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3.   Allele-Specific Primers

5   An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in

10   conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows

15   a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of

20   the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4.   Direct-Sequencing

The direct analysis of the sequence of polymorphisms of

25   the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind *et al.*, *Recombinant DNA Laboratory Manual*, (Acad. Press,

30   1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita *et al.*, *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A.   Forensics

Determination of which polymorphic forms occupy a set
of polymorphic sites in an individual identifies a set of
polymorphic forms that distinguishes the individual. *See
generally* National Research Council, *The Evaluation of
Forensic DNA Evidence* (Eds. Pollard *et al*., National
Academy Press, DC, 1996). The more sites that are
analyzed, the lower the probability that the set of
polymorphic forms in one individual is the same as that in
an unrelated individual. Preferably, if multiple sites are
analyzed, the sites are unlinked. Thus, polymorphisms of
the invention are often used in conjunction with
polymorphisms in distal genes. Preferred polymorphisms for
use in forensics are biallelic because the population
frequencies of two polymorphic forms can usually be
determined with greater accuracy than those of multiple
polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set
of forensic markers in an individual is useful for forensic
analysis. For example, one can determine whether a blood
sample from a suspect matches a blood or other tissue
sample from a crime scene by determining whether the set of
polymorphic forms occupying selected polymorphic sites is
the same in the suspect and the sample. If the set of
polymorphic markers does not match between a suspect and a
sample, it can be concluded (barring experimental error)
that the suspect was not the source of the sample. If the
set of markers does match, one can conclude that the DNA
from the suspect is consistent with that found at the crime
scene. If frequencies of the polymorphic forms at the loci
tested have been determined (e.g., by analysis of a
suitable population of individuals), one can perform a
statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

p(ID) is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y, the probability of each genotype in a diploid organism is (see WO 95/12607):

Homozygote: $p(AA) = x^2$
Homozygote: $p(BB) = y^2 = (1-x)^2$
Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$
Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e, the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity p(ID) for a 3-allele system where the alleles have the frequencies in the population of x, y and z, respectively, is equal to the sum of the squares of the genotype frequencies:

$$p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of n alleles, the appropriate binomial expansion is used to calculate p(ID) and p(exc).

The cumulative probability of identity (cum p(ID)) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

cum p(ID) = p(ID1)p(ID2)p(ID3).... p(IDn)

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

cum p(nonID) = 1-cum p(ID).

If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

B.   Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced. Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

    p(exc) = xy(1-xy)

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

    (At a triallelic site p(exc) = xy(1-xy) + yz(1- yz) + xz(1-xz)+ 3xyz(1-xyz))), where x, y and z and the respective population frequencies of alleles A, B and C).

    The probability of non-exclusion is

    p(non-exc) = 1-p(exc)

    The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

    cum p(non-exc) = p(non-exc1)p(non-exc2)p(non-exc3)....
p(non-excn)

    The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

    cum p(exc) = 1 - cum p(non-exc).

    If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

    C.   Correlation of Polymorphisms with Phenotypic Traits
    The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell
mutation confers resistance to malaria, but a homozygous
sickle cell mutation is usually lethal. Other
polymorphisms occur in noncoding regions but may exert
5   phenotypic effects indirectly via influence on replication,
transcription, and translation. A single polymorphism may
affect more than one phenotypic trait. Likewise, a single
phenotypic trait may be affected by polymorphisms in
different genes. Further, some polymorphisms predispose an
10   individual to a distinct mutation that is causally related
to a certain phenotype.

     Phenotypic traits include diseases that have known but
hitherto unmapped genetic components (e.g.,
agammaglobulimenia, diabetes insipidus, Lesch-Nyhan
15   syndrome, muscular dystrophy, Wiskott-Aldrich syndrome,
Fabry's disease, familial hypercholesterolemia, polycystic
kidney disease, hereditary spherocytosis, von Willebrand's
disease, tuberous sclerosis, hereditary hemorrhagic
telangiectasia, familial colonic polyposis, Ehlers-Danlos
20   syndrome, osteogenesis imperfecta, and acute intermittent
porphyria). Phenotypic traits also include symptoms of, or
susceptibility to, multifactorial diseases of which a
component is or may be genetic, such as autoimmune
diseases, inflammation, cancer, diseases of the nervous
25   system, and infection by pathogenic microorganisms. Some
examples of autoimmune diseases include rheumatoid
arthritis, multiple sclerosis, diabetes (insulin-dependent
and non-independent), systemic lupus erythematosus and
Graves disease. Some examples of cancers include cancers
30   of the bladder, brain, breast, colon, esophagus, kidney,
leukemia, liver, lung, oral cavity, ovary, pancreas,
prostate, skin, stomach and uterus. Phenotypic traits also
include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5   individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the
10   individuals, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be
15   performed by standard statistical methods such as a κ-squared test and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with
20   heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In
25   the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular
30   monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the
possibility of transmitting such a polymorphism from her
husband to her offspring. In the case of a weaker, but
still statistically significant correlation between a
5   polymorphic set and human disease, immediate therapeutic
intervention or monitoring may not be justified.
Nevertheless, the patient can be motivated to begin simple
life-style changes (e.g., diet, exercise) that can be
accomplished at little cost to the patient but confer
10   potential benefits in reducing the risk of conditions to
which the patient may have increased susceptibility by
virtue of variant alleles. Identification of a polymorphic
set in a patient correlated with enhanced receptiveness to
one of several treatment regimes for a disease indicates
15   that this treatment regime should be followed.
        For animals and plants, correlations between
characteristics and phenotype are useful for breeding for
desired characteristics. For example, Beitz et al., US
5,292,639 discuss use of bovine mitochondrial polymorphisms
20   in a breeding program to improve milk production in cows.
To evaluate the effect of mtDNA D-loop sequence
polymorphism on milk production, each cow was assigned a
value of 1 if variant or 0 if wildtype with respect to a
prototypical mitochondrial DNA sequence at each of 17
25   locations considered. Each production trait was analyzed
individually with the following animal model:
        $Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \ldots \beta_{17} + PE_n + a_n + e_p$
where Y_{ijknp} is the milk, fat, fat percentage, SNF, SNF
percentage, energy concentration, or lactation energy
30   record; μ is an overall mean; YS_i is the effect common to
all cows calving in year-season; X_k is the effect common to
cows in either the high or average selection line; β_1 to β_{17}
are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent
environmental effect common to all records of cow n; a_n is
effect of animal n and is composed of the additive genetic
contribution of sire and dam breeding values and a
5   Mendelian sampling effect; and e_p is a random residual. It
was found that eleven of seventeen polymorphisms tested
influenced at least one production trait. Bovines having
the best polymorphic forms for milk production at these
eleven loci are used as parents for breeding the next
10   generation of the herd.

     D.   Genetic Mapping of Phenotypic Traits
     The previous section concerns identifying correlations
between phenotypic traits and polymorphisms that directly
or indirectly contribute to those traits. The present
15   section describes identification of a physical linkage
between a genetic locus associated with a trait of interest
and polymorphic markers that are not associated with the
trait, but are in physical proximity with the genetic locus
responsible for the trait and co-segregate with it. Such
20   analysis is useful for mapping a genetic locus associated
with a phenotypic trait to a chromosomal position, and
thereby cloning gene(s) responsible for the trait. *See*
Lander *et al.*, *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357
(1986); Lander *et al.*, *Proc. Natl. Acad. Sci. (USA)* 84,
25   2363-2367 (1987); Donis-Keller *et al.*, *Cell* 51, 319-337
(1987); Lander *et al.*, *Genetics* 121, 185-199 (1989)).
Genes localized by linkage can be cloned by a process known
as directional cloning. *See* Wainwright, *Med. J. Australia*
159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6
30   (1992).
     Linkage studies are typically performed on members of a
family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a
set of polymorphic markers. The distribution of
polymorphic markers in an informative meiosis is then
analyzed to determine which polymorphic markers co-

5   segregate with a phenotypic trait. *See, e.g.,* Kerem *et
al., Science* 245, 1073-1080 (1989); Monaco *et al., Nature*
316, 842 (1985); Yamoka *et al., Neurology* 40, 222-226
(1990); Rossiter *et al., FASEB Journal* 5, 21-27 (1991).
       Linkage is analyzed by calculation of LOD (log of the

10 odds) values. A lod value is the relative likelihood of
obtaining observed segregation data for a marker and a
genetic locus when the two are located at a recombination
fraction θ, versus the situation in which the two are not
linked, and thus segregating independently (Thompson &

15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders
Company, Philadelphia, 1991); Strachan, "Mapping the human
genome" in *The Human Genome* (BIOS Scientific Publishers
Ltd, Oxford), Chapter 4). A series of likelihood ratios
are calculated at various recombination fractions (θ),

20 ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$
(unlinked). Thus, the likelihood at a given value of θ is:
probability of data if loci linked at θ to probability of
data if loci unlinked. The computed likelihoods are
usually expressed as the $\log_{10}$ of this ratio (i.e., a lod

25 score). For example, a lod score of 3 indicates 1000:1
odds against an apparent observed linkage being a
coincidence. The use of logarithms allows data collected
from different families to be combined by simple addition.
Computer programs are available for the calculation of lod

30 scores for differing values of θ (e.g., LIPED, MLINK
(Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446
(1984)). For any particular lod score, a recombination
fraction may be determined from mathematical tables. *See*

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Smith *et al.*, *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component) except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, *e.g.*, mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, *i.e.*, 80, 95 or 99% free of cell component contaminants, as described in Jacoby,

5   *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is

10   secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene

15   and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. *See* Hogan *et al.*, "Manipulating

20   the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. *See* Capecchi, *Science* 244, 1288-1292

25   (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30   In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active
fragments include any portion of the full-length
polypeptide which confers a biological function on the
variant gene product, including ligand binding, and
5   antibody binding. Ligand binding includes binding by
nucleic acids, proteins or polypeptides, small biologically
active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that
specifically bind to variant gene products but not to
10   corresponding prototypical gene products are also provided.
Antibodies can be made by injecting mice or other animals
with the variant gene product or synthetic peptide
fragments thereof. Monoclonal antibodies are screened as
are described, for example, in Harlow & Lane, *Antibodies, A*
15   *Laboratory Manual*, Cold Spring Harbor Press, New York
(1988); Goding, *Monoclonal antibodies, Principles and*
Practice (2d ed.) Academic Press, New York (1986).
Monoclonal antibodies are tested for specific
immunoreactivity with a variant gene product and lack of
20   immunoreactivity to the corresponding prototypical gene
product. These antibodies are useful in diagnostic assays
for detection of the variant form, or as an active
ingredient in a pharmaceutical composition.

V.   Kits
25   The invention further provides kits comprising at least
one allele-specific oligonucleotide as described above.
Often, the kits contain one or more pairs of allele-
specific oligonucleotides hybridizing to different forms of
a polymorphism. In some kits, the allele-specific
30   oligonucleotides are provided immobilized to a substrate.
For example, the same substrate can comprise allele-
specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table.
Optional additional components of the kit include, for
example, restriction enzymes, reverse-transcriptase or
polymerase, the substrate nucleoside triphosphates, means
5   used to label (for example, an avidin-enzyme conjugate and
enzyme substrate and chromogen if the label is biotin), and
the appropriate buffers for reverse transcription, PCR, or
hybridization reactions. Usually, the kit also contains
instructions for carrying out the methods.
10   The following Examples are offered for the purpose of
illustrating the present invention and are not to be
construed to limit the scope of this invention. The
teachings of all references cited herein are hereby
incorporated herein by reference.

15   EXAMPLES
        The polymorphisms shown in the Table were identified by
resequencing of target sequences from three to ten
unrelated individuals of diverse ethnic and geographic
backgrounds by hybridization to probes immobilized to
20   microfabricated arrays or conventional sequencing. The
strategy and principles for design and use of such arrays
are generally described in WO 95/11995. The strategy
provides arrays of probes for analysis of target sequences
showing a high degree of sequence identity to the reference
25   sequences of the fragments shown in the Table, column 1.
The reference sequences were sequence-tagged sites (STSs)
developed in the course of the Human Genome Project (see,
e.g., Science 270, 1945-1954 (1995); Nature 380, 152-154
(1996)). Most STS's ranged from 100 bp to 300 bp in size.
30   A typical probe array used in this analysis has two
groups of four sets of probes that respectively tile both
strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect
complementarily with one of the reference sequences. Each
probe in the first probe set has an interrogation position
that corresponds to a nucleotide in the reference sequence.
5   That is, the interrogation position is aligned with the
corresponding nucleotide in the reference sequence, when
the probe and reference sequence are aligned to maximize
complementarily between the two. For each probe in the
first set, there are three corresponding probes from three
10   additional probe sets. Thus, there are four probes
corresponding to each nucleotide in the reference sequence.
The probes from the three additional probe sets are
identical to the corresponding probe from the first probe
set except at the interrogation position, which occurs in
15   the same position in each of the four corresponding probes
from the four probe sets, and is occupied by a different
nucleotide in the four probe sets. In the present
analysis, probes were 25 nucleotides long. Arrays tiled
for multiple different references sequences were included
20   on the same substrate.
        Multiple target sequences from an individual were
amplified from human genomic DNA using primers for the
fragments indicated in the listed Web sites. The amplified
target sequences were fluorescently labelled during or
25   after PCR. The labelled target sequences were hybridized
with a substrate bearing immobilized arrays of probes. The
amount of lable bound to probes was measured. Analysis of
the pattern of label revealed the nature and position of
differences between the target and reference sequence. For
30   example, comparison of the intensities of four
corresponding probes reveals the identity of a
corresponding nucleotide in the target sequences aligned
with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the
nucleotide occupying the interrogation position of the
probe showing the highest intensity (see WO 95/11995). The
existence of a polymorphism is also manifested by
5   differences in normalized hybridization intensities of
probes flanking the polymorphism when the probes hybridized
to corresponding targets from different individuals. For
example, relative loss of hybridization intensity in a
"footprint" of probes flanking a polymorphism signals a
10   difference between the target and reference (i.e., a
polymorphism) (see EP 717,113). Additionally,
hybridization intensities for corresponding targets from
different individuals can be classified into groups or
clusters suggested by the data, not defined *a priori*, such
15   that isolates in a give cluster tend to be similar and
isolates in different clusters tend to be dissimilar.
Hybridizations to samples from different individuals were
performed separately. The Table summarizes the data
obtained for target sequences in comparison with a
20   reference sequence for the individuals tested.
      From the foregoing, it is apparent that the invention
includes a number of general uses that can be expressed
concisely as follows. The invention provides for the use
of any of the nucleic acid segments described above in the
25   diagnosis or monitoring of diseases, such as cancer,
inflammation, heart disease, diseases of the CNS, and
susceptibility to infection by microorganisms. The
invention further provides for the use of any of the
nucleic acid segments in the manufacture of a medicament
30   for the treatment or prophylaxis of such diseases. The
invention further provides for the use of any of the DNA
segments as a pharmaceutical.

All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5   individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
WI-7070	226	C	T		---	TGTGAAACTCCACTTGAAGCCAAAGAAAGAAGAAAACTCACACTTAAAACACATGCCAGTTGGGAAGGTCT GAAAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATTT GTACTGGCCAAATACTGAATAAACAGTTGAAGGAAAGACATTGGAAAAAGCTTTTGAGGATAATGT TACTAGACTTTATGCCATGGTGCTTT[C/T]AGTTTAATGCTTGTGTCTCTGTCAG
WI-10744	61	G	C		---	AAGCCATTGACGTAACATCTCAGAGGTTATTTGCATGGATGACTCCTGGGACAAAAGGAC[G/C]AA AAACACTCTTCTGTGCGGATATCTGTGCAGATAGCCAAAGATCAGATGCTACCCAGATGTGTTTT GATAATACATAAGCCCCTAGGATTTAGATACAACAATCTTGAAAGAAACTGAGACAGATAATTCTGAATT AAATGAGGTAAAGTTTCAGGCACTCA
WI-9975	126	C	T		---	GGGCAAATTACCAGCAAAAAGTCAAATTACCAGCATCAAAGTCAGGTGCAAAGGAGGTAGAACAA TTACAGTAACTATGTCAATCTTTTGTATATTAGTATTATCTGCCCAATGCCTAGAATA[C/T]AGTG GGTCCCTAATAGTTATTAGTTCCTTTTCTCCTCTTCTCTGAATTTATTTTATACTTAA GGGATTAGTTACCACCAAAAATGTGTATGTATCAAATTGATTCTTACTGAA
WI-8010	247	G	T		---	GCTAGGTTTTGTTCTGTTGGCTGTCTCACTAGACTTGAGATGACTTGATTTACAGTAATCCCTATGT GATGTAACTAGTCTAGACCTTCCCTCTCCGCAATTCCCAGCTCCAGGTTTCAGAAAGTATGCCACAC TCAACCCTCTCTCCCAGTTCATCCTGTATTAATTTCTTCCCATATTAATTCAAAGGGAGTGGACAGGT CCCTGGCTGAAAAGAAAATAAAAGAGATCCCCAAAGTGGTGGGG[G/T]CTT
WI-5222b	85	G	C		---	GCCCGGCCTATCTCTTTAATTTAAACTTGTATCTTTGGTGTTTCTCCATCCTA[G/C]GATTCTGCCTTAT CTTTGTCCTGTCTGTA[G/C]ATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAATTCTTCAGGTGTCTCTTGAATTTTCTCTGCTATTGAGGACATTCCCACTTTCTACTTA TCTCGACTCTATAACAACTCCAACAGAA
WI-5222	52	G	C		---	GCCCGGCCTATCTCTTTAATTTAAACTTGTATCTTTGGTGTTTCTCCATCCTA[G/C]GATTCTGCCTTAT AATCTTTGTCCTGTCTGTAGATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAATTCTTCAGGTGTCTCTTGAATTTTCTCTGCTATTGAGGACATTTCCCACTTTCTACTTA TCTCGACTCTATAACAACTCCAACAGAA
WI-8007	242	C	A		---	TATGCACTTCCACAAAAGCGGATATAATTTAAAAGTTTTTTCATTAGAAATAAAATGTATAAAAATAA ATATGTTATTATAGGCATTTATTATTATGAGTGAATTCTACTATATACATATTTACTATATACATATTCTCACA ATAAAGTACATGTAATTTATAGTAACATATTTACTATATACATATTGAAAAAATCATATTCTCACA GAAGAGCTGAACAGACATTCACCAGGATACGACTGTTGGAC[C/A]AGCTGCTG
WI-9823	97	C	T		---	TCAGTTGCAAAAATTGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGTATGTGTTTTTGTTAG TCTATATTCACACATAGTGAGTGAAATTC[C/T]GGGGCATGGGAAATACATCTTTATGAGACATTGA ACTGCTCACCACTATCACATCTGATTTGTATGACTATTGTACAGTTGGGATCACC ATGCTTCCAATCTGATTTGATTGTGTATGCCAGTATTGTGACTATTGTACAGTTGGGATCACC

Marker	Pos	Alleles		Sequence
WI-9651b	105	A	T	TCTCTACATTCTATGGACAACCTCCATGCCTTTGCACATGCTGATCCTCCTCCTGGAATTCCTTTCCT ACTTGTCCTCATGTACAATTTTCTGCTCGTCCTTCA[A/T]GGGGCAGCTTGCAAGCCTCCCTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATCGCCTCCATGCTGTTTGAATGTCTCTG TCTTTAAACCTGTAATGGTATATTAATCCTTGGTGTTTGAATGTCTCTC
WI-9651	139	T	C	TCTCTACATTCTATGGACAACCTCCATGCCTTTGCACATGCTGATCCTCCTCCTGGAATTCCTTTCCT ACTTGTCCTCATGTACAATTTTCTGCTCGTCCTTCAAGGGGCAGCTTGCAAGCCTCCCTTTAGACACCT C[T/C]ACAGGTACAGCCGACCATGCCCTACCTCCATGGCCTCCATGCTGTTTGAATGCCCTCTGT CTTTAAACCTGTAATGGTATATTAATCCTTGGTGTTTGAATGTCTCTC
WI-7676b	309	A	C	GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGCTGCTGGGACTTGGCCCTGCTATTTATTTTTG TATTTATGTCTTAATCTCTTCCCACTGATGCATCCTCCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGGGCTTCTTGGTGCCTGCTGGGTTGCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTGGTGC TCCCCCCGTCTCTCCTGGAGGCAGTATAGGAGAGAGAGAGAGCAAGGATT
WI-7676	139	C	T	GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGCTGCTGGGACTTGGCCCTGCTATTTATTTTTG TATTTATGTCTTAATCTCTTCCCACTGATGCATCCTCCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GC[C/T]GGGCTTCTTGGTGCCTGCTGGGTTGCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTG GTGCTCCCCCCGTCTCTCCTGGAGGCAGTATAGGAGAGAGAGAGAGCAAGGATT
				CATTATCTTGTCCTTGGGTCTGTGTTCATTCACTTCCTCTCTCCAATGAAGAGGATATTTAAGCATCATT CATCTGGCCCTTTTTGAGTTTGAATATTTTTGT[G/A]TGACTCCTATGCACATGATAAATTTGTTA TGCTTGTCTCTTATCTTTTTGTTATAGGAGTTTTGGCCATGACCCTTTATGAGGAGAAAAGGGA TCACCCCCTTTTTGCCTCTCTACAACCTTATAGATATTTAAATATCTTTT
WI-10072	105	G	A	TTGGTGTGAACTCAGAATATAGGGAAAATAAGACAATTTGAA[T/A,C]GTACCCCAGGAAACAAGAG CCCTGCACTTGACTCCAAAAGGAGTTCTATTATTCTGGCTGTTTCCAGACTTATTGTATCTTGAGAA GAGAACTGTTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTCACAAGAACATGTCA ATATCAAATAGCATAGCATATGGGGTGTTGGATTCTTGGAACTTATTGCAATT
WI-9986	42	T,A	C	GTCTATTGCAGGAGAAACGTCCCTTGCCACTCCCCACTCTCATCAGGCCAAGTGGAGGACTGGCCAGA GGGCCTGCCACATGCAAACTCCAGTCCCTGCCTTCAGAGAGCTGAAAAGGGTCCCTCGGTCTTTATTT CAGGGCTTTGCATGCGCTCTATTCCCCCTCTGCCCTCTC[C/A]CCACCTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGTAACAAGCTCATTGTAACAGTGTCGTTCATGTAATAA
WI-7041	174	C	A	ATAAACCCTTGTGTATGTATCACCCAACTCACTAATTATCAACTTATGTGCTATCAGATATCCTCT ACCCTCACGTTATTTTGAAGAAAATCCTAAACATCAAATCAAATACTTTCATCCATAAAAATGTCAGCATT[T /C]ATTAAAAAACAATAACTTTTAAGAAGAAACATAAGGACACATTTTCAAATTAATAAAAATAAAG GCATTTTAAGGATGGCCTGTGATTATCTTGGGAAGCAGAGAGTGATTCATGCTAG
WI-7224	134	T	C	

WI-10826	132	A C	TCTTATTTGCATTCACAGTAGCCCCATGAAGTAGGTATAACCAGCCTCTATTTAACATGAGAAGAT GGAGGCCTTTCCAAATGACTAAGTAATGTGTCTCAGGTTTTCTCAGGTTTCTCAATAAGCAAAGACCTGCA[A/C]]CCCTGGCTTCCTGACTCCAAAGCTTATCCCTTCTCATGCTTGCTGTCAGCCAGGACCCCATGCGGCA GAAAGCCCAGCCTCTCCATCCCCAC
TIGR-A004S25	145	G A	AGATCTGCCATTAGTATTATTCCTTGAAGATACTTTGGAGATTCATTTCTTGAGTGGCACTGCAT GCTCATTCAGTGAAAACTTGTGGGGTATAGAAATGGAATGGAGAGTTCAAACAGCTTTGCTGAAAC TGTACTTTGG[G/A]CTCCAGACTTCACTGTCCTGTCCTTAGGCATTGAAACCATCACCTGGTTTGCATTCTTC ATGACTGAGGTTAACTTAAAATGACTGAGGTTAACTTAAAAC
WI-1021	24	A T	AAACACACAGAATCATCAAAGCAC[A/T]ATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG TAAGAAGTAACTCTGAAATAGTAGGATAGTATTATCATTCCTGTAATAGATTCACCTCTCAGCAAT TGGGTCTGTTTTCATTCTATGGAAACTCTCCGTACTGTAATTTTCATTCTATGGAAACTCCCCATACTGT AATTGGACAGTTTTGGTTTCCAC
WI-4687	121	G T	TAGTATGTCACTGCCATGGTAAGGGACTTTGATCACTAGGAAATAAGAACACTTTGAATGGTCTTGTCC TTTCAATAAAAAGAGGTGACATGATTGAACATGTGTTTAGATAAAGGGCACTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAGGAAGATCAGGAAGAAAAGTAGCAATGGGAATGAAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAAACCAAGAGAGAAAGAAACTTGAT
WI-4719b	107	T G	TTCATTTCCCTCCAAAATCCTTAGGAAAATTTACATTATGGGCTAGTGCTTGGGTGTGAGCGGATT ATGTCTGACGCGCCATGGGTGTTCATAAGTGACTTGAGAGTT[T/G]ACTGTGAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCATTCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCCCCACTTGTCAACTTATCCTTAAGACATTTTCACAGGA
WI-4719	70	G A	TTCATTTCCCTTCCAAAATCCTTAGGAAATTTACATTATGGGCTAGTGCTTGGGTGTGAGCGGATT AT[G/A]TCTGACGCGCCATGGGTGTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCATTCAACAATCTGCTATGCTTCTCAGATTGCAGAAAATCAC TGCTCAAAATTCCCCACTTGTCAACTTATCCTTAAGACATTTTCACAGGA
WI-9484b	216	G C	TCAACACGCTTTATTGCCACTTCTGCTCCCCTGTCCCCAGCAAGATTCCTACCTCCTTACCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGGGTGTTACCACTTCTCCTCTGCACACTGCCAAGT TAAAGAAAACCCTGCTTGCTGGAGAGGGAGGCCAGAGGGCCAGACAGGGAATTCAAGGGCATGTATGGCTC AGTCCCACTTCTT[G/C]ACTGCAGAGTATAGGGACCAGGGTTCCAAACTTT
WI-9484	178	G A	TCAACACGCTTTTATTGCCACTTCTGCTCCCCTGTCCCCAGCAAGATTCCTACCTCCTTACCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGGGTGTTACCACTTCTCCTCTGCACACTGCCAAGT TAAAGAAAACCCTGCTTGCTGGAGAGGGAGGGCCAGACAGG[G/A]AGGAATTCAAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGACCAGGGTTCCAAACTTT

Marker	Pos.	Allele 1	Allele 2	Sequence
WI-7330	207	C	T	AGGATGGAAGGAGGACACGGGCAGGGAGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTGTCTTAAATGCTGACTACAGCCACTGACATGGTGGCTGGCTAAGTTTAATTGTGGCATATAGGTTTGTGACACAGAAGTCATACTTTGGTGGCTAAGTTTACTAAGGAAAATAACTGAAAAGATTAAAAGTGAGAG[C/T]TGAAAAGAGAAATGATAATGCTTCCAAACTGTAGCTGTCACAG
WI-9443	211	G	A	TTAAAAACAGTTCAGGTTGGTGAAGCAGAAAAGGGATGGTGATTACAATTTAAATGAATCAGTCACTTGCACAATTAATCCTCTTGGCATCATACAAAACTGGGTTTAATGGCAAATGATGACATCATAGCATGACCAACACTCATGGAAGGCAGTCTAGAGTCCATCACGCTCACCTGAGGGGGAAGGCACTGCACCCACTGACGAGGAC[G/A]CAGAGACCTTGGACTACAGAGACCATGACCACATGCCCACTT
WI-7166	59	C	T	TCTCTCAAAAGAGAAAAACAAAACCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGATCATCAAACAAGATTTCCTTGTGCAAAATATTGACTATTCTGTATCTTTCATCCTTGACTAAATCGTGATTTTCAAGCAGCATCTTCTGGTTTAAACTGTTTGCTGTGAACAATTGTGAAAAGAGTCTTCCAATTAATGCTTTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCGAG
WI-7259b	189	T	C	GCTTCTTCCCCAGGAAGCGGGGGTCTTGGCCTGGAAACCTTCAGAGAGAGGGGGAGCAATTTAGCCCCACCCTGCTCCCATCTGCCCCCCTGCCAACAGCTGCAGGCTGCTTCCTCCTCTCTGAGTTCCTCTGGGCTGCGCAGGCTGCCCCTGGGAATAGAGCAAGACGTGAGTCCTAAACCTGGCCACAGT[T/C]TGGGGGAGCAGAGCCAGCAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCCTGGAGCTC
WI-7259	188	G	T	GCTTCTTCCCCAGGAAGCGGGGGTCTTGGCCTGGAAACCTTCAGAGAGAGGGGGAGCAATTTAGCCCCACCCTGCTCCCATCTGCCCCCCTGCCAACAGCTGCAGGCTGCTTCCTCCTCTCTGAGTTCCTCTGGGCTGCGCAGGCTGCCCCTGGGAATAGAGCAAGACGTGAGTCCTAAACCTGGCCACA[G/C,T]TTGGGGGGAGCAGAGCCAGCAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCCTGGAGC
WI-7322	275	A	G	GTACTTTAGGCCTGTGTGGAGGGTGGGCATTTAGTGGTGACCCTTGCACCAGGGTTTCTAACAGATGACCCTGTGAATCATAATTTAAACCTGCATATATTTTATAGCCAGTCACATTTGCCCCTCTCACCCTATATGGCCCATAAACTGCCTAAGCACTCAGCCTCATCAACCCCTTTGACCAGGAAAGAAGAGCACTCTGGTTCTCTATCCCCTTGTCACATAGGAGTTTGTCATGGGGCCCTCTGGCTG
WI-7685	46	T	C	TCAGTTCTAGTCTCTCTGGGGGCCACACAGAAACTCTTTTTGGGGTCT[T/C]TTTTCTCCCCTCTGGATCAAAGTAGGCAGGACCATGGGACCAGGTCTTGGAGCTGAGCCTCTCACCTGTACTCTTCCGAAAAATCCTCTTCCCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTTCCTCCTCCCTCCTGCCGACTCCTGGGTTGAGCTGTTGCCTCAGTGCCCCCAACGATGCTTTTCTGTCTC
WI-563	87	G	A	TGTGACCAATTGTTATTTTAGAGGGTTAACAATGGCCTGACTATCACCTGACTGATGGTCGCCAGAATTCCTGGGGGAGGGGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTCTAGCACTACAGGCACATACTTGTGGTATGGGGATCCCTAAGCCAATTTTAAATCTCTTTGGATAACCCAGGGCACAT

Marker	Pos				Sequence
WI-931c	191	C	A	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACCAACCTTCGCACACCCCTGGAGTT TCTCTCCCCTCCCTATCCCCTCACCAACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCTTCT GTTGCTGCACTGTCATTACTGTTGTATGGGGAAAGATGTGTCAGA TACAGAAAAGGCAT
WI-931b	81	A	G	---	GACCAGGGCACCAGAAAGCCACGGAAGCCAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCCTCCCT[A/G]TCCCCTCACCAACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCATTACTGTTGTATGGATTTATAATTATTGTCCAAAAAGCCCCGAGCCTGG TACAGAAAAGGCATGGGGAAAGATGTGTCAGA
WI-931	31	A	G	---	GACCAGGGCACCAGAAAGCCACGGAAGCCAC[A/G]GCCACTAGCCCTGAACCTTGCACACCCCTGGA GTTTCTCTCCCCTCCCTATCCCCTCACCAACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCATTACTGTTGTATGGATTTATAATTATTGTCCAAAAAGCCCCGAGCCTGG TACAGAAAAGGCATGGGGAAAGATGTGTCAGA
WI-10870b	91	C	T	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAATTACAAGAAATCTTGGGACCTGTACTCCTGATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCC
WI-10870	103	G	A	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGGCACCTACTTAGA[G/A]CAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAATTACAAGAAATCTTGGGACCTGTACTCCTGATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCC
WI-7719b	281	T	C	---	AGTTATTCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTGGGTCTGGCCAAGTCTACAATGTCCCAATATCAAGGACAACCACCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGGACATTGCCCATGTATAATCCTCACTGATTTCAAGCAA
WI-7719	163	A	G	---	AGTTATTCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTGGGTCTGGCCAAGTCTACAATGTCCCAATATCAAGGACAACCACCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAA
WI-10396	72	C	A	---	GCCTTGGAGTATATCTAAACTGTGGCCTCCACTTTCATTTTCTTGAAACATTGCTATCAACTGGGAA GAGT[C/A]GTGACTTTATGCCCAGTTCCCCTCTCAGATTTTTATGACGGTTGTTTTCTTTTCTTTTGTTA TGCCATTTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCCATTGCTGTTCCAGG TTAACAGCCCACCATTTGTAAACACTTTGT

WI-10673	94	C	G	---	TCCCTTTATGCACCCAAGAGATATTTATTAAACACCAACCAATTACGTAGTAGCAGGCCATGGCTCATGGGACC CACCCCCGTGGCACTCATGGAGGGGG[C/G]TGCAGGTTGGAACTATGCAGTGTGCTCCGGCCACACA TCCTGCTGGCGCCCCCTACCCTGCCCCAATTCAATCCTGCCAATAAATCCTGTCTTATTTGTTCATCCTG GAGAATTGAAGGGAGGTCAAGTTGTTTGTCAATGATTTGTCAGAGAACCT
WI-7842	57	T	C	---	CACAGCCATGCCCTTGAGGAGACGCGGCCACCAGATGCTGAATCCCTATCCCATTCTGT[T/C]GTATGAG TCCCATTTGCCTTGCAATTAGCATTCGTCTGTCTCCCCCAAAAAGAATGTGCTATGAAGCTTTCTTTCCT ACACACTCTGAGTCTCTGAATGAAGCTCTTAGTACCAGAGCTAGTTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGAACTTAAGATGAAAGCAAATGATTCAGCTCCCTTATA
WI-7721	145	A	C	---	CTGCCTCATCACGCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGCCACATCCCACCCCAGCTGTTACCCAGCCCGGGCAGGTGCAGCCCTTCCTCCC TGTCTCTGC[A/C]TCGACTCTCTCTTTGAGGTCCCTGTATGTCACCTCTGACTTCTGTGGTCCCTCTG TGTCTGCTCATCCATTCCTCTTACTGGGCCTGGGGGCCTGAGCCCAA
WI-4767b	173	C	A	---	TTTCCAGTCTGTTTATCCTTTCATTGTCAAAAAGATGTCTCTTAGACTGAAATTCATAAAGAGTTCCT CAGGTCTCGGGTAATCCTAGATCTTCCTATATCCATTGAGTGTGATGGAGTTGGAGAGAGGGTATGTTT CTTGCCTTGAGAAATCCTAGAAAGCACAGGGATGACACA[C/A]AAATCACTAAGGAATTCCACTAAGA CTCCTCTAACCCAGAGATTTTAACCT
WI-4767	50	A	G	---	TTTCCAGTCTGTTTATCCTTTCATTGTCAAAAAGATGTCTCTTAGACTGA[A/G]ATTCATAAAGAGTT CCTCAGGTCTGGGTAATCCTAGATCTTCCTATATCCATTGAGTGTGATGGAGTTGATGGAGAGGGTATG TTTCTTGCCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCCACTAAGAC TCCTCTAACCCAGAGATTTTAACCT
WI-7718f	222	C	T	---	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACACTGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAAGAGGTGAAAGCTGAGTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAGAAAAATTACAAAGAAGAA[C/T]CATGCAGGAAGGAAGAAACTATGTATTAAT
WI-7718e	60	T	C	---	ATTGCACTGAAGTTTTGAAATACCTTTGTGAAATACCTTTGTGAGTTACTCAAGCAGTTACTCCCTACACTGA[T/C]GCAA GGATTACAGAAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGGTGAAAGCTGTGTTGAAACAGAAATAAGTC AAAAGGAACAGAAAAATTACAAAGAACCATGCAGGAAGGAAGAAACTATGTATTAAT
WI-7718d	31	G	A	---	ATTGCACTGAAGTTTTGAAATACCTTTGTA[G/A]TTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGGTGAAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAGAAAAATTACAAAGAACCATGCAGGAAGGAAGAAACTATGTATTAAT

ID	Pos	Alleles	Sequence
WI-7718c	91	C G	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTACTCAAGCAGTTACTCCCTACACTGATGCAAGGATTACAGAAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACACATGTTCTGGGGCCCGGAGATAGATGACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAATAAGTCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAGGAAAACTATGTATTAAT
WI-7718b	248	A G	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTACTCAAGCAGTTACTCCCTACACTGATGCAAGGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACACATGTTCTGGGGCCCGGAGATGATGACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAATAAGTCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAGGAAAACTATGTATT[A/G]AT
		C	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGC[A/C,T]GTTACTCCCTACACTGATGCAAGGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACACATGTTCTGGGGCCCGGAGATAGATGACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAATAAGTCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAGGAAAACTATGTATTA
WI-7718a	42	A T	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTCCGTGGACCAATTCATCTTTCAGACAAGCTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGCTTTGGTTAGTATCTGTGTTTCCGGTGGGTGTAATAGGGGATTAGCCCAGAGGGACTGAGCTAAACAGTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227d	99	G C	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTCCGTGGACCAATTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTTGGTTAGTATCTGTGTTTCCGGTGGGTGTAATAGGGGATTAGCCCAGAAGGGACTGAGCTAAACAGTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227c	291	G A	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTCCGTGGACCAATTCATCTTTCAGACAA[G/T]CTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTTGGTTAGTATCTGTGTTTCCGGTGGGTGTAATAGGGGATTAGCCCAGAAGGGACTGAGCTAAACAGTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227b	93	G T	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTCCGTGGACCAATTCATCTTTAGAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTTGGTTAGTATCTGTGTTTCCGGTGGGTGTAATAGGGGATTAGCCCAGAAGGGACTGAGCTAAACAGTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24	A G	AGGGAATTGTGTTGCTCCTGGAGG[A/G]AGCCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTCCGTGGACCAATTCATCTTTAGAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTTGGTTAGTATCTGTGTTTCCGGTGGGTGTAATAGGGGATTAGCCCAGAAGGGACTGAGCTAAACAGTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234	A C	CCACAATGCCTCTCCCACGATGTCAAGGACTCCTGTCTGTCCTGGAGGTGGGAGACAAGGAACCTCCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCCTTCATCGAACAAACTGATGCGAAAACTTGAATCTGTTACTGAAATGAGGAGGAAGGACATGTGCTATTGAACTGAGCCAAACACTGTAAATATCCACAGACTCCCTCCCCTGCCCCTCCCCA[A/C]ATGATCTTGAGATTTC

Name	Pos.				Sequence
WI-7310a	64	T	A	---	CCACAATGCCTCTCCCACGATGTCAAGGACTCCTGTCTGTCTCCTGGAGGTGGGAGACAAGGAACC[T/A]CCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCCTTCATCGAACAAACTGATGCGAA AACTTGAATCTGTTACTGAAATGAGGAGAAGGACATGTGCTATTGAACTGAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCCTGCCCCCATCCCAAATGATCTTGAGATTTC
WI-7878b	162	A	G	---	CCAGCAACACCTACACCCTTGTCACCTGCCTGGGACTCCTATGATGGCCTGCTGGTTGATAATAATCA GATCATGCCCAAGACGGGCCCTCCTGATAATCGTCTTGGGCATGCAATGGAGGGCAAATGCGTCC CTGAGGAGGAAAATCTGGGAGGAGCTG[A/G]GTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGT CTGTGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAACTA
WI-7878a	51	C	G	---	CCAGCAACACCTACACCCTTGTCACCTGCCTGGGACTCCTATGATGGCCTG[C/G]TGGTTGATAATAA TCAGATCATGCCCAAGACGGGCCCTCCTGATAATCGTCTTGGGCATGCAATGGAGGGCAAATGC GTCCCTGAGGAGGAAAATCTGGGAGGAGCTGAGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTG TCTGTGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAACTA
WI-7381c	213	C	T	---	CTCCACATTCCCACAGGCCTTGAGCAGAATTTCTGAGACTGAAGGGAAATCCCCCTTTCTTTCTACC AGCCCTGCAAGTTTCCTCATGGACGCTCGCGGAGGAGCAGGCTGCAGGTTTCCTGCCTATGGTGAGATC AGATGGTGGCCAAGGAAGGAGCTCTGGTTCCAGAGAATTTGCACAAAGTTCCCTCTGTACAGAGACA AAACGGCCCTC[C/T]GGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54	C	G	---	CTCCACATTCCCACAGGCCTTGAGCAGAATTTCTGAGACTGAAGGGAAATCC[C/G]CCTTTCTTTCT ACCAGCCCTGCAAGTTTCCTCATGGACGCTCGCGGAGGAGCAGGCTGCAGGTTTCCTGCCTATGGTGAG ATCAGATGTGGCCAAGGAAGGAGCTCTGGTTCCAGAGAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCCCTCCGGCTCTCGGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53	C	G	---	CTCCACATTCCCACAGGCCTTGAGCAGAATTTCTGAGACTGAAGGGAAATCC[C/G]CCTTTCTTTCT ACCAGCCCTGCAAGTTTCCTCATGGACGCTCGCGGAGGAGCAGGCTGCAGGTTTCCTGCCTATGGTGAG ATCAGATGTGGCCAAGGAAGGAGCTCTGGTTCCAGAGCATAATCCTTGGCAGGGCTCAGCAGG ACAAAACGGCCCTCCGGCTCTCGGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93	G	A	---	AAATTGCTCTATTCGGACCCTCATATTAAATAAGAGCAATGAGAGCGAGGGAAAATTGAACTCTCTG AGGTACTGACTGTGGGACCAGCAGACAAG[G/A]GATGTAGATTGTCACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTTGTCCC
WI-1017a	92	G	A	---	AAATTGCTCTATTCGGACCCTCATATTAAATAAGAGCAATGAGAGCGAGGGAAAATTGAACTCTCTC AGGTACTGACTGTGGGACCAGCAGACAA[G/A]GGATGTAGATTGTCACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTTGTCCC

WI-1795b	130	T	C	GAAGCAACCAGAAAGTATCTTTATCCCCATCTAGATTATGTCTGGGTTCTTCCAGACTCCTACGATTA AATTGTATGCATGTGAACAACTGATGAGGTACTTAGATCTCAGTGCTTTGCAGAAAGAAAAGT[T/C]C GTCTACCATTTTCACCAAATTTCGTAGTACAATTTAAGTATCTCTGTTATCTCCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-1795a	47	T	C	GAAGCAACCAGAAAGTATCTTTATCCCCATCTAGATTATGTCTGGGT[T/C]CTTCCAGACTCCTACGA TTAAATTGTATGCATGTGAACAACTGATGAGGTACTTAGATCTCAGTGCTTTGCAGAAAGAAAAGTC GTCTACCATTTTCACCAAATTTCGTAGTACAATTTAAGTATCTCTGTTATCTCCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-10616d	136	G	A	CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCCACATAGAGAAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCCTGGTCTCCTATCACATTGCCA C[G/A]TAGCCCTCCCTTCCCTCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
WI-10616c	136	G	A	CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCCTGGTCTCCTATCACATTGCCA C[G/A]TAGCCCTCCCTTCCCTCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
WI-10616b	141	C	T	CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCCTGGTCTCCTATCACATTGCCA CGTAGC[C/T]CTCCCTTCCCTCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
WI-10616a	116	G	C	CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCCTG[G/C]TCTCCTATCACATTG CCACGTAGCCCTCCCTTCCCTCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
WI-1126c	52	G	A	CTCTTATTTCTCTGGGCACTGCTTCTTTGGGGGCAAACTTCCAGTATCACT[G/A]ATACTAATATAA AAACCCTGTAAGTCTGCTTGCATTTCAAGATTCAATATATATCCAGCAAGAA AATTTATTTCTCAAGATATAAAAAAATAAATATTTAATTTCAGTTCCTCAAAAGGAATATGAAATT TGTTAAAATGCAAATCCAGCTGTAACTTTTTGGACTTGTCTTTATTTCTT
WI-1126b	230	T	C	CTCTTATTTCTCTGGGCACTGCTTCTTTGGGGGCAAACTTCCAGTATCACTGATACTAATATAAAAAA CCCTGTAAGTCTGCTTGCATTTCAAGATTCAATATATATCCAGATTGTTTCCCAGCAAAAATT TTATTTCTCAAGATATAAAAAATAAATATTTAATTTCAGTTCCTCAAAAGGAATATGAAATTTGTT AAAATGCAAATCCAGCTGTAACTTTTTT[T/C]GACTTGTCTTTATTTCTT

WI-1126a	97 T C	---	CTCTTATTCTTCTGGGCACTGCTTCTTGGGGCAAACTTCCAGTATCACTGATACTAATATAAAAA CCCTGTGAAGTCTGCTTGCATTTCAAGAT[T/C]CAATATATATATCCAGCAAGAAA ATTTTATTTCTCAAGATATAAAAATAAAATATTTAATTCAGTTCCTCAAAAGGAATATGAAATTT GTTAAAATGCAAATCCAGCTGTAACTTTTTGACTTGTCTTTATTTCTT
WI-11183c	124 C T	---	TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGTATTTTTGCCCTTGT[C/T]ACTAACA TTTATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192 T C	---	TAGTGCTAATTTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGTATTTTTGCCCTTGTCACTAACATT ATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAA[T/C]ATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118 C T	---	TAGTGCTAATTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGTATTTTTGC[C/T]CTTGTCACTAACA TTTATGACATACAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174 G A	---	GCTTGGTTGCTTAGTCTTATTGTCTCAGTCTTGAGTTCTCCCTTCTGCCTGGCCCTTTGTATT CCCATACCTCTATGCCTGCTCTCAGACCATTCCTCTATCTGGAGCGGCGTCTTCCTTGTACTTCTCCTG TTCACCAACCTTCTTTATTCTTCAGGACACTCA[G/A]TTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCCTTTCCC
WI-10770a	49 G T	---	GCTTGGTTTGCTTAGTCTTATTGTCTCAGTCTTGAGTTCTCCCTTCT[G/T]CCTGGCCCTTTGTATT TCACCCATACCTCTATGCCTGCTCTCAGACCATTTCCTCTATCTGGAGCGCTCTTCCTTGTACTTCTC CTGTTCACCAACCTTCTTTTATTCTTCAGGACACTCAGTTCCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCCTTTCCC
WI-9667b	82 C T	---	GATGACAACTTCTGCTGTGACCCTTAGTCCTTGCTCATGACACTTTCAATCTCTGCCTTGTATCATGG TTATCACTGGACA[C/T]AGCCACCTCCCCAGCAGGCTTAGAACTCCATGAGTAAGGGACCCTGTCTA ATGTGCCGTTCTCCTTATGGTATTACACACAGTACCTAAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTGTCTCT
WI-9667a	68 G C	---	GATGACAACTTCTGCTGTGACCCTTAGTCCTTGCTCATGACACTTTCAATCTCTGCCTTGTATCATG[G/C]TTATCACTGGACACAGCCACCTCCCCAGCAGGCTTAGAACTCCATGAGTAAGGGACCCTGTCTA ATGTGCCGTTCTCCTTATGGTATTACACACAGTACCTAAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTTCTGTGTACCCAGTACCTAAGTCCAAACTTGCATTCT

ID	Pos			Sequence
WI-10400d	189	A	G	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTCAGAGACATCTGCTG GTTAAC[T]GTTATAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAATTTT TCTTTCCCTTACCTTACTTGCAAATTATTCAAAGGCGTAATGCCATGTAG
WI-10400c	166	A	C	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTCAGAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAATTTT TCTTTCCCTTACCTTACTTGCAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTTGGTTCATTTACTTGCAAATTATTCAAAGGCGTAATGCATTATG
WI-10400b	165	A	G	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTCAGAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAATTTT TCTTTCCCTTACCTTACTCCCCACCC[A/G]AAAATAACGTAAGGCGTAATGCATTATG TTTTTTGGTTCATTTACTTGCAAATTATTCAAAGGCGTAATGCATTATG
WI-10400a	46	T	C	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAA[T/C]TGCATTCAGACATCT GCTGGTTAACTGTTATAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTA ATTTTCTTTCCCTTACTTTACTTGCAAATTATTCAAAGGTACCTATGTCATGCCATGT AGTTTTTTGGTTCATTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10809b	78	C	T	AAAGGGCTACAAACTAAGGCCAAAAACCATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTCACCA[C/T]TTAGAAAAGGGCATTCAAGCACCATTCAATGAGGCTTCATATACTGGTTAG CAAACAAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCCAGTGATGAGGCCACA GTGAATATCCACCTAACGACACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33	C	T	AAAGGGCTACAAACTAAGGCCAAAAACCATGAA[C/T]GGTATAAGGAGGGTAAATGCAAGGGGAGA CCCCACCTCTCACCACTTAGAAAAGGGCATTCAAGCACCATTCAATGAGGCTTCATATACTGGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCTATGGACCAAAAGTGCCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266	T	C	CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTTGTCC CAATGAAATACTGAGATGCTGGGCGTGTCTCCCTTCCAGGAATGCTGGGCCCCCAGGCCCCAGCCCAGAC AAGAAGACTGTCAGGAAGGGTCGGAGTTGGCTTTTTCACATTGAT CATTTTTATATGAAATAAAAAGATCCTGCATTTATGTGTAGTTCTGAGTCC
WI-7038b	140	A	C	CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTTGTCC CAATGAAATACTGAGATGCTGGGCGTGTCTCCCTTCCAGGAATGCTGGGCCCCCAGGCCCCAGCCCAGAC AAGA[A/C]GACTGTCAGGAAGGGTCGGAGTCTGTAAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTTATATGAAATAAAAAGATCCTGCATTTATGGTGTAGTTCTGA

ID	No.	Allele		Sequence
WI-7038a	31	G	A	CGAGCTTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCTCAGCTTTCCCTGCCACATCCAGCTTGTTG TCCCAATGAAATACTGAGATGCTGGGCGTGTCTCCCTTCCAGGAAATGCTGGGCCCCAGCCTGGCCA GACAAGAAGACTGTCAGGAAGGGTCGGAGTCGTGTAAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTTATATGAAATAAAAAGATCCTGCATTTATGGTGTAGTTCTGA
WI-3429b	64	G	T	ATACGGCTTCTGTCTGTCCCACAGTGGAACCAGCACCACCCAGGTGGCCAGGGTCGGGCTCCAACACA[G/T] CCCTCAGCCCCCTTCAGCTTTGCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACCTCATGTGA CAAAAATACAGATTCCCAGTCTCCTCTCTGGATTTGGATCTAGCAAGACCAAGACGGGTCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTCTTAAGACCAAGCACGGAGC
WI-3429a	62	C	T	ATACGGCTTCTGTCTGTCCCACAGTGGAACCAGCACCCAGGTGGCCAGGGTCGGGCTCCCACA[C/T]AG CCCTCAGCCCCTTCAGCTTTGCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACCTCATGTGA CAAAAATACAGATTCCCAGTCTCCTCTCTGGATTTGGATCTAGCAAGACCAGAGACGGGTCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTCTTAAGACCAAGCACGGAGC
WI-6786c	151	G	A	ATTTTAGGACAGTGAAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAGGAT[G/A]TGGGATAAGGTGAGTGACGGTGACCT GTGAGCCCCATTCTTCT[G/A]TGGGATAAGGTGTCCATTGTTTCTTGGAGGGTGAAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCATTGCTCAGTTTCATCATT
WI-6786b	111	A	T	ATTTTAGGACAGTGAAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAGGAT[A/T]AAGAAGTGAGTGACGGTGA CCTGTGAGCCCCATTCTTCTGTGGGATAAGGTGTCCATTGTTTCTTGGAGGGTGAAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCATTGCTCAGTTTCATCATT
WI-6786a	106	A	T	ATTTTAGGACAGTGAAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAA[A/T]GGATAAAGAAGTGAGTGACGGTGA CCTGTGAGCCCCATTCTTCTGTGGGATAAGGTGTCCATTGTTTCTTGGAGGGTGAAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCATTGCTCAGTTTCATCATT
WI-6711b	226	G	T	GGCTATTTGTAAATGCTTGGTTATTTGACTCCAAAATTGAATAAGTATTGGGGAAGAATCCCTACCT ACTTCACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCTAAACCTTCAGTTCCAATCACTCT TTCATATACCTCCATTATTAAATTCAATACATCATTGCAGAGAAAAGACAACGGTGCCAACTGGGTT TGGTTGGTCCTGCACACCCACA[G/T]TGCAACTAAGTGTAATCTCTAAA
WI-6711a	36	T	C	GGCTATTTGTAAATGCTTGGTTATTTGACTCCAAAA[T/C]TGAATAAGTATTGGGGAAGAATCCCTC ACCTACTTCCAAATCCTTACATATCAATTTACACAAAGCCCTAAACCTTCAGTTCCAATCACTCT GAATTTCATATACCTCCATTATTAAATTCAATACATCATTGCAGAGAAAAGACAACGGTGCCAACTG GGTTTGGTTGGTCCTGCACACCCACCACAGTGCAACTAAGTGTAATCTCTAAA

WI-10613b	172	A	C	ATTGTATGCCAAAATCATAATACCCTGCATTCTAGAAACATACAGTGTAATAGAATTTTGAGCCATA TGGTGAAAAATTTAGAAGTATTATTCTCTATATGTATATACTACGTTTAACATCAATGAATGTGATTT TTTGTCAACTTTTGACAAGGCCAGGCAATTTATTTG[A/C]GCCCTAGGAGGGTTACTATAATTTAGA AAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-10613a	44	G	A	ATTGTATGCCAAAATCATAATACCCTGCATTCTAGAAACATACA[G/A]TGTAATAGAATTTGAGCC ATATGGTGAAAAATTTAGAAGTATTATTCTCTATATGTATATACTACGTTTAACATCAATGAATGTG ATTTTTTGTCAACTTTTGACAAGGCCAGGCAATTTATTTGAGCCCTAGGAGGGTTACTATAATTTAG AAAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-7587c	133	A	T	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCTTGAAGC ACATCCCCTTCTGGATCTGAAAAGAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCCTGAGGAAA T]GGAATGAACCACTCCCTGCCCATTCCCTATAAGAATATCCCAAGACCCAGGCAATTTGCCCCTCT TCCCACATGCCCCCATATGTCTGAGCCAAACTGCACTGGGGGCTGCCCTC
WI-7587b	81	G	A	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCTTGAAGC ACATCCCCTTCTG[G/A]ATCTGAAAAGAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCCTGAGGAAA AGGAATGAACCACTCCCTGCCCATTCCCTATAAGAATATCCCAAGACCCAGGCAATTTGCCCCTCTT TCCCACATGCCCCCATATGTCTGAGCCAAACTGCACTGGGGGCTGCCCTC
WI-7587a	28	C	T	GCTCTAGTGGGAAACCTCAGGTAGCTCC[C/T]GAAGATCTGTGCTTTCCAACAAGTGACTACCCTTGA AGCACATCCCCTTCTGGATCTGAAAAGAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCCTGAGGAAA AGGAATGAACCACTCCCTGCCCATTCCCTATAAGAATATCCCAAGACCCAGGCAATTTGCCCCTCTT TCCCACATGCCCCCATATGTCTGAGCCAAACTGCACTGGGGGCTGCCCTC
WI-10681b	103	T	A	ATGACTCAGGTGACAAAAGAAGCATGTCCTAGACCCCATTGACTTACGCAAACTCAATCAGCCAACC ACAGAAAAGCTAAAGACATCCTTTTTAAAAAGCC[T/A]AAAGACAGCCATTTTAATCCTAATTCG TAGTTTATGATTTTCTCAAAATTTCCCCACACAGAAAGAAACTTCAAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTTGGGAAGGAGGAGGTGACGCTCTGTTAAAAG
WI-10681a	41	A	T	ATGACTCAGGTGACAAAAGAAGCATGTCCTAGACCCCATTG[A/T]CTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCTTTTTAAAAAGCCTAAAGACAGAAAGAAACTTCAAGGTTCTAATGTTA TAGTTTATGATTTTCTCAAAATTTCCCCACACAGAAAGAAACTTCAAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTTGGGAAGGAGGAGGTGACGCTCTGTTAAAAG
WI-7222c	126	G	T	GCCTCTCCTCAACTGTCCTGGACCACCAAGGCTAGGAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCTGTTCTCAAGTTGGGGGATGGG[G/T]AATAA AGGAGGGGGAATTCCCTTGAACAAGAAGAGAAACTGGGGATTAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTTGTGTAAGGTTGTATTCAAAGACTGAATTCATTT

ID			Sequence
WI-7222b	255	G A	GCCTCTCCTCAACTGTCCTGGACCCAAGGCTAGGAAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCTGTTCTCAAGTTGGGGGATGGGGAATAAAGG AGGGGGAATTCCCTTGAACAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAT GACAGTGAITTTGTATTTCAAAGACTCGAATTCAITTTCTCA
WI-7222a	126	G T	GCCTCTCCTCAACTGTCCTGGACCCAAGGCTAGGAAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCGAGGTGTCTCTCAAGTTGGGGGGATGGG[G/T]AATAA AGGAGGAGGGGAATTCCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGAITTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCAITTT
WI-8054d	41	C A	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTT[C/A]TATCTCCTCCCAGTTCAAAATG CTTGCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCA CAATCTTCTTCTTGTAGTTTTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-8054c	237	G T	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTTCTTCTTGTAGTTTTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCTTCC TGTCATAACGCCGCTTCCCTGGGCGTACAGA[G/T]AATCCTTGCCCTT
WI-8054b	148	T C	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTCTTCTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTTCTTGTAGT[T/C]TTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-8054a	131	C G	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTCTTCTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAG[C/G]A CAATCTTCTTGTAGTTTTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-10854b	152	G T	TTCCACAAAAACTTCCCTGGGCCGCGGGGTGACTAAGAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAAACA[C/T]GAAGACGATAGTTAACGTCTGGTAAGTT ACGGGTGTGCGAGGCAACAGAGGGAGAGGTACGGGAATAGTTCTACTTCCTTGTTTTATTCTTGTG TTTTAGACACAGGGTCTGCTGTGTTG
WI-10854a	102	C T	TTCCACAAAAACTTCCCTGGGCCGCGGGGTGACTAAGAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACA[C/T]GAAGACGATAGTTAACGTCTGGTAAGTT TATACGGGTGTGCGAGGCAACAGGGGAGAGGTACGGGAATAGTTCTACTTCCTTGTTTTATTCTTGTG TTTTAGACACAGGGTCTGCTGTGTTG

ID	Pos			Left	Right	Sequence
WI-9826b	127	G	A		...	AATTTATATGTGAAGGGTTAGCAAAACTATGGCCCACAGGCCCATTCTAGCCATGCCTATTTTTTGTG TGCCTGATGGCTGTTTGGTGTTTTGCACGCAGTCAGTTGAGCCAGTTGACAGAGGCTGTTAT[G/A]GCCTT CAAAGCCAAAAAAAAAATTTACTCTCTGGCCTTGACGGGAAAAGTTTGCTGATTCTAGATATTTAAA GGCAGAGAAGATCAGAAGTGTTGAA
WI-9826	125	A	T		...	AATTTATATGTGAAGGGTTAGCAAAACTATGGCCCACAGGCCCATTCTAGCCATGCCTATTTTTTGTG TGCCTGATGGCTGTTTGGTGTTTTGCACGCAGTCAGTTGAGCCAGTTGACAGAGGCTGTT[A/T]TGGCCTTC AAAGCCAAAAAAAAAATTTACTCTCTGGCCTTGACGGGAAAAGTTTGCTGATTCTAGATATTTAAAG GCAGAGAAGATCAGAAGTGTTGAA
WI-15986	60	T	G	TGACATTATAT AAACGTAAAA GAAAATGT	TTTGTTTGTGTGT GTGGGTTTTT	CGGACACGTGTATATACAAATACAGATCGTATGGGTTGTTTGTTGTGTGTGGGTTTTTTTTT[T/G]TTAC ATTTCTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A	G	AACTGCAAAT AGGAAACCAG	CCACCTGGGGC TCCC	TTCAAGTAACTGCAAATAGGAAACCAGAG[A/G]GGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCCAACAGAACAGGGGGAGGAGGTGGCCCCTACACCTTTAT
			AG			GCACTTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACCAGAACCG TGTTTAATAGCTGCTGATAAATGAACCTATTTTAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGGAGAGATTACAAGGTTAAGATCATGTGTCCATCAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACAAGA
WI-8170b	259	G	A		...	GCACTTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACCAGAACCG TGTTTAATAGCTGCTGATAAATGAACCTATTTTAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGGAGAGATTACAAGGTTAAGATCATGTGTCCATCAAGTGCAATCCTATCAATCAGAA A[T/A]JAAAGGTAAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACAC
WI-8170a	204	T	A	CCTTTATTAAA GAAGAGAAAT ATTGTTTTCTT GTAATACCTGT AAAGGTAC	...	CAGGATTCCTTAAGTCATCTTCCAATACTCCAGGTCACATGGTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAAACAAGCTTTAAAATCCTTCGGTAACTCCCTTTATTAAAAATTGTTTTCTTTGACAT A[C/G]JAGTACCTTTACAGGTTATTACATTTCTCTTCACCGTTTACA
WI-8172	136	C	G	A[C/G]GACA		AGCAGGGTTTGAAATTGATCCCTTTATTTTACATGAAATAAAAACAATTTCTGTTGTGC[G/A]GCAGGTT TGATTTCAACACAGTTGAATCTGTAAAAACGAGCTGTTTCTGATGCAGGACAAAATATCCACAAT ATTTAAAAACTGCAAGCACCATGC
WI-8183	56	G	A	TGAAATAAAA ACAATTTCTGT TGTGTTGAAAT TGC	CAAACCTGC	AGCAGGGTTTGAAATTGATCCCTTTATTTTACATGAAATAAAAACAATTTCTGTTGTGC[G/A]GCAGGTT TGATTTCAACACAGTTGAATCTGTAAAAACGAGCTGTTTCTGATGCAGGACAAAATATCCACAAT ATTTAAAAACTGCAAGCACCATGC
WI-14149	83	C	T		...	GCTTTATTGGGATTGCAAGCGTTACAAGGTTAAAGACAAACCCAAGCATGGGATTTTGCCGGAAAT ATTAGGCGTTAAAGGAG[C/T]TGAGTTGAGTCAAACACGGG
WI-8712	44	G	A	G	CACAGGGAAG AGGTAGTGGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAACAGCACACAGGGAAGAGAGGTAGTGGAG[G/A]GAGATGGTCAGGCTTCCTG TTCCTTAACCAGCAGAGCCCCAGCAACCTAGAAGCGCCTCACCTAGCCTCTTAAT

Marker	Pos					Sequence
WI-8827	22	C	T	TCCCCTGGGGAG ACTATGG	GCGATTAGGAT TTAGTGTTCA C	GGTGTCCCCTGGGGAGACTATGG[C/T]AGTGAACACTAAAATCCTAATCGCCATGCCATTGGAATTATT CCGACTATTACTTTCTTTAGTTCCTTCTTATCCAGTCTTCT
WI-8833	51	A	T	TCTTCCATGCC ATTCTCTG	CCTCACACATT ATAGGGGCA	CTCCGGCCTCTTAAAGCTCTCTGTGTAGACTGTCTTCCATGCCATTCTCTG[A/T]TGCCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACTGCCTTGTCATAAAAGGTCAGCTATGT
WI-8377	63	A	G	---	---	ATTTTTAGCCATGTTGGTAAAAGTTCATTTCAGTACATGGGTAACACCCAGGCCCTTTCCC[A/G]T TATATCCAGGTATGCTACAAGTTCTTTAACTCTTATCAGAAGTTATTATTACTGTTCCTTAGAGAG GCTACCAGGCTAAAATTCACTTAGTTTGGTTTGTCTAATGTCCTCATTATTTATCCTGAAGCTCGTG
WI-8850	21	A	G	GGGACTTAAC CTTTGGCCT	CAAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCCT[A/G]CCTGCCTGGCTGTTGGCTCTGCCGCTTGCTGCTGTTTTGGTTTCTT TCTCTTCTACTGGTCTTTCCTTTGTCTTTGCCAGCCACCTATGCTGCTGT
WI-8853	79	C	T	CCCGGGCATTG AGGATA	AGTCTTCCTGA GCCTTCCAT	ACTTTTTCTTGAGCTGAGCAACCTCATCATCCTTTAGCTTCTGGTTGATAAACGCTGGTTAATCCCGGGG CATTGAGGATA[C/T]ATGGAAGGCTCAGGAGACTTCATTCTCAA
WI-8865b	52	A	G	---	---	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGAACAGTCATGGTCGAACA[A/G]ACAACATGCT TCGGACTTACCAAAGGGGAGAGTCGAGCTTTCCATATAAA
WI-8865a	42	T	C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGAACAGTCA[T/C]GGTCGAACAAACAACATGCT TCGGACTTACCAAAGGGGAGAGTCGAGCTTTCCATATAAA
WI-8895	32	A	C	---	---	GTGCCACAAACCTGGACACCAACCAACCAACAGAAT[A/C]CTCCCGGTCCTTGAAATTTCCATTAAGAGCA CAATGGGGTAATTATACCAGGGATGCTCCAATCGCTCTTTC
WI-8456	93	G	C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTTGTGAAATATAATAAAACTCTTTCC AAGGCTCCCATGCCATGGGATGTCACA[G/C]TTATGTCAAGTTAATATAAACATTTCTAAGTGCTCACTC TCAACTTCTGTTATCTTGCCATGGTCCAGTAACAGTTCACAGGCAGACCACAAGTTGTGTAGCAC TGGCATAGACGAGGCGTTCTCAAACTCCCGTCTGCGTCTCAGTCACCCAC
WI-8496b	157	A	G	---	---	TTTCATCATCAAAAGTTTTCTTCCATAGAAGAATGGTAAT[G/A]TTGTATCAGTGCATATTCTATGGAAA AAAATTCATATCTCAAGTAACTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGG TCAAAGACACAAATGCTGCCAATGCA[A/G]TTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41	G	A	---	---	TTTCATCATCAAAAGTTTTCTTCCATAGAAGAATGGTAAT[G/A]TTGTATCAGTGCATATTCTATGG AAAATTCATATCTCAAGTAACTAGCTTCAGTGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTC TGTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28	A	G	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGAAGGCCAGC[A/G]TCCCCTCCTGCGTTGTCACCCATCCCAGAGCA GCCTAGTGCCAAGTGGCCAGCGCAGCCACTGCCACCACGGGAACAGGACCGGCCATGCTGC

ID	Pos	Alleles	5' segment	Variant segment	Sequence
WI-12108	40	C/T	TGGAAAAGGG TTAAACTCAA ATA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTGATTACTTTCTGGAAAAGGGTTAAACTCAAAATATC[C/T]GAAATACTTTCATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTATTTAA
WI-5989	29	G/A	CCACAAAGGT CACAGGCA CG	GGGTATAACAG AACCGTATGTA	CAGGCAAACGTCCACAAAGGTCACAGGCA[G/A]CGTACATACGGTTCTGTTATACCCATATATAC CCTTCATGTCCTAAAGAAGACATTTCTCCTAGAGATTTCATTTAGTGTGTATCTTTAAAAAAAAT
WI-12201	61	C/T	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGTCTTTTAGCCTTTTCCTGGAGTGTTTATGTCCCAAGCCCACTGATCACCTGCATG[C/T]GCCA GGTATGTGGTCGGGGTGTGATGGACGTGGGTTGCAGCCCTCCCACTGCTCGATAAAGGC
WI-12018	31	A/T	GGCAGCCAGC TCTGACTT AG	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAGGCAGCCAGCTCTGACTT[A/T]CTCTCTGTTTCTGTCATCTCTCCCCACATACCA ACTTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	A/G	TGGCCCTCGCTG CCTC	AGGGATCAAA GAGAAAAGGC	TTTTCGTTGTTTAATGATCCGAATGCTTGAGAAGAAACCCTGGCCTCGCTGCCTC[A/G]GCCTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAAATGAGAGCTACCAAGATGTAGTCG AGCGGG
WI-15407	92	A/G	CATGCCCTTTA AGGATTAAGT TT	TCTTTTCTCTT TGGTAGTGTGG	AGCATGTAAGGAGCAGTTTATTTGATGGTATATTCAGGTTTCTAACCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAG[A/G]CCACACTACCAAAAGAGAAAAGATTTATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T/C	GTTGAGTATTT GTTCTGTCAT AATT	GGGAAGGTCTG GTACATATTGG	TCTGATGTCATTATTATTGGCACAAAAATTATTCTGATACAACATGGTGTCTCAGACATGGCTACACTTTA TACTTTGTGTCATTTAGTTGAGTATTTGTTCTGTCATAATT[T/C]CCAATATGTACCAGACCTTCCC
WI-12326	25	G/A	GACAGACTTC AAAAGCAATT CA	AGGTTTGAAAA TATGTATTAAG TACTTTGT	CTGACAGACTTCAAAAGCAATTCAC[G/A]CTTCCAGAATACAAAGTACTTAATACATATTTCAAAC CTGTTTGCATTTCAAACAAAGTTAGCGTTTTTGTAAATCAAATTTGATAACCCGACTAAAAAT
WI-12361	63	C/T	---	---	TTAAATTCCACACTGAAGATCTGAGTATGGGGGGGATATAGGGAATTTCAGCATATGTATTATT[C/T] ACC TGAACTAAATTTACAAAGTGGAACAGTTGGAAGGTACTTATAGGTAGCTGAGGGTCGTTACC
WI-11305	87	C/T	CAGACACAGC ATCACACCA	GACCCTCCCGT GGGC	ATACTGGTTTAATCCATGTCAAATGTAGTTTACAAAGGAAAGGACAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[C/T]ACAGACACAGCCGGGGAGAGGAGGAAAAATCCAATAAATTTTTTAAG AAAGG
WI-11321	67	A/G	GGGAGGAAAA TCCAATAAAT TTTT	CATTGGGGAAT AGCTAAACCTT	ATTTTTATATGAAAGGTTTTCTGGTGAAATCTTTTAAGCAGGAGGAGGAAAAATCCAATAAATTTTTTAA[A/G]AAGGTTTAGCTATTCCCCAATGCTATTTAATACAATTGAGGTTAGGACGTTAAGTCTTTATATGA CTGTGTACTGGAGCCCCG
WI-11324	40	C/G	GGATAAATCA TGTGCCCCA	ATCAAGCTTTG GGGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCCA[C/G]AGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACACAAATGTATCTGAAGAAGTTATCTGTTCTTGTCC

ID	No.	Bases		Fragment	Fragment	Sequence	Fragment	Full sequence
WI-11352a	69	T	C	G	AGCACAGCAC ATAGTGGAAA G	GACCTCTCGTA GGACACTTAGC CACTTA	AG[T/C]GCTAAGTGTCCTACGAGAGAGGTCAGATCATCATCCATAGAAAAACAGCTCTCTTTTACTTGCA	TGACACATGGTTTCTGTTTCCAGAAGGAGAGAGAGAGTCATCTACATAAGCACAGCACATAGTGGAA
WI-11371	84	C T	G	CAGCTTGGAG ATTCTGATTCA GCCCCGCCTGA GCAC		GGAGATTCTGATTCAG[C/T]GTGCTCAGGCGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGGT GATTTCGATGCGTATAT	TTAGCCCATGCTGTCATTGCAATCACCTGTGAAACCTATGAAACTATACCTGCCCAGGCTCAGCTT
WI-11385	75	T C	G	ACAGAAGACT TTCATATTCTT GTTTTT		TCTTCAG[T/C]GAGGAAAAAGCTACAGATTTAAAAAATATGACCATGACTAGAATAGAATCAGC	CTTAAAGCATTATAGTTTGGCCTGATGGTGGACACAGAAGACTTCATATTCTTGTTTTTAAAAGTC
WI-11388	88	C A	GATTCTATTCT AGTCATGGTCA TATTTT	TGTTTGAAATT ACACGTAACT AAGTTC	CAAGTTAAAAAT T	AAATTACACGTAACTAAGTTC[C/A]TATAATTTAACTTGGATACAAGGCATTGTTATGCTAAT	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAATTAAAGAATGAATGTTTG
WI-11392	55	C A	GGTTATGTGTT CTTGAACTTTA TGTTTTGTAAA GATAAATAC	T	GTACATTCACG TGTTTTGTAAA AAG	TTCTATCATTCCATTAAAATGGGCAGGTTATGTGTTCTTGAACTTAATAAATAC[T/G]CTTTTTACA AAACACGTGAATGTACTTTTCTTGTCAGAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCCTTCCCCAGA	
WI-11396	52	A	TTTTGTTTTTG AAATGGTGTTT TC	AGCTTATTTTC ATATTCACCCA TC	AAAGAATAAGATGGCATTTGTTCAGTTAATTTGTTTTTGAAATGGTGTTTT[A/T]GATGGGTGAATA TGAAAATAAGCTTACCTCATCCCACTCTAAAAGGTAGTTGGTGATTTTGAACCGTTGTCAAT	
WI-11441	100	C A	TCCCCACCAAC CAGC	TGCCAGGGCCT TATTTG	CTGTCAGTCTCTTCCCAACTAAACCGTGAGTTCCAGTATGTCTGGCAGCACGTCTGTCGTTCTTGGTG TATTCCCATTACTGAATCCCCACCAACAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGAATGAAT	
WI-11466	26	C T	TGAGAAGCCA TGGCAGCCAGG TTTATTTTGCA	GTTTATTGTTA TAAAAATGAC CTACAACTT	ACTTTGAGAAGCCATTTATTTGCAG[C/T]CTTCAGTCCAAAAAAAGTCAACATTTTCAGAATTTT TATATAAGTTGTAGGTCATTTTTATAACAATAAACTTTCTATTATCTCATTATCTCACATACATTT CATGTATCCTG	
WI-13364	35	A G	---		TTTTTCTTTTGTCTCTTTTTTTTTTTAGTAGAAGC[A/G]GGAACAGTTGTCAATACTACCTTCTGTTGG TCCCCTGTTAGACAACATACCTTTCTTGAAATGTAAAATGTCA	
WI-11276	41	A G	GGCAGCCAGG AGCAGAC	TGTACTGAGGA GCCGGTG	AGGCAACACTGCTTTATTAGGCCGGGCAGCCAGGAGCAGAC[A/G]CACCGGCTCCTCAGTACACATT CCCCCACCCCTGCCTCGGTGCTCCCCACTCAGGGCTGGCATGGAGCGGTAGGCAGCGTTAGGTCTGGAA	
WI-12210	76	A G	ACTGGGAAAA CAACTATTGC A	TGCTAGTTTGC ATATGTTTTCC	ATTGGAAACAACTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAACAA CTATTGCAT[A/G]GGAAAACATATGCAAACTAGCATCATTGTCTCTAGA	
WI-14186b	88	A G	---		AATGGTCTGGTTTATTGAGAAGTCATTTGATGGAAAGACACATACGGTACAAAATTACA GGTGGTTAGTTCATTACATG[A/G]TACAAATCATTACAAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT	

Marker	Pos					Sequence
WI-14186a	52	C	T	GGTCATTTGAT GGAAAGACAC A	AACTAAACCA CCTGTAATTTT GTACC	AATGGTCTGGTTTATTGAGAAGCTGTTGGTCATTTGATGGAAAGACACATA[C/T]GGTACAAAATT ACAGGTGGTTAGTTCATTACATGATGACAAATCATTAGAGTCTTTACAAGTCTTCATTAGAGTCTTTGGAT TTT
WI-12234	66	A	G	GAGAACACTT GTCGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTGGCTATAGGTCAGTGGTTCTCAAAACTTGAGCTTGCAAGAGAACACTTGTCGGGCTT[A/ G]TTCAAACATGACTGATAGGTCCCACCCCAGATTTCTAACTGGGTAGGTCTGGGGTG
WI-12345	37	C	A	GTGGCAGGAA AAAGAGGAA	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAAAGAGGAA[C/A]CCTGAACCCCTCGCAAGTATTCTCT TTCCTGACCAGCTGGGGCTTGCGCACTTTGTGAGGATTTTGCAAAA
WI-13416	71	C	A	AAATTTTTGG AAGTTTTTCAG AAA	AGTGTTTATAG TTCAATGAATA ATTTCAA	GAAAAGGCTGTAATTTTATTTTCAAATTTTGGAAGTTTTTCAGAAAAAATAAAATGACAAGAACA CATA[C/A]AAATATTGAAATTATTCATTGAACTATAAACACTTAGCAGAGGAAGGGACTTTTGAT
WI-12310	46	G	A	TTATTCCCAAG TATAATTTTA AAAAGC	TGTTTAAATAT GTTTGGGTCCT AAA	TTTGAAAAGATGCTGAATTTATTCCCAAGTATAATTTTAAAAAGCT[G/A]TTTAGGACCCAAACATA TTTAAACATCTCTTACACATACAGAATTTCAGTTTACAAATATTCCAGAAGGCATTTCTTAAGCAG T
WI-12086	72	C	T	CCGGGAAAAC TTGGATTT	GGAGTCTTCGG GTCTTGG	GAACCGAGCTTTATTGGAGCAAAGAGTGTGGACACTGTTTACAACAAACGTTTCCGGGAAAACTTG GATTT[C/T]CCAAGACCCGAGACTCCTCCAAGTTCTCACTGTTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102	T	G	GGCATAAAGT TCATAATATTC TTTTTATG	GGAAAGTCTGT ACAAATCCCC	ATGTCTTCACAGGTTGTATTTGTTAAGAGTTTGTCTATCTAAATTTCATATTTATTGGCATAAAGT TCATAATATTCTTTTATGTGATCTTTAAATATCTG[T/G]GGGGATTTGTACAGACTTTCCTC
WI-11585	79	T	C	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACTTCC	TTAGAAGGAAAGAAATAAAACACGGTAATGGGAAAATCAGTTCAGAGGTAGGAAGAAGCTGGGTT TGCAAAACAAAA[T/C]GGAAGTATCAGTGAAGCATGGCCTAGAAGTCCAAGAGCAGGGGTAGAGT TT
WI-11604	68	G	C	---	---	TTAGTTGGTTCCTGAAACTTTATGCTGTTTATTTTAACCAATAGGATGTTCCAGTTACCAGCATT[G/C]AGAACTAGGAGGACTTTTCCATGAAAATAATAAGAGCTAAGGAATTCTGACGCTCACCATTTTTC TTTGTTACTCTGCAGTT
WI-11614c	108	C	A	---	---	CAAAATCAAAAATTGAGGAGGCAAGAAACAGAAGTAAAATCCAGAAGACTCAGCTGCTTGAGGCAT GTTCCCACCCTGGACTTGCCAACTTCACTGTGAAACTGCAA[C/A]ATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60	A	G	CCAGAGAGACT CAGCTGCTTG	AGGGTGGGAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAGAAGAACAGAAGTAAAATCCAGAAGACTCAGCTGCTTG[A/G]GG CATGTTCCCACCCTGGACTTGCCAACTTCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83	T	C	---	---	TTGATTTTACTAAGGTCTTCCACTGGAACATGAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTAAAATAAA[T/C]TACTTAATAATAAGAAATTAGCCATACCACATTGTTCCATTGCTAC AAGAACAAATTGGCAATGA

Marker	Pos			Seq A	Seq B	Sequence
WI-11626a	39	G	A	TCCACTGGAA CATGAAGGTA G	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGTCTTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGTACAGGATAATATACT CAGATATTTTAAAATAAATTACTTAATAATAAGAAATTAGCCATACCACATTGTTCCATTTGCTAC AAGAACAAATTGGCAATGA
WI-11627	23	T	C	CCTTTCCTTCC ATTGTCCTC	CATTTGCAACC CATCTCAAG	ACCCTTTCCTTCCATTGTCCTCT[T/C]CTTGAGATGCCTTTTGTCTGGCTTACTCCATTCCGCATGTCAAGTCCATCATG AGATGAGAAATACTGATGCC
WI-11636	61	A	G	GGACTTAAAA AGATCTGCTTA GTCCT	AGAAACTTGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAATACTATTTGTAAAGGTGGACTAAAAAGATCTGCTTATCCT[A/G]TA TATCCACATAACTCTAGTGTTACATAAAATATTTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTTGGTA
WI-11537	119	C	G	ATTGCTCATCT TACTCTGACCA T	GACCCAGCAA AAAGAATGAT T	GTACCATTTCTTATGGTGGCAAATAAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTTACAG TATACAATATTAGAGAATATATGTTGCAATTGCTCATCTTACTCTGACCAT[C/G]ATAATCATTCTT TTTGCTGGGTCCAGGACC
WI-11654	37	G	C	GCCAAAAGAC TATTCAGCAA CTG	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCAAAAGACTATTCAGCAACTG[C/G]AAACTGTCCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATACTCTACTCAGAGTTCACACTCTCATATTTTT ATTTTTGGGTGTTGGGT
WI-11656	28	G	A	ATTGATTTTAG AAGGAACTGC AA	CAAGGCTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAACTGCAA[G/A]CTTTACTTGAGGACAAAGCCTTGCCTGCAGTTGTTT AAAAATGTCCTGAAACAATCAGATTCCCAGCCTGGAT
WI-11680	55	T	C	...	...	ACAGATACTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCCTTTT[T/C]TTGCATAAA GGCTGGGAAGGTGGTTTGGCCAGACCGTACATCTTTTT
WI-11696	47	T	C	TTATCACAGC AGGGGACAG C	GGCATTAGAGA AGCCAACCTT	GTCCAAGAACAAAGATACTTTGACATCTTTATCACAGCAGGGGACAG[T/C]AAGGTTGGCTTCTCTA ATGCCCCACCATCTGTGTTTCAGAATCTTCCACTTCGCC
WI-11702	69	C	T	GAATAAATACT GAAATAACCA CAGCAG	AGAACAACTT AAGCAAATTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACTTTCAATAATTAAAAATCGAATAATAACCACAGCAG[C/T]T TTCAGTATAATTGCTAAGTTGTTCTAGAAAACACTGCTAATTTTTGTTTCTGCAGA
WI-11706	60	C	T	TGGCTGGAATT TTCTCTTCTT	ATCACCAAAG AACAAATTCCA	TGCTGATTCATCGCTTCTACCATCTGGCTGGAATTTTCTCTTCTTGTACAATTTATTTGC[C/T]GG CTGGAATTGTTCTTGGTGATTTGTCCCCTTGTGCTGCT
WI-11709	105	T	A	AGAAGCTTGC TTCAGTTTGC	TCATTTCTTCT AATTTTACGGG A	AATATCATCACTCATATCAGGCATGTTTATAAAAATGAGAGATTATGTCCTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAAGCTTGCTTCAGTTTGC[T/A]GTCCCGTAAAATTAGAGAAATGAAT GGCCAGATGGATGGAAAA
WI-11710	103	C	A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCCAGCTTTCCAGCACAACAGCCAGCCCACACTCTAGACACGCCTTCAC[C/A]CTCCTCCTCCTCCACACTCCTTCTCCAGTCCATTCTGCGCACCTAGCCTCAGTCTTCA

ID	Pos	A1	A2			Sequence
WI-11715b	123	C	T	AGGCTGGCCTGC AGCTT	TCCCCATCCTG TGGCT	AGAATGGAGCTGTTGGGGAGGAGGACATGCACACAATGTAAAAACAGACAAAATGCATTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTT[C/T]AGCCAC AGGATGGGGACTGGGGGAAGA
WI-11715a	49	A	C	GCACACAATG TAAAAACAGAC AAA	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGGAGGAGGGACACTGCACACAATGCCCTGGGGAGGGGACACTGCACACAATG TGGTGTAATGTGGCCACTATGAATCCCTATGAATCCTATGTGTATAAGAGAGGAAAGAGGCTGGCTGCAGCCAC AGGATGGGGACTGGGGGAAGA
WI-11727	43	G	C	AACAATCCTT AAAAACAACTA TCAACA	CCTGTGGGTTG TGTTGCAG	CTGGAATTCCTATACCTAACAATCCTTAAAAACAACTATCAACA[G/C]CTGCAACACAAAACCACAGGC AAAATGAAAAACAGATGCCCCAGACAGCACCCCACCACATGGCACACAC
WI-11728	16	C	G	---	…	TTTTATTTATCAAACT[C/G]CAATTCCATTTCACAAATGTAAGTTATCATCAGCTCCCCATCCACTTT CTCCCATCTCTTATCTCTTCCCACCCTCACACTTTCTCTCCCTACAACCCGGGTTCCAAA
WI-11758	61	A	G	ATCTGTGTGGTTT TCGCCCTG	TGATTGGCCCT GTGGTCTA	TTTTTCCTCTTTTATTAAGTCCGCTACTAACTAGAAGGAGAATCTGTGGTTTTCGGCCTG[A/G]TAG ACCACAGGGCCAATCCACCACAGCTTCTGTGAGAACATGGAGAGTGCCAAGATCACCATCA
WI-11295	37	A	G	GCCTCACAAA GTATTTTCTAA AATATAA	AAAAGTGCTCA TCTGTGAACTC T	CCGGGCCTCACAAAGTATTTTCTAAAATATAATTTGCT[A/G]TAGAGTTCACAGATGAGCACTTTTCA CATTAGGTGATATGCAAACAAATCACTATTGGCTCAGCAGGAAACAGACTTT
WI-11773	93	T	C	…	…	AGCACATGATATTCTGCCTGGAGTTTCTGTGAGCTCAGCAAACAGAGTCAGAGATTAAGAATT ATTTATTGCCTCCTTTTTTCCCCC[T/C]GTGATTGTTAATTAGGGAGTCAAGGCCAAGTTATC
WI-11282	42	C	G	GGCTCAGAGA GCAAGGGAA	AAAACTCAGA CTGTAAATTTT GTGTG	CATGACAACCTCTCTTTATTAATGGCTCAGAGAGCAAGGGAA[C/G]CACACAAAATTTACAGTCTGA GTTTGCGCGCAGAGACCCCTCCACCTTTTCATGCCTGTGTGTACACACTGTCCAAGCCTC AGA
WI-11790	28	A	G	TCATCTAATCT GTGAGGTATTT AGTATACA	GATAGTTGAAC CTCTTCACTTT ATAAAAA	TAATTCACCCAACTTACCAAACCTCTGT[A/G]GCTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACCTACAATGGCAAAATCATCTAACACAAAGC
WI-11879	61	C	A	GTTTTAATGT GGTATTAGAA AAGTTTAAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTTTAATTCCCAAAGCTTACAACCATCTTTCATCTAATCTGTGAGGTATTTAGTATACAG[C/A]AGT GATTTTCTCTTCTTTTTTATAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91	C	T	TGTTATAACAT CAAAGAAAGA AGTCTGAA	TTAATTTCTGC ATCTGAA	TTTACTAATTTCCATTTCCTCCCCTTTTAATGTGGTATTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATATTCTATTTCTA[C/T]TGACAGCACAGTTCTTCAAAGTTTGCTATAGACAATCTGA AAATTGGGTTCTGAACT
WI-11906	52	A	G	…	AGTCCCCTCA	ACATTTGAGTAGGAATGACTTTGTTGTTATAACATCAAAGAAAGAAGAATCTGAAT[A/G]TGAGGGAACTG CAGAAATTAAACTTTCAGTCTAATTCTCAGAATGCCAGAGTAAGATGAACCCTTTACAG

Marker	Pos			Seq 1	Seq 2	Sequence
WI-11909	78	A	G	TTTGTTGTTGGG TGGTCAAG	CCTCCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGATTGTGGAGCATACTGAAGACTATTCCTAAATGGCTATTTGTGTTG GGTGGTCAAG[A/G]CTATTCAGAAATCTCAGAGAGGAGACAAATGATAGTGCACTGCGAGCCAGCTCG GACTGGCTTGCAAGAGTC
WI-11806	60	T	G	CATGAAGAGT GGGGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATTGCCCCAAGTTTGGCCAGGCATGAAGAGTGGGGCAGTTCA[T/G]GTT TTATTAGTATATAAAAATTGGCTTTACAGGAAGCATTATGG
WI-11946	31	C	A	...	...	CCCTAGTGAATACAACCTTTGTCCTGGAGAC[C/A]CCAGCTAGTCTAAGAAAACTTCCTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCCTGGGAAGAAGGGAA
WI-11965	65	T	G	TGAAGATCAG ATCTCTGGTTT ATTT	CAGCTGTGGTG AATGTTGAT	ACAAAATTCACAAGTACAACACTGCTTATTTCTTGCTTGAAGATCAGATCTCTGGTTTATTTAA[T/ G]ATCAACATTCACCACAGCTGAAGGAAATTAAACTGAACCT
WI-11027	90	T	A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAAACTGCAGAAAGGGCAGGACAAAACAAATCACTTCATAGATTTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAA[T/A]AATAAAAATACTGTAACACATTTCCTCATTTCTCTACGA ATACTTCTTTTGATATTGCAAATTCTATGGCATACACAGAGCACCTCCTCAATGCCCTG
WI-11049	95	C	T	...	...	TTCTGCTGAAGATCACAAAAACAATTCAACCTCTGTGGTTCAAAATAATTAAGGATCTTGTACCTTT GTGTTTATTTCTGTTCAACTAAGGA[C/T]AGACTTCAGAAGGCATAGCTTCCCTTGTAACGTTTTT AAACATCTTTTCATTTGTAGGAAGGAACATTTCAAAAGCCCAA
WI-15488	69	C	T	AAAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAAACATGGTAGGGAAAAGTTCTCACTCTGCACTATAAAAGGACAGCCAGATATCA AC[C/T]GTTACAGAAATGAAATAAGATGGAAAATTTTAACAAATTG
WI-13654	49	A	G	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAA TGATGTCAT	TGCTCAATTAATGTGATAATCTCCAACAGTTAATGAAACACATCCGTA[A/G]GTATGACATCATTT CACCAGCCAGCTACTTCATGTGGCAGAAAGGTAACCTTTCCCATTTACAGACAAAACCAGT
WI-11070b	135	C	T	...	...	ATGAGACCCTGCTTGAACGTTTAAACGTTTGGAATAATGGAGAGCTAGGACAATTCTTGCTT TCAAGTAAAATTGTGACTGAGCAGAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCAAGTA C[C/T]GTGGGGGGTTCTGATGACTTCACGGTCACTGGGGATCCAACAGAAGGGAA
WI-11070a	110	G	T	CAGAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCCTGCTTGAACGTTTAAACGTTTGGAATAATGGAGAGCTAGGACAATTCTTGCTT TCAAGTAAAATTGTGACTGAGCAGAAATCAGCCAGCTATCTT[G/T]GGTGCAGAGAGGTACTCCAA GTACCGTGGGGGGTTCTGATGACTTCACGGTCACTGGGGATCCAACAGAAGGGAA
WI-12020	121	T	C	...	...	AATCTTTATATTTCCAGCTGTTGAGACAGTATTTTTGAGGGCTGATGTTACCTCTAGCGGCGAAACC AGAGCCAGCTATTAAGCACTATTAGAATACATGACCATT[T/C]CTCTTTTAGC ACGTTCTTTGTTCCTC

Name	Pos.	1	2			Sequence
WI-11076b	142	G	A	...		CATGGTTCTGCCAGCTTACAGGAAGCATGGTGCTGCTGGCATCGGCTTATCTTCTTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAGGCAGGGGGAGCAGGCATGGTCACATACCCAGAGCAGGAGGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACTCACTCACTGTCAT G
WI-11076a	106	T	C	AGGCA	TCCTGCTCTGG GTATGTGAC	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGCTGGCATCGGCTTATCTTCTTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAGGCAAAGGGGGGAGCAGCAT[T/C]GTCACATACCCAGAGCAGGAGGAGA GAGAAATGATGAGTTCTCTCAAGGAACTCACTCACTGTCAT G
WI-14263	49	T	C	CGCAGAAAAA GGCATATTCA	GGTTATTCAAA AATTAGTATGG GACA	ACCTTAAAGTTTCTCCCCACCTACTCCCGCAGAAAAAGGCATATTCAA[T/C]GTCCCATACTAATT TTTGAATAACCTAACTCTCCCTTGTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-14267	28	T	C	...		AATTATTGCTGAAATTAGGAAGGGAGCA[T/C]TGAAATGGGAAGGGGGAGGTTAGAGAAGACAGAG ATTTAAAAGAAGCAAGTACCATTTCCAAGTATAAAACTCGTA
WI-13892	50	G	A	CTTTTCATTTT TGCTTTTTAAA TAGAAC	TGATGATGTCA TATACTAAAA ATCAAAG	GATTTGTTTATTCATTCTCGCTTTTCATTTTGCTTTTTAAATAGAACA[G/A]CTTTGATTTTTAGTA TATGACATCATCATGAATTTTTCTCTTACTTTGTATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGAATGAGTTCA
WI-15288	108	C	G	CATGAGAGGA TTCCCTCTCTC	AAAAGCTTCTT TCCCTTGGA	ACCTCTTTCTGATGACACTTGTACCTGTAAGGGGTCTAGAGAGGAAAAGAGTAGTAGACTCCTACTTTGC TACAATTCAGGATGCAGGGCATGGAGAGGATTCCCTCTCTC[C/G]TCCAAGGGAAAGAAGCTTTGGC
WI-13951b	88	G	C	...		AATAAATGGAAGAAGGAGGAGTGAACAAAGTAATGAACAAAA[C/T]AGACCCCAGATCAGAGGAAGAG GCTTTCTTGTTAATTCTGGAGCAGATTCAAGCAGCAAATATTTACTGAACACTTGCTATGTGCTG G
WI-13951a	39	C	T	GGAGTGAACA AGTAATGAA CAAAA	TTCCTCTGATC TGGGGTCT	ATGGCTTTCTTGTTAATTCTGGAGCAGATTCAAGCAGCAAATATTTACTGAACACTTGCTATGTGCTG G
WI-13264	25	G	A	AAAAAGGCTC TTGCCCAT	GGAGGGAGAG ACGGGAATA	GAGACCCAAAAAAAGGGCTCTTGCCCAT[G/A]TATTCCCGTCTCTCCCCTCCTGACTGACCCCAGTGTCTT ACAATGAAACATCCCTCAGCCCCATGGCATGGTGCATCCCCTTCTTCTTGGGGATCCTGTGAATATAACCA ACTGTCTTGTCAATGGC
WI-13960	39	A	C	AGCAAAAGGA AGTTAAAATAC TGATAGA	CATGAAAGGA CAAATTTGCAT C	TTATTTGTCATTAGCAAAAGGAAGTTAAATACTGATAGA[A/C]GATGCAAATTTGTCCTTTCATGCA TTTGTGGAGCAAGTACTAACTTGTCACTGTCATTCCCTCACAAGGAGTTGAGCCCCTAGATGAC
WI-15843	62	C	T	ATCTTATAACC AAGAAGCCTT CAG	CTCTGGCTCAG ACTTGCTCT	AACTCTTTATTGTTTAGCTAGCCCCAGTGACTTTATGCATCTTATAACCAAGAAGCCTTCAG[C/T]AG AGCAAGTCTGAGCCAGAGGTTTATCACACACTTGTCTCAGGGTCCACCAGGAACCAGGTCTTGGCT

ID	pos	allele	seq A	seq B	flanking sequence
WI-13983	52	G A	TCTCTCCCACT CCTTAAACCT	CAATACTCTCT	TTGTGTATCTGATTTCCGAAACATAGAAATCTCTCTCCCACTCCTTAAACCT[G/A]CCACTGGGCTAA
WI-13850	51	A G	AATCTCAGGG TCACAGCTTTA TT	TGTTCCCTGAC AATGTTTGTAA	GAGAGTATTGTACAGAATGACTCACTGACTTAACAGAATTAGAACATCCAGGCACTCACTGAGA CATGAATCTCAGGGTCACAGCTTTATTTTTATAGATTTTTAACACAGCCAT[A/G]TTACAAACATTGT CAGGGAACATTTACAAGAATAAATAAGATGGACTTGCAGGTGTAAAAGATTACACTTCA
WI-15295	27	G C A	TGTCAGTTTGA ATGTATTCCTG A	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTGAATGTATTCCTGAT[G/C]TTTTCCTTGCCAACTATTCATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAAGAAAAAGGCCCGAAAATATGAGTGAGACTCA
WI-14284	55	C T	...	...	ATTTCAAACAAATCCAGAAACACAGGTTCTCACACTTTAGTGCAAAAACA[C/T]TATGCCAT GCGGGGAAATAAAATGCTTATCCAGTGGGAGCGGCGCTCCCCTGATGCATTGA
WI-14288	85	G C	CCGCTGCTATT CCCAGAT	GGTCTCCTTCC ACCAAATCTT	ATGACCAGACCAGAAGCCCTGTTCTATATGAAGACAAACAGGTGGCCATACTTGGGTGGAGGGATA CCGCTGCTATTCCCAGAT[G/C]AAGATTGGTGGAAGGAGACCATGACAGATGACAAACGG
WI-13522	33	C T	TGATGTAGTTA CCCCACTAAT ACAAC	CATAATATTTG AAGTCAGTGGT TCTC	TTTATTTGATGTAGTTACCCCACTAATAACAAC[C/T]GAGAACCACTGACTTCAAATATTATGAGAG AAAATTACTCCAGGGAATTTTTGCAGAGAAGATAATA
WI-13529	42	T C	CACAAACATT TATTGAACAG TTACCA	TCTATACACT CTCACTCTCT GCTT	AAATATGATTCCATTCCACAAACATTTATTGAACAGTTACCA[T/C]AAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGTCCTCGAGGGTTTATATGTCTAACAGGGGAACAACCTCTC A
WI-13859	84	G A	...	...	TTATTTGTCAGAATTCCAGAATCAGAGTCTCTACTGGGCAAGTAGAAAATAGAAAAGTTACTAC TTTGAAAAGGAAACTATT[G/A]ACAAACAAGTATATATTCAGGAAGGACTCCTAGAACTTGAGCA ACA
WI-13536	29	T C	...	...	TGAAAGGATACAGAAAAAAACTCAGCGAAGT[T/C]GAAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAGCTTGTCCTCTCCCAGTGCCATTACATGGAGTACACTTAATTTCTCAGCA
WI-13373	52	G A	...	...	TTTTATTGTTGGTGAGAAAACAGGCTCTTAACACTGAATAAACATCTCAC[G/A]AACTGTCGCTC CTAGATTACAAAAAGTCAAAACCAATTCCTTGACGCGGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAAACCAGAGCT
WI-13477b	61	A G	...	...	TTGGTTTTAATACCTCTTGTTGGATAAAAGGACACATTGTTTTCATTAGCTTGTCTTCAAA[A/G]GAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAAATAGAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32	A G	TTAATACCTCT TGTTGGATAA CAATG	GAAGACAAGC TAATGAAAAA AAGG	TTGGTTTTAATACCTCTTGTTGGATAAAAGGA[A/G]CATTGTTTTCATTAGCTTGTCTTCAAAGAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAAATAGAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

Marker	Pos.	Allele	Seq A	Seq B	Sequence
WI-14297	86	A / T	AATGTGGGTACTTTTTCCAAG	TGTGCACATTCAGAAACATTTT	CTGACTTTATTTAGCATGCAATGCAATTTATTCTGGCAATAAATTAATATGTGCAGTTATAAAAATGTTGGGTACTTTTTCCAAG[A/T]AAAATGTTTCTGAATGTGCACACTAGAATATGCAGAATCCTTTAAACAGTGGACT
WI-12229	89	T / G	CATGTGCACAAAAAGAGTAAGAAA	ACATGTGAATTGTCCCAAAAA	TCCATGTAAATATTCTCAACAGAGAACACTATCTTAAATGAAGAGATTACCATTAAGAAATCAACATGTGCACAAAAAGAGTAAAAAT[T/G]ACCAAAAAATTAAAGATTTTTGGGACAATTCACATGTTCAAAAT
WI-13582	43	C / A	TGCAATCTAGAGACTGGGGA	TCTGCGCAGTTAGATTCCA	AAGGCTGCCCCTTACTGGACCAATGCAATCTAGAGACTGGGGA[C/A]TGGAATCTAACTGCGCAGAGAAATCAAAGACCGATGGTGTGAAATCTGGGGCAGCTTCAAAATTTCTGCCTCCTAAAAACATTTCACCCAATTTTCATTATTGCC
WI-13857	28	A / G	...	...	TCTGAGTTGATAAAATGCTTTTCTGAAC[A/G]TACATTTTAGGTATCTGGCACAATTAACCAAATGTCTGCCCCATTTTGTGTAGCTTTCATTACAGATTTCATTGATGTCGCTCCACATCTG
WI-15809	77	T / G	TGGTTTTCTGTGTGTAAATGCCGTAAA	TAAGGTAGCTAATTCAATGTGTTGTAAA	GTTTTAAGTTGCAGAGATGTGAATGGTTACAAATCTGAAGCTGAAGTCAATCTTTGGTTTTCTGTTGTAAATGCC[T/G]TTACAAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123	A / T	...	...	TTAATCAGTCTGTGTCAAGAAGAAACAGGACTTGATCAAGCTTCCAGCCCTCCACCACTCTATCAGCATAGCAATTTAAGGATCAGAGCTTTGTTGTTCTAAAACCAAGAGAAGGAA[A/T]GGAATCAACTCCACAGATCAACATGT
WI-15801b	81	T / G	CATACTCCACTCTAGCTGCAGTAA	AGAAGAGTGGATGGGATGC	TCTTTTATTCCAAGAATGGGAAGCGCCATTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACTCTAGCTGCAGTAATAC[T/G]GCATCCCATCCACTCTCTCTTTTGACTGAAACTCTTCAAAGAACTGCTGAATGTCCTCTCTC
WI-15801a	24	G / A	TTTATTCCAAGTCATTCAAGCC	AATGGGAAGCAATGAAAATG	TCTTTTATTCCAAGAATGGGAAGC[G/A]CATTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACTCTAGCTGCAGTAATACTGCGCATCCCATCCACTCTCTCTTTTGACTGAAACTCTTCAAAGAACTGCTGAATGTCTCTCTC
WI-13763	59	T / C	GGCTGGACACTGCAGTGTGAT	CCCACACCTGCCCCT	GCTCGTAATGAAGACAGAACGCTACAATCTGTTCAACACTGGGCTGGACCACTGCGACACTGCAGTGATT[T/C]AGGGGCAGGTGTGGGGGAACGCAGGGTGGGGCCCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA
WI-13578	48	T / A	TCAATAAAGAGCAGAAAGAAAACC	CAGTGTGTAAGAACATCTTTTTGTC	TTTTTTTTGGTGAGTGTTTGTCTTCAATAAAGAGCAGAAAGAGAAACC[T/A]GAGACAAAAAGATGTTCTTACACACTGAGCTTCACCAGTCACCCAAACATTGATATTTGCTTTTCCCGAGGGCAAAAAGAGAGTCTTCCCAGAAACCTC
WI-13789	62	G / A	TTGGATGGCTGAGGGAG	CAGTGCGCTTCCTCTGTTC	TCCAAGGAAAAAGAAAGAAGAAGAAAAACCAATCAGTGAGAAACTCAAGAATTGGATGGCTGAGGGAG[G/A]GAACAGAGGAGAGCGCACTGGGGCTGGGGACAAATGTCAGTGGATGGTGAGGGTCCTCACTCTCTTGAGGTCCCT
WI-13594	66	G / A	TTTTTAACACAGATCACAAAAAGC	CCTTTGCGCCAGTACTTTTT	AATAACAAGTTAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTAACACAGATCACAAAAAGC[G/A]TGCACAAAAAGTACTGGCGCAAGGACAAAATAATGTCTAAGAATTAGGCCAAACAGCTGC

Name	No.	A1	A2	Seq 1	Seq 2	Sequence
WI-15625	40	C	T		...	GTTCTCCCCACCTACTCCCGCAGAAAAAGGCATATTCAA[C/T]TGTCCCATACTAATTTTTGAATAA CCTAACTCTCCCTTGTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-13367	84	C	G	CCACACTGAA GACTCACCAG A	TCCCCACCCCA CCCT	GTCTCACTTCTTGTCTAGGCTGTAAATTTCAGTTAACAAGTTCTTATGTGATTGTTGTGGCCACACT GAAGACTCACCAGAA[C/G]AGGGTGGGGTGGGGAATACTTAATCAATATTGTGGAATTACCGAT GAAATCCAGTTATTCCT
WI-13600	26	G	T	CATATTGAAAA TTGTTACTAGA AAGCATCCAT	TTAATGAGCC TGATGG	CTCACTTTAATGAGCCAAGCATCCAT[G/T]CCATCATCTAGTAACAATTTCAATATGCACATTATAT TATACTGGAAACAAGAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCTCT TGATTCCCTCTCTACCC
WI-13602	89	G	T	TCCATTCTGGA GACAACACA	GCATACCTCAT ATATTAAT	GATAGGAAAAGAAGAGAATGAAGTCAATAGTCTTTAGCAAGCCAACTAGCTCAAGGAATAGACAGCCC CTTCCATTCTGGAGACAACACA[G/T]AAATCTATTAATATTAAATATTGTCATGAGGTATGCACCT GCCCA
WI-13650	76	A	T	AAAGATTCAC AATATTTCACT TTTAAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTTT	GCATTAACATTAAAAATTCTGAGGGATATTGATGAGAACTATGATGAAAGATTCACAATATTTCAC TTTTAAAAC[A/T]TAAAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAAGTTACCGG
WI-14319	83	C	T	CAATTCAAGG CACAAAGCTA A	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAGGAAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTGGGGGTGGGACAGTACAGAATT
WI-13528	80	A	G	CAATACATTT GCATTTTCCTA AAAA	CATGATACCAC AGTTTTCTG AA	ATTGGATACATGCTTTAAAAATGGTAGCTTTAAACTGTAATCAATACATTTGCATTTTCCTAAAA AAAGAAGACATTT[A/G]TTCAGAGAAAAACTGTGGTATCATGCAGGAAAAGCAGAAAAAATT
WI-13909c	93	A	T	...	...	ACTTAAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCCAGTGAAGTTCATCTTCCTCACACT CTCTTCAAACTCGAATATCTTTTC[A/T]GAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80	G	C	TTCCTCACACT CTCTTCAAACT C	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCCAGTGAAGTTCATCTTCCTCACACT CTCTTCAAACTC[G/A]AATATCTTTTCAGAGATGCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86	C	A	...	...	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAAACAAATTATAAAAGGGACAGAAAAATTAAG AATCAAACATCATTCTGGAC[C/A]ATGGGAAACCTTGAAAAGGCATGGCGAGACCAGTAACTA
WI-14323a	78	T	C	ACAGAAAAAT TAAGAATCAA ACATCA	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAAACAAATTATAAAAGGGACAGAAAAATTAAG AATCAAACATCATCA[T/C]TCTGGACCATGGCGAGACCAGTAACTA
WI-15389b	104	G	A	AGATAATGAA ACATCTGCGA AAA	GATGAGGTGAT TCCCACACTT	AAAATTGACAAATCAACTAGCTTGCTTTTGTCGTTTGGAAGACTACCATTATTCAAATTTATTATGT AATACACTCATCCAGATAATGAAACATCTGCGAAAA[G/A]AAGTGTGGAATCACCTCACCTCGTGTGC

Marker	No.			Seq 1	Seq 2	Sequence
WI-15389a	33	G	A	AATCAACTAG CTTGCTTTTG TC	TTTGAATAATG GTAGTCTTCCA AA	AAAATTGACAAATCAACTAGCTTGCTTTTGTC[G/A]TTGGAAGACTACCATTATTCAAATTATT ATGTAATACACTCATCCAGATAATGAAACATCTGCGAAAAGAAGTGTGGGAATCACCTCATCTGTGC
WI-15747	88	T	C	TGCTTCATTTT AAACTAATTT AGTGTTT	CATAATTCACC AAAAGTTCATA TAATTT	TGTAATCTGCTTACAGTCCTTGCAAAGACAGACATATGTTTTGCATAAAGATATAAATTGCTTCAT TTAAACTAATTTAGTGTTT[T/C]TTAAACTAATTATATGAACTTTGGTGAATTATGAACTGTACCAAAC C
WI-13752b	117	C	T	...	...	AAGAAAGCACATACATTTCCAGAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCTCGTTAAGTGCTGGATATACTTGGCTTGCAC[C/T]GGACACCTTTTACG GAGGGATTCCGGACAACT
WI-13752a	106	T	C	CCCTCTCGTTA AGTGTCTGGA	CCCTCCGTAAA AGGTGTCC	AAGAAAGCACATACATTTCCAGAATTTGGAAAAGTTCACTCTGCGATGAGTTCCTTCTCGTTAAGTGCTGGATATAC[T/C]TGGCTTGCACCGGACACCTTTTACG GAGGGATTCCGGACAACT
WI-14339	102	T	G	CCCAATCAAA CAGTACATGA GTTAC	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCTCACTGGGCTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCAATCAAACAGTACATGA[T/G]CGGTTTCCAGAAATCTGGATAC
WI-13744	115	C	T	TGGTGCTGAAC AAAACTGAA	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAAACAGTAATGGAACTTCATGCAGCTTAGAT TTCCTTTGCCCAGCTAGGAGCTTGTGTATGGTGCTGAACAAAACTGAA[C/T]GCTGTGTGCTTATCTTTC CTGATTCT
WI-14061	68	C	T	...	...	CCTTTGACTATATTGTTTTTCCAAAAATAGGACTATGTGTAGAAGAGAGCCCCGTACATACCTTAT [C/T]AACCATTTCATCCACCATTGTAAAAATCTGTGGGTCTCTGGATACTCAAAAACAGAT
WI-15719	69	A	C	ACCCTTTCATC AAGAGTTTTAA ATT	TGATACTTGGC	TTACAGTTGGATTAAACACTACCACACTGAATATACTGAATTAACTATTCAACCCTTTCATCCATTCAG [A/C]AATTTAAAAACTCTTGCCAAGTATCATCGAACTTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106	T	C	CTCTAAATCG ATACATCCAA AACTT	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAAATCACACATACTAGATCAAACAGAAGTACCACAGTATGCTTTATTTGCA[T/C]AGTTAGCAGCAAGCATCAGTTCTTC GGTATTAATTGGTTCTCTAAATCGATACATCCAA
WI-15736a	27	G	T	ATTTTATTCAC ATTAAACTTG CACA	GTTCTTTGATA TGTGGCTTAGT TTT	GGATTTTATTCACATTAAACTTGCACA[G/T]TAGCAAAAAATCAAAACATAAAACTAAGCCACA TATCAAAGAACAATATACAAAGTGCTTTCTCAATTGGAAGGTATTCCATAAATA
WI-13785d	72	G	A	CACA	...	TCAAAACTGCACACTATAAAAAGTGCTTTAAAATGCAGCACTACAAGCTGTCACAACACAGTG AAGTGC[G/A]TAGTGACACTATAAAAAGTGCTTTAAAATGCAGCACTACAAGCTGTCACAACACAGTG
WI-13785c	56	A	C	...	...	TCAAAACTGCACACTATAAAAAGTGCTTTAAAATGCAGCAGCAGGAGATGTGAAGCA[A/C]CAAATG AACAAGTGCTCAGTGACACTATAGCTGCTGTCACAACACAGTG

Marker	Pos	A1	A2	Flank 1	Flank 2	Sequence
WI-13785b	40	C	G	---	...	TCAAAACTGCACACTATAAAAGTGTCTTTAAAATGCAGCAG[C/G]AGGAGAGATGTGAAGAGACACAAATG AACAAGTGCGTAGTGACACATAGCTGTCACAACACAGTG
WI-13785a	27	T	C	AAAACTGCAC ACTATAAAAG TGCTT	TGTTGTGACAG CTATGTGTCAC T	TCAAAACTGCACACTATAAAAGTGTCTT[T/C]AAAATGCAGCAGCAGGAGAGATGTGAAGAGACACAAATG AACAAGTGCGTAGTGACACATAGCTGTCACAACACAGTG
WI-13793	88	C	G	GGATTTTACAT TCAGCCTAGAT ATAGG	GGGCAGGAGGA TTTGTTACT	AGAAACCAAGTATATCATAGGCAAATAAAAATAGTTTTTACCCCCATTGATACAACATAAGGGATTT TACATTCAGCCTAGATATAGG[C/G]AGTAACAAATCCTCCTGCCCATAAATCTATGACTTG
WI-13794	52	A	G	TTCCTCACCCT TTTCTTCTC	AGAAATGGGCTC TTAACCTTGTA	TAGTCTCCTACAATTCCTTCATTTCTTCCTCACCCTTTCTTCTC[A/G]TACAAGGTTAAGA GCCCATTCTTCAAACAAACAAAAAACAACACATAGAGCAAT
WI-15729	35	A	G	CTTTGAACCAT GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACTTTGAACCATGTGTAGACTGC[A/G]GGCACTTTAGAAAGAAGCTGAGACTGAA AAGTCTGTCTTGACTTCCAAGGAAGGGTAGTCCCTGTTTGCAGCCCCGGGCCTGCTCATTGTTA
WI-13424	66	G	A	TGAGGTTTTC ACCCTATTCTT C	TTTTTCTCCCC AGGGTCTA	GTCCTTTGCACAAGTCTCCCAACTGGTTTGGAGTTTTCCCTTCTGAGGT[G/A]TAGACCCTGGGGAGAAAAACACACATGTGTAAGTGGCTCAGGACGCCGTTCACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29	T	C	TCTTATAAAA GGTCAGAGGC AATT	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTCAGAGGCAATT[T/C]GAGATCCCAGATTCAGCTTGTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAATTCTTGTCTGCTTTAATCCTGAACATTCTTGAAGCACGAA
WI-13446	22	G	C	GCCATGTCTT CTCACTCATCA	AAGGGAATCA AAATCAGAAAG G	TGCCATGTGTTCTTCACTCATCA[G/C]CCTTCTGATTTGATTCCCTTTCTGCTCTGTAATTTTTTCTTC TTCCCTTTTTAGGGCCTAGTCTGTTAGAAATTCTGGTTTTGAGAGTAGTGAGCCCTTTTACTTTTT CTGACTGCCTAATT
WI-13725	56	A	C	TGAGCACATA TGGGTGCC	CCTGCTGTCTC GGGC	TCACACAAAGGCATTTGGAAATGTCACCTTACACGTGGTGAGCACATATGGGTGCC[A/C]GCCCGAG ACAGCAGGATAAGTTCACAAAACTTGACCAGGCAGGTTAGAAGCAAGGCATGGTTCAGGATG
WI-15702d	107	T	C		...	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAGAAACTGTAACCCTGTAAACAACTAA[T/C]GGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101	T	C		...	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAGAAACTGTAACCCTGTAAACAA[T/C]ACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90	C	T	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAGAAACTGTAAC[C/T]CTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA

Clone	Pos	Allele		Flank 1	Flank 2	Sequence
WI-15702a	48	G	C	AACAAAATAA AGGCTTTCAA AAAG	CCTCACCCCTT TACCCC	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTCAAAAAG[G/C]GGGGTAAAGGGGTG AGGAAAGCATGTGAGAGAAACTGTAACCCTGTAAACAATACTAATGGGTTCTTTGAACACAAATAGTTT TGA
WI-13831b	113	T	C	---	---	TTTTTTTTATGGATGCACTGTTACATGTTTATTTATTTAGCGAAGGTGACTTGGAAAAGGAGAATTCACAT ACTTCCACTGTATCCTCCGGGTAAGTTTCCTTCTTCTTCTTGTGAGA[T/C]GTCTCCATGTTACAGTCAAC TATAAAACATGGCTCA
WI-13831a	56	G	C	---	---	TTTTTTTTTTATGGATGCACTGTTACATGTTTATTTAGCGAAGGTGACTTGGAAAA[G/C]GAGATTCA CATACTTCCACTGTATCCTCCGGGTAAGTTTCTTCTTCTTCTGTGAGATGTCTCCATGTTACAGTCAAC TATAAAACATGGCTCA
WI-13806	62	G	A	---	---	TGATTGAGCTTAGAAAGGAAGTCATGTTGAAATCAGAGAGAGGCCAAAACTAGGCCTCAGGT[G/A]C CCATTAAGCATGCTGTGAATGCAAAGGAAAAGCTTAAAAAAATTTTTTAAGGGTGACTCCAGTAAA CAT
WI-14372	86	A	G	---	---	CACATTTTCAGCAACAAATCGAGGTGCAAACAGGGTTTATTTCACATTAATATATTAACTGGATTT TTTGTCAAATAAATAGGGA[A/G]TTCTCTTTAAATAACCATCTCCTCACTTCATGGCCAGT
WI-14373	95	A	G	---	---	AGGCTGTTTTTTGAGGCCTGAGGACCCCAACGTAAGACTGTAACCATGGTCATGTGTGAGTT ATGAGCTAGGAACCCTGGACGAAACCA[A/G]CACATATACAATCATCTCCCACCTCCCAAGCGCCTTT ACTTTCACAGCGCCTCTGCA
WI-14078	61	C	T	AAAGAAGTAA ATTAGGAAGA GCAAGA	TGTGTGCATGT CTCTTACTGC	AGAAACCGAGAACTCAAAGAACCACATGGTGTATCAAAGAAGTAAATTAGGAAGAGCAAGA[C/T]G CAGTAAGAGAGACATGCACACAAATCGAAACAAGGGCATGGAGGAAGGACTTTAGATGGTCACG
WI-14083	47	C	T	AGACTTGAGA GCTTAAAAACA ACACT	GCCTACTGGAC CTCTAAACTAC TGA	TTGCTACATAACACATTACTCCAGACTTGAGAGCTTAAAACACACACTC[T/A]TTTGTTATTTCACAG CTCAGTAGTTTGAGAGGTCCAGTAGCTTGGCTGAGTTGTTGCTTAAGGTCTTACAAGGCCAA
WI-14085	31	A	G	CATTTATTTTC ATGTGTAAGA AGAAAAA	CAGTCATGTTC ACGTGCTAGTT	TGCATTTATTTTCATGTGTAAGAAGAAAAAC[A/G]TAACTAGCACGTGAACATGACTGCATGGATAC ACGGGCTCAGCAGTGAGAGGCTAAAGTCAGAAGTGAGTGAAAACAAAATAGCATGTTGATTTAAGTGAAA TAACAGAACAGGAGGCCTTT
WI-12169	121	G	C	AATAAAACTT CCTATTTTCTT TTGCTT	GGGTTCTGAGG TGAAAGAAAA A	GTCAAAGGTTGGCAAATTTATTTCCACTTATCAAGAACTTACAAAATATTTTGTTTCATTTCTAAA TTTTCACCTTTATTGCTAAGTTATATAAAATAAAACTTCCTATTTTCTT[G/C]TTTTTTTCA CCTCAGAACCCCTTA
WI-15705	50	A	G	GGAGGGGAGAT TTTAGACTGA GATC	AGCTGTAGTCG TCAAATACTCT AGAA	TTGTTTTTATTTGGGAGAATGAAGGAGGGAGGAGGGAGATTTAGACTGAATC[A/G]TTCTAGAGTATTT GACGACTACAGCTCTCTCTCTTGTACTACGGAGACCCTGCTTATAGCCCCAACAGAAATCCTCA TCTGCGGTTGCCAGACAG

ID	No.						Sequence
WI-14379	102	C	T	TCTATTAACA GGGTTATGTCA CACC	ATCATCTGTTT TGAGGTTGACA		TTTATGCTGTGTTGTTGTTCTACTGGTCGGTCGGTCGCTCACTAATATCCAATCCTAGTATGATTTTCTTT TACTTGTGTCTATTAACAAAGAGGGTTATGTCACACC[C/T]TGTCAACCTCAAAACAGATGATACT TAAATAAAAACAAAGCAGAGAAA[C/A]CCCACCATTAACAGAGAGGACACTGCAGAGGCTTATGTGTACA ACACGTGTCCCGCGAGGAG
WI-14102	22	C	A	...	...		...
WI-15937	24	A	G	A	CGCAGAGCTG CTGTGTATTTAAAA A	GCAGAGATCCA GACGCCTTGT	ACCGCAGAGCTGCTGTGTATTTAAAA[A/G]ACAAGCGTCTGGATCTCTGCGAGGGGCTGGGACCAGCTGC AGTGGGGGCTCCGGCACTGCTCCTCCCAGGACTCTTCCCACCACCCC
WI-15944	24	A	C	A	AAAACTGAAAC GTATTTCCTCC A	GGCCTTTAAGT TTCTACGGTG	TGAAACTGAAACGTATTTCCTCCA[A/C]ACACCGTAGAAAACTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCCGGCGAAAAAGGAAGTTTCAGGTGATACAAGATGTCCTGCCATCACACCTGAAGGAT GGTT
WI-14124	92	A	G	---	---		ATGTTTTATGATCAATTCCAAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAGAAAAAAATCAT ATTTAAGTCCCGTTAACACTAAGCC[A/G]TTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14125	88	C	T	GGTTTGACCTG CATAGATTTTT	GGAATGGCATG GCCAC		GACAAAGAGGCAGTTTCTGTAGTTCCAGCAGGGCCAGAGCAGTTATCAGAACGGGGTTGGTTTGACCT GCATAGATTTTTGACGACTA[C/T]GTGGCCATGCCATTCCTGTAAGTGAAATTAATGAACA
WI-14136	120	G	A	GCTTCTCACC ATGTCTTCACA	CTTGTTCTGTC TCTTTGGGC		GTTTATTTTCTCACAGTTCTGGAGGTTAGAAGTCTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTACAGCTGGCTGCTGCTTTCTCACCATGTCTTCTCCACCATG[G/A]GCCCAAAGAGAC AGAACAAGCTCTCTGGT
WI-14138	23	C	T	TGTTGGCACCA GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAAACA		TTGTTGTTGGCACCAGAAAAGCTC[C/T]ATGTTCTATGTGTTCTATGTCACTGTACATACTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTTGTTTCAATG
WI-13551	74	G	A	TCCTTCAGTAG TAGTATATTCA GACAATC	GCTCATTTCTT TTAGTGCTAAG TAATATT		GGCAGGTTTATTCATAATTTCAAAAACTTGGAAGCAACCAAGATGTCCTTCAGTAGTAGTATATTCA GACAATC[G/A]AATATTACTTAGCACTAAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-15953b	59	C	T	TTTTAAGAGTG TCCTTCACATC ...			TTTTTTAAGAGTGTCCTTCACATCATTTATATTGTGATTGCACACAAACTTTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC
WI-15953a	26	T	G	A	T	TTTTAAGAGTG TCATCTGTTCT TGTTGTTTTG AT	A	TTTTTTAAGAGTGTCCTTCACATCAT[T/G]TATATTGTATTGCACACAAACTTTTTTAACTCCGTCAA AACAACAAGAACAGATGAATAAGGAAGCCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC

ID	Pos					Sequence
WI-14631	82	G	A	---	---	TGAATTCAATGGACAGTTTGCCTCTGTTTAGTGAAACCCTCACAAGCACTCTGCATAGTCCGCTTT CTGTCTTCTTTAAC[G/A]TGCCTGGTTCCCTCTGCCCAAACTTTAGGATTGGGCCTCCTCAGGCCTT GTCCTGA
WI-6053	24	A	G	---	---	ATCACCACCGTGTCTCAAGAACAAC[A/G]TCTTCATGTCCAACTCATATCCCGGGACTTTGTCAACTG CAGTACACTTCCTGCATTGAACCTGGCTTCCTGGAGGGAAGCCTCCTAGAGGCCAGGTAAGGGGGTGC AGCCAGTGAGGGGTATATCTGGGCTGGCCAGTTGGAACCACGGAG
WI-15964	99	T	A	GCTCTCTGTCC CCTCTTGC	GACTTCTCCAC CTGGAGGTA	CAGAAACCTCTTCTGTGTATTAAGCTGATGCTAAAGTCAGAGCAGTCAAAGGCAGGAGGCTGCCTT GGGAGGTAGTAAGCTCTCTGTCCCTGGAGGTA[T/A]GCAAGAGGGGTGGAGAAGTCTTGGCAAG
WI-12075	103	G	A	AGCAGCTGGG GGCAC	CCCCTTCTTTC TCTTCCTTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAAGCCAGGCAAATACCCATCAG AGACAGTGACAAGCAGCTGGGCACGGGGGCAGGAGGC[G/A]GAAGGAAGAAGAAGAGGGGAGGAG CCT
WI-12179	96	G	A	GGAGGTACGG TGGGAGGTCA	TCGGAATGACCC TGTAGATGC	TAATTTAAAAACACGCCCTTCCCACATAGTGCGTGAGGCATCTGCACATTTTCCTAGAAGGACATGA ATAGTGATGTGGGAGGTACGGTGGGAGGTCA[G/A]GCATCTACAGGGTCATTCGAGGAGGAACAG
WI-14651	49	C	G	CAAGAATCAT TCTCATTTAAA GATTGT	GGAGATATTGA TCTTTTCTGA CTTATTT	CACAAATAGTGAAATTATCTGAGCAAGAATCATTCTCATTTAAAATTGT[C/G]AAATAAGTCAGAA AAAGATCAATATCTCCCCTGCTTCAAAAATGACACTCCCAATTTCACAGGTAACCACTGTTA
WI-14666	105	T	A	---	---	AATGTGGACTTTCAAACAAGGGTTTAAAACTAATCTAATACAACTTCTACAACACCATTCCAGAGCAT TATAACAAGAATTATTTACAGGCAGCTAATGTATTAAA[T/A]AACCATGAAAAGAAAAAACTTG
WI-13473	31	C	T	---	---	ATCTAGATGTCAGCAAATGGGCTGAGACTGT[C/T]TGTCTGGTAGATGCAGTGTTGTATGTTTCTAC TCTATTACAAAAAATTAACAGAAATATGGCTTCGCTTTGTGTGCAAATGTTTATCACAGTC
WI-13967	103	A	C	AAAAGACTAC AGATACAAGG AAAATAAAAA	TTGTGTTTTCA TCTCCTAAAAG TG	AATTTAATAGCAGCTCTGTCTGTGTTGTGATTTAAAGAACAAGATAAAAATATGTCATTCAGCAGTCATTT AAAAAAATAAAAGAGACTACAGAGGAAATAAAAA[A/C]CACTTTTAGGAGATGAAAACACAAA
WI-14408	60	T	A	GCAGACACAC TATTACAGGCT G	TTAATTGTGTA AAACTCATTTG TTACTTT	TTAATATTTCAGCAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTG[T/A]AAA GTAACAAATGAGTTTTACACAATTAAAATATTAACACATACTTATGGGATTTGTTGAATGA
WI-13683	47	C	T	---	---	TTTTGTTAAGAACAGCATTTGAAAATAAAACCTATCTGCCCATG[C/G]TTACAGCCTTTAAAT TTGTAATATTTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63	C	T	CACCATGGCA CGTCCT	CATTGAGATAA AGCACACTTAT CAC	TTAGAAAACTGATAAAAGCAACACAACTTTTGGGGAAAGCACCATGGCACGTCCTTTTGTGCTA[C/T] GTGATAAGTGCTTTATCTCAATGAAGCAACCCCA
WI-14635	22	G	A	---	---	ACATGGCAGATACAGAGCTGTC[G/A]TCTTGAAGCACCACACTGACCAGGAAATGCCACTTTTACAA AATCATCCCCCTTTCATGATTGAACAGTTTCCTGACCGTCTGGGAGCGGTTGAAGGGTGACCAGC ACATTTTGCACATGCAAAA

ID	No.			Probe/Primer	Probe/Primer	Sequence
WI-16002	59	T	C	GATAACATAA AATGATCATG AGAATTC	GCCATCCTC TTTGACTTT	CCAACATTTAAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAATTCA[T/C]GTTA AAGTCAAAGAGAGGAGGATGATGGCTAATGCATGCTGGGCT
WI-15361b	101	A	G	A	CCCACTTGAAAC TCAAGTCATC / AAACTAAAAC CTTTGTGCCTA	GTGGAATTTATTAAGCCATCACAAATTCCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAACTCAAGTCATCA[A/G]TTTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTAACCA
WI-14759	73	T	C	GCGTTTGACTT GTGCGG	TCCCACACTGC CCCC	TGAGTTACAACAAATGAGCAACAAGTTAGAAAAATTGGTTTTATTCAAACTTCCTAGCGTTTGACTT GTGCGG[T/C]GTACTCAAATGGGGGGCAGTGTGGGACGGGGAGGGATTGCAACCAGAGTTCATACTG CAA
WI-12535	50	A	T	CTAGGAGGGTT GAGGTGTAGA TAT	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTTCAGGTGGTGACTAGGAGGGTTGAGGTGTAGATAT[A/T]CTTCCTCCTCTC GTGGAGCCTTACTGAAGACAGGATCGCCGTTCTTGTGTTTATCAGCTGAGAAGGCAGTCTCGCCATC TTAAAGACCTGCCCTCC
WI-13805a	112	G	A	AAAGGCACAC GGGGAA	CTCAGCCTGCC TTGACC	TTCCATTCATTATGCTTGGCTTTACCAATTTTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCCAGAAACCATGAGATTTGGGTCAGAAAAAGGCACACGGGGAA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18	T	C	...	...	ACACAATATAATTCCATT[T/C]CGAGTGATTAAAACCTATTTGTTGTTTAGAACCAAACAAAACTAC AAGAAAACATTTCAAAACCTTTTTTTCAGGCTGA
WI-14808	52	T	A	ACCCACCACA CTACCCTGT	GAGGGCATCACA ATGTTAAGGATT TT	CTTTGAAACACTTAAGCAACAGTTAAAAGTACCCACCACACTACCCTGT[T/A]AAAAATCTTAAC ATTGTGATGCCTCTGCATCAATTTTTAGAAAAACAAAGAAAACAACAACTGAAGGCCCCATGTA
WI-14816	29	A	T	...		AGTTAAAAAAATCGAGTCAGCATTATT[A/T]AAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTTGTATCCCAAGCCCCTGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTTC
WI-12542c	71	G	T	...		CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70	G	T	...		CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]GTAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45	C	T	GCTATTAGGC AAACTGAACA TTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGT[C/T]ATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57	C	T	GGATACAGCA GTAAAGAATA CAAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATTCTAGAAACTGGGATACAGCAGTAAAGAATACAAAAAATCCTGC[C/T]CTTATA GAGCATACATTCTAGAGGTGTGGGAAAGAGGCCAATAAATA

Clone	Pos	Allele 1	Allele 2	Fragments	Sequence
WI-14836	28	T	C	...	TCTTTGGAGGGATAGAGGAGCAGAGAGTGTT[T/C]GTTGATTTTCGTTCGGTTCAGTTTGGTTGTCATT GGTTTTGTTTTGCTAATTTTGCCCCACCCTATAAAAAGCAGTGCCACCCAGAGGCAG
WI-14856	60	A	T	TTTGTTGCTA CTTTTTACAAA CTTT / TGGTGACACG GAAAATACTT AA	ACATTCCTTATGATAGCAACAACTAAATATGATGGTGACACGGAAAATACTTAAT[A/T]TAA AGTTGTAAAAAGTAGCAAACAAAATTGAGTATATACTATAAGTGATAGAGGATGTATATGAAAAA GGCTATAAAAAGCTCCAAAA
WI-14863	61	G	A	...	ATGGCAATTTACTTTATAGCAATGAACAACAAATATTTGTCAAAGGGCAAATATTTTTGTCTG[G/A]AG TTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACTATTATTGATTGCCACT ACCTGGC
WI-14867	46	T	C	TGGGGCTGCAG ACACTC / GACATTCCAA GGCTCTCTAAC A	TTTTAATTAAACGTAAAAAGGCAGGACATTCCAAGGCTCTCTAACA[T/C]GAGTGTCTGCAGCCCCA TTCGCTTGAGATGTGAATGTGTTAACCCAGGGTGGA
WI-14733	98	G	A	CCAAATTGAC AGATATTCTGC GCCATTTATT / GATGAGGTCAG A	ACGGAGTGCTCTGATGTATTCTTGTCAAAAATGTTTGCCTGATTCATCATGAAAGAACAATT AGAAAAAAATCCAAATTGACAGATATTCTGCA[G/A]AATAAATGGCCTGACCTCATCAAAAACATCA ATGTCATGAAAAACACAAAA
WI-14898b	79	A	C	... / GCCTGTGTTCTGTCTT	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGAGTTGTCTCATAAGGTGCCACTAAGGAAA ACTTTCTCCATTA[A/C]AAGCTGCCTGCCTGTGTGCACGTTGCCTGGCTTTGCTAACCCCTGGTGCTGCATCT GCCTGTGTTCTGTCTT
WI-14898a	50	A	C	CATGTACAGG AAGAGTTGTCTT AGTGGCACCT CA / AAGTTTTCCTT	TTTTGTACCTATTCCCTGTTTCAGTGCATGCATGTACAGGAAGAGAGTTGTCTCAT[A/C]AGGTGCCACTAAGG AAAACTTCTCCATAAAGCTGCCTGTGTGCACGTTGCCTGGCTTTGCTAACCCCTGGTGCTGCATC TGCCTGTGTCTGTCTT
WI-14907	48	G	A	GGCACACATT GGACTCTGAC GGGAAT / TCTGCTGCAAG A	TGGTATTTATTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC[G/A]ATTCCCCTTGCGCAG ACATTGTGAAGCTGCTGGTCGGCGACACCCATCAATCAGTGACTCCTGCAGAGGGGCCACATG CACGATGCTCACGTGTG
WI-14911	52	G	A	CCAATACATT CAGTTCCTGGT C / CAAACCAGGA AAGGACCTT	CTAGAATCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCAGTTCCTGGTC[G/A]AAGGTCCTTTC CTGGTTTGCAGACAGATACCTTGCTGTATCCTCACATGGCAGAGAAAGAGAGGAAGTAATCT
WI-14913	88	C	A	...	CTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGCTACTTCTCCTGGGACCAGCCAATTTC TAGTGATAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTCATATACAGATCAACCAATCCAAAAC CTACACCTCCAACCACCT
WI-14914	66	G	C	CTGGACACAG TTTTCTCTAGC A / CAAGCCCAGGA CAATAAATTC	ATTTCCTTGATTGGCTGCTGCGTGCGTGTAAAGCCTGTGAAGTCATGCACATCTGGACACAGTTTTCTCTAGCA[G/ C]GAATTTATTGTCCTGGCTTGATGGCTTTCACAGC
WI-14926	49	T	C	...	GTTTATTTTCAAAATGACACATCCCAGATTGAAATGGCACTTAGCGAA[T/C]ACTTGTGGACCACA AGACTTGTCTGAGAACATGTTCAAAGACAGTTTCAAATAAAAATTTCCTTAATCAGGTCCA

ID	No.					
WI-16083	89	C	T	ATGTTAAACA CAAACATATC AAGGAT	TGGAAAAGATT CCAGCCC CATTAAAGCAG	GCATCTTTATTACCACAGAAACTCATTTATGTCCTTAATCATTGTTAATATATATAAGCATGTT TAACACAAACATATCAAGGAT[C/T]GGGCTGGAATCTTTCCATTCTATAGAAAAGCACTAACCATC
WI-14930	55	C	T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTTCTGTGTTCTGGAACAGCTCTCCTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG GTTGGTTGTGGTGATTGGGGAGCACGAGGGAGAGCAA
WI-14946	47	T	C	---	---	TCAATACTGAAGGTGTCAAAGTGGTCTATTGCCCCCAGACATAACA[T/C]CTCTAAATCATCCTCTA GATCAGGGAGGTCATAAGGACCATTACACACAGTACTTTATGGAAAGGATT
WI-15987b	80	A	G	---	---	ACATTAAAACAGCACAATTAAAGGGGTCCCAACGAGGTTGGTAGTGCCTTCCACTATGTGAGGA TAAGAGATGGTC[A/G]TCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32	C	T	CACAATTAAAA GGGGTCCCAA	GGAAGGCACTA CCAACCTC	ACATTAAAACAGCACAATTAAAGGGGTCCCAA[C/T]GAGGTTGGTAGTGCCTTCCACTATGTGAGGA CACTAAGAGAAGATGGTCATCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56	T	C	AGGGAAACTG CTAACTTGTCA G	GATGATCTTAC ATCAGTTGTTG GA	GAATAAAGTTCTTATTGCCGGTCCTTCAGGGAACAGGGAAACTGCTAACTTGTCAG[T/C]TCCAACA ACTGATGTAAGATCATCTTCTGACCATAGCGAACCTGTGAAGGCTTGCTGTTCCCTCCAGCTGA
WI-16100	52	A	G	CAAAAAGCTA TTTCCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCCTACACTTGAC[A/G]TAATATACTG TTTTCTGACATTCCTGTTATCAACTCCTCTGAAAATC
WI-14958	83	A	G	AATAATTTAT CTCTTTCTTTT CAAGGG	AATGCATTCAT TTGGGTTTTT	GTGATTGATCTGTAATTATTATTTATTGGGATTATTATTCAACTCTAAAATTCCAAGATGAAAATAATTATCT CTTTCTTTTTCAAGGG[A/G]AAAAAACCCAAATGAATGCATTTCAGTTTCTCCAGGCCTTGAACTGC AGCAGAAAATTCAAGGA
WI-14976	35	C	T	GTTGATTGCT TCGTTCAAAG	TCAAACTAAAT CTTCCATTCTA AGC	TATTTTTTAATTGGTTGATTGCTTCGTTCAAAG[C/T]GCTTAGAATGGAAGATTTAGTTGAGGAG GGGCAGGTTGGGGGTAGGCTCAGCGGCCATAGTGCCACAAGAAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
WI-14981	31	G	T	TCAGTGGTGTT TATTGGATTTT T	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTCAGTGGTGTGTTTATTGGATTTTT[G/T]TTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTCACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80	C	T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCCT	TGATTACATTTTTAAAATCATGCTACCAGCCCATCTAAGCCAAATTCAAACACCACTCTGCATTA AATGAAGCTGCAG[C/T]AGGAAAGCTAGCACCCAACTGATCGGAAAGAAACGTA
WI-15002	72	T	A	---	---	AAATCTCTTCTTCACACACAGATGAACTTTAATAAATTACAAATGCCTTCTTGA TTTCC[T/A]TTCAGTTTAGGCCTCAAATGGGCTCTCCTCCAAGGCTGGACCTCAAAGGCCCAGTT
WI-15000	90	G	A	GACAGAAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCACAACAATAACATGTATTGAAAGGTATAGAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTCAGACTCTAAGTA[G/A]TGAAGTTGTGCAGAACTAGAAACAAAATCCACCT

Locus	Pos	Allele 1	Allele 2	Sequence (left)	Sequence (right)
WI-12323	68	G	A	CACTGGGACATA TTCCCTACCTG	AATTTGTTGATGTGGTTAAATCTTATCTCTTTTTATACACAATACTTCATGTGTACCTATGAAATAA[G/A]ACAGGTAGGGAATATGTCCAGTGCAAACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91	A	T	AAGGGACGAT TTAGTATCTAA GGCATGTCCCA GTGTTTTT	CATAAGTTGCATTATTCACGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAAGGGACGATTTAGTATCTAAAAAACA[A/T]CAAAAAAAACACTGGGACATGCCCCCTGAATTGCAAGTTGGAGTTCGTAAGAATCTAC
WI-13470	100	C	A	CCTGCCTTTAT ATTGGAATTTC GGGAGACCATG GGTCTCT · T	AATTTGTTGTTTATTTAGCACCTGAATTTAGGCAAGAGAAACATTCTACCTGAAGACTCCATGCAGTCAAATTCCCTGCCTTTATATTGGAATTTCTA[C/A]AGAGACCCATGGGTCTCCCCAAGTGAGGGAAGCCAGGGCACTCAGCCCTTC
WI-14712	38	T	A	TGAATGCTTCC AAGTACAAAT CA	TTTGGTGCTACTTGTGAATGCTTCCAAGTACAAATCA[T/A]CTCACAATACCATATACAACATACTTTCAATCACAACTCAAATATAAAAATAAACCTACAAAATCACATTGC
WI-13712	40	A	C	TTTACTTTGTT GTCATTTTAT CCATAAGGTCT CACACTTTCT TAT	TGGGATACCCTTTACTTTGTTGTCATTTTATTCTATTG[A/C]ATTATAAGAAAAGTGTGAGACCTTATGGCCTTCTGCTTATTGGGCAATATGCAATATAATATTGTGTGTTGTTAAAATTTATGCAT
WI-16163	35	C	T	TCTGGTGATGC AATTGAAATA GCTGCCAATTA CATTAACTTAC AA	TCTAAGATTTACTCTGGTGATGCAATTGAAATAA[C/T]ATTGTAAGTAATGTAATTGGCAGCATTGCCCAAAGTTAAGAGGACTATTCTTTAAACAAAGACAGTGTCTGACATTTATTTCAGGT
WI-13453	88	T	A	AATGCACAAA ATCTTGTCTCT TCAGATTTTA CATCTCTTCT AGCA	TTTTTTTATTTGCATTGGAGTGCTTTATTATATTGGGAATTGCAGTGATATTAACATTGTACAAAT GCACAAAATCTTGTCTCTTC[T/A]TGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTTAATGAACTCATTGTCCAT
WI-16167	58	T	C	CGCCACTCTAA ATTAGAGATA TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTTTTCTGATATACATT[T/C]CATCTTATTCACCACGAGCACACACGCACCACGTAGAACAGTTCCACACCTGATAAATTGCACAAGATG
WI-14482	17	G	A	···	GCAGAACCAATTAATAA[G/A]AATCTGCAAGTTTCCCAAGAAACTCTGGAACCATAGTGCCTAATGCCCTTAAAATCGATACTAAAGGAGAGAATAAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T	C	···	TGTAGTTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATACTATGTGTATTCCCAGTATCATGTAC GCACTAAAAAAAA[T/C]GTGTGCTTGCTGTGTGAGTGAACCATTGCTTAAGATAAA
WI-16156	97	A	C	TGAAGATTAA CCCAGAGTCGC AATTGTGTGCA TTTTGAAGAGA	ATCTGGTATTTGTGTATCCCAACAAGTATACAGAATACTCTATAAAACCAACCCTTCAATATTACACTAATGAAGAATTAACCCAGAGTCGC[A/C]TCTCTTCAAAATGCACACAATTAAGACG
WI-15012	59	G	T	GCAGCAAGAT TACATCAGTA CTCCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATATATAATACAGCTTTTTCATTGAAGCTTT[G/T]TACCT TACTATACTCTAGGCTATTTGGGAGTGTTCCCCCAC

ID	Pos	Allele	Primer 1	Primer 2	Sequence
WI-15100	74	G A	...		TCTTATTCACAGCCAAGAAAATACCCAATTATTCCAAATAAGCAAAATTGGAAACAGAGACTGGAGTGAGAAC[G/A]GGTTCCACCACCAAGCCCCTCAAGACAAGATGGACAAGATGGACAAGATGGTTCTGGGGTGCATTTCTAGTTGGACTTTAT
WI-14492	92	A T	GTCACCATGTTATATTTTCTTTTAAGAC	CCTTTATTTTCCAAATATAAAATTACT	TGGTACAGAATGTTAATTACAGCAGGCAGTGATCCAGTTAAATAAAATTAAAAACCTTTATTTTCCCAAATATAAAAATTACTAAATTAA[A/T]GTCTTAAAAGAAAATATAACGTGGTGACAGCTTT
WI-12002c	89	T C	...		TCTTTAATTTTATGGAATCCAGGACACAACAAGAAAAACACCCAAAAACCACCACCGGAGACAGAAGACGAGACACAACTCCTCCCCAC[T/C]GCCTCCCTGCTCTAGAGTGGGGGACAAAGTGGGGGTGAGACAG
WI-12002b	68	G A	...		TCTTTAATTTTATGGAATCCAGGACACAACAAGAAAAACACCCAAAAACCACCGGAGACAGAAGAC[G/A]AGACACAACTCCTCCCCCACTGCCTCCCTGCTCTAGAGTGGGGGACAAAGTGGGGGTGAGACAG
WI-12002a	30	C G	TGGTTTTTGGGTGTTTTTCTT	TCGGAATCCAGGACACAA	TCTTTAATTTTATGGAATCCAGGACACACAA[C/G]GAAGAAAAACACCCAAAAACCACCATGGAGACAGAAGACGAGACACAACTCCTCCCCCACTGCCTCCCTGCTCTAGAGTGGGGGACAAAGTGGGGGTGAGACAG
WI-15116	96	C T	CCTGAATATGCAATTATTTATTATGACA	GGGAGCCCTAGTTGCAGTAA	TTTTCATTTATTTTCCAGAAAAAGAAATCACATTTCAGTAACAACTTACATATAGAATTAAACTTTGTTCTGGAATGGGAGCCCTAGTTGCAGTAA[C/T]GTGTCATAATAAATAAATTGCATATTCAGGATTTTGTGAAATAGGTGATTGGGA
WI-12578	37	C T	TCAAGGCGACCACCAACAC	GGCCTAAAGGAATGGGAA	GCAAAAGCAAAGCTATGGAGGCCTAAAGGAATGGGAA[C/T]GTGTTGGTGGTCGCTTGATACTTGGTGCTTGTGTGCCATGGAGCAGAAGTCTTCCTGGTCCATGCAGGGGCGTCACATATTTAACTGCACTAATTTGGGCAAACTGTCATTC
WI-15153	40	A G	AACCTCAGATAAGTGCAGTGTCT	CCCTTATGTTGGCATTGCA	ATTTCACGTTGGCCAAGATCTCCCTTATGTTGGCATTGCA[A/G]AGACACTGCACTTATCTGAGGTTAGAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAATTACCATTTCCTAA
WI-15215	84	G C	CCAACAGGGGAAAAGTCA	TGGCTTAGAAGCTCAAATGGG	CCTTTGCTCTCTGAACTGGACCAGGATGTGAAATAATTTTGAATCTGATGCAGGTCGAGGTATGGCTTTAGAATCAAATGGG[G/C]TGACTTTTCCCCTGTTGGTGGAAAACTCTGTGAGGGTTTGGCA
WI-15225	80	C T	TTTGATTGGCATAATCACTCC	CTTGAGGACCTAGAAAGCAAAC	AGGAAAGAGAGTGTAAAGCAAGCAAAGGGATCATCATTGGATGATGAATGATTATGTGTCACGAGCACTTGAGGACCTAGAAAGCAAAC[C/T]GGAGTGATTATGCCAATCAAATTGCAAGGTTGGAGATATGCTAAAA
WI-15152	51	G A	...		AATTTGCTAGTGCAAATGACCCAGAATTGGAAGGGCTATGTAACTACACACA[G/A]ATGCACACCACAGCCATGTCAGTGTCAGTAGATCCTCTTGTCATTCAGCTTTCTTAAAAACACATCAAAGGCTGCA
WI-15123	55	C T	TTGCTTAAGGGCAAACAGAC	TGTTAGTGACAGACAGATAAAC TTAGGATG	TGACTGTATACCAAATGCTGTGCTTAATGTTAGTGACAGAACAGATAAATAGGATG[C/T]GTCTGTTTGCCCCTTAAGCAATTTACAACTCACTGGGGAAGAAGAACATGCAAACGAGATAAAAACACAAT

ID	#					
WI-15182	49	C	A	GCACAACCAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACTAGCTAGCTGCACAACCAGGCAAACATA[C/A]TGCTGGATTAACCC ATGCTAATGGGTTACCTTTATTTAGTAATCATGGGTCCCTCATAAGCATGGTCCAGATCCG
WI-15198	38	T	C	GGGCCCTTGGC ACTATG	ACTTATCCGTC AGGCAGAGTAG	GTGGACCTCTACAAGTACCATGGGCCCTTGGCCACTATG[T/C]CTACTCTGCCTGACGGATAAGTTGGC ATATGGTTCAGATTGCTTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTCTT
WI-12601	42	T	C	CATTTATTGAG TATTCTTGCTT TGAT	GTTGTAGTCTT ACATGCTTACG TAGAC	TCAAGTGGTAAATAGCCATTTATTGAGTATTCTTGCTT[T/C]GTCTACGTAAGCATGTAAGACT ACAACATTACGACCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAAAAACATTTGTCATTCAGAT T
WI-14510	104	A	T	TGGCAAAATA TGCATAACAA AA	TTGAAAATGGT TAAACTGGCA	ATGTTGAGAGTAAATATGCCTACATATTTAGTGTAAGTACACCCCAGATATTTTGGGGAGAAGAG TTGTTTGCTTTTTGTGGCAAAATATGCATAACAAAAT[A/T]TGCCAGTTAACCATTTCAAGAGT
WI-15239	57	T	C	CATTTGCAAT AAACACCATC A	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGTGCATTTGCAATAAACACCATCATT[T/C]CCTGAG TCCACAGATAAGGTCCCGGAGAAGGGCTTCCCCTCCTTTCTGCGTGGGTTGACGTTCCCAGGCGAGT GAAGCCTTTTCTGGAATG
WI-12634	52	T	C	GCATCATATG AACTGTCTAGC AGT	GGACAAATTGT AAACATAGCT AATAGC	ATGAGTTTATAAACTGGAGACAGCGCATCATCATATGAACTGTCTAGCAGTATTA[T/C]GCTATTAGCTA TGTTTACAATTGTCCTGAAGGGGTCTAGATGTGTACACCCCAGAAAGTGGTGATTCCTGA
WI-15249	34	T	C	GGGCTTGACAC AAAGTTCTAA A	GGAAAGCCAG AGATTTTTAAC AA	TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTT[T/C]GTTGTTAAAAATCTCTGGCTTCCTGGCTGG TGAGGAGGCACAGGCTGGGGTATCCCAGTGGTCCCGCCATCGTGTTCCCTCCCACTCCCCAG CCCACATTCTTGGCTCT
WI-12159	28	C	T	AAGACACCGT GCAAATGC	CCCTCTCCTCA GTGCACTTT	CTGTCCGGGGAAGACACCGTCGCAAATGC[C/T]AAAGTGCACTGAGGAGGAGGGGAGGGTCTGTGACTC CCAAACCCTCGAATATTTTATGAATCTAAGAGTCCAGACGCAGTTCATCCACGGAGATCTGC
WI-12648	41	A	G	CCTAGTGGCAT TAAGGATGC	AGTGGACATCC T	TCCCCAGATTGTATGGAAATGCCTAGTGGCATTAAGGATGC[A/G]GTAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCACTACTCCATGTTAGGTGCTTTACTTGGATTATCTCACTTAAAAACCACA
WI-12684	64	G	T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAAATATTCAGTGTAAACAGCTGTGTGC[G/ T]CCATTTAGGCTTGTGTTGTCCATTTAGAGAGCACAGGAGAGAGAGAAATTTAGCATAATTCTT
WI-15260	75	G	A	AAAGGATGAA GCTAATCATG GA	TCTCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAAGAGGTCGACACAGCGGACACTGTCATAAGTGGAACAAAGGATGAAGCT AATCATGGA[G/A]GCAAGCTCCCTGGAGAGAGACAAGAGGGACAAAATCAAGAGCTGGAGAAATTAA TCCTG
WI-15325	39	T	C	CATGTGGCTGG GAGGC	CCTTCCACCAT GATTGTGA	AAGGTTTAATGGACTCACAGTTCCATGTGGCTGGGAGGC[T/C]TCACAATCATGGTGGAAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGGAATGAGAGC
WI-13936	123	C	T	C AGTTGGCATTC AATAGCCTAT	TGAAACTCCCA CATGGAGTT	TATTTGAGTATTTCATCCATGGCCGCTTCTCACTCCCCTATACATTCTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTCAGAACCTATGTATCTTCAGTTGGCATTCAATAGCCTATC[C/T]AACTCCATGT GGGAGTTTCATAATAA

Marker	Pos					Sequence
WI-14528	62	T	G	TTTTAACTTTT TCTGGATGGTA TAAAT	CTCGATTAGCA CTTATTATAAA AATTAAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTAATAATATATTTAACTTTTTCTGGATGGTATAAAT[T/G]TTGAATTATAAATTTAATTTTTATAATAAGTGCTAATGGAGACATCACTGGGTATAATTGA
WI-15347	74	C	T	GACTTCAAAG GAAAAGAACA AGTCTTTT	TCACTCCCCCA	TATTTCTTTCGGTTCGGATGCAAATCAAAACAAAAAAATTTAAAAGAAATGTGACTTCAAAGGAAAAGAACA ACAAATTT[C/T]CAAAGACTTGGGGGAGTGAAGGCAGAGGCCTGGTGCAGATGGACGAGGTCTGCAGA CG
WI-14546	95	C	A	CCAATTTCTAG TGATAGTAGA GGACTCA	AAGGTGCACGT GCAGG	GTATTTCTGATGCTTGACATCTGGGCATTGCTGTCTCTAGAGAGACTACTTCTCCTGGGACCAGC CAATTCTCAGTGATAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTCATATACAGATCA
WI-15353	37	G	A	---		TTTATTGGCTGTCTGTCTGTAATACAATGTGGTGAAAAC[G/A]TCTTAATTCAGGACATCTTCCACCTTG TTTGGCTTCCAGTTGTACTGCAAGACCAGTGTCAGGCACATAGGCTGATTAATCAGTGG
WI-14580	100	G	A	CATTCCCATCT GTCTTGCA	CCGACCAAGAT CCCTCC	AGAATTTTTCCTTTTTAACAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAAATAC CTAGTTATTATACACATTCCCATCTGTCTTGCA[G/A]GGAGGGGATCTTGGTCGGCTTAACA
WI-8540	73	T	C	GGCCTGCATTT GGCTTA	GCCCTTCTTT TCAGGCAC	CCAGCTGGAGGTGGAATAAATGCGGCAACCACAGAAAAAACACACAGCTACACACAGCCTGCATT TGGCTTA[T/C]GTGCCTGAAAAAGAAGGGCGACCTCTGATAAAGAATGTCT
WI-8039b	97	T	C	---		AAGTAGAACACAATAGAATGGCTCAAAAATATCAGAATGCCACTACGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTTCAGTTAAATATGTA[T/C]GTGTCCGTGCATGTCATGATTAAATATCCTTCT TACCACAGTCACCCTAAAGAACCAAAGCTTAGGGACTAGGGACACAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGTGAGATGATTAATGCCGAGCCGACCACCCACA
WI-8039a	87	T	C	---		AAGTAGAAACACAATAGAATGGCTCAAAAATATCAGAATGCCACTACGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTCAGT[T/C]AAATATGTATGTGTCCGTGCATGTCATGATTAAATATCCTTCT TACCACAGTCACCCTAAAGAACCAAAGCTTAGGGACTAGGGACACAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGTGAGATGATTTAATGCCGAGCCGACCACCCACA
WI-8044	107	C	A	---		CACAACATTCAGAAGTTTTTCTGCATTGTGTCTTCTGATGTCTAAAAAGATTTGAGCTTTGACTAT ACGATTTCCCACACTGAACGCATTCATAAGGTTTCCCC[C/A]AGTATGGATTCTCTGATGATTAATA AGCCCCGAATTCTGGCTAAAGGCTTCCCACATTCAAGACATTGTAAGGTTTTTCCCAGTGTGTGGAC TCTCTGGTGTTGCACAAGAATGGAACTTCGGCTGAATGCTTCCCACACT
WI-8550	32	G	A	GGGAACATCA ATGCAACAAG	TTTGTGGCTTG AGTTTACAAAT T	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAAACTCAAGCCACAAACTTAGTTA ATAATCATGGTTAAGGGACATTGCCAAAGAGCAACTGATGCCTCAGTGAA
WI-8057	87	T	A	---		TATTAGATAAAACCCTTGTTCCCGATTCAGGATGTTTAATTTGCTTCTCTTTAAACTCTGTGACTTTT CCTGGTTCAAAAGGACAGT[T/A]GATGGACAGCAGCAGAGGAGTGGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACTCTGTGGCCTCACAACTGCCCCCGTCAGGGGATGCTGCCTTCCAGCCCTAAAG ACACTAGGGCTTTCAATGGACGGGGTGTTGAAGCAGCCAGATGGTAAGG

ID	Pos				Sequence
WI-6192	91	A	G	GACTGCTAAG GATTTAATTTG GAT / TGAAGTGTTAG ATGGCTAAGTA TTAAAA	AAGAGGAACAAATTAGCTCAGTCCAACATGATTGGCAGTTGGCATATTCTAGTGAGCAAGTGTTCT GACTGCTAAGGATTTAATTTGGAT[A/G]ATTTAATACTTAGCCATCTAACACTTCAAGCATAAC
WI-6194	105	T	A	CACATGGCAA TGATAATAAA GAAA / TCTATCCTCAG AGTGTAGTCTG CA	AAGTGATGTGTCCTCACAAATACATTCTCAAACTCAAACACATCATGCTTGAAATATCACTGAACTT GTCACCAAAGAAGTCACATGGCAATGATAATAAAGAAA[T/A]ATGCAGACTACACTCTGAGGATAG AGCTCTAAAGAGTAAAAACAATGGAAATTGGAAAAAATAGGAGTAAA
WI-6213	164	C	T	...	CATATGCTGCTTTATTTCTGTAAGGATACACTGAAACGTTAGATGATAATAGCTAATGACAGAATGT AGAAATGAGGCATCAGCTTCTCTAACCACTCTCACAAGATGTTAGTATGTATTGTCATTACACATGTTT ACTTTTGATATTGTCTCATTATACTATGT[C/T]TATATAATAAGTGAATAACAGTAAGTAGGTGATCC TGCATTTCAGGTAAGCGGTAGGTGGAAATCCAGATTTCCTCTTGAGGAAAA
					CGGGTTAAGAAAATACCTTAAATTTAGGTAAAATAAAGCTCAAGGAGGTGGGGCTGTCATCTGTGGTG TCAGTCCTTCTGGCCCCCTGGCTGTGCAGTGTGCCTTGACAAGCAGCTCATTCAAG[C/T] GGCCCACCATGGCCCTAGGGTCGTCGTCAACAAGTCCAGCAGCAATCATGGCGTTCTCGTATATCTGATCC AC
WI-6217	131	C	T	...	ATAGTCTTTATTTGTCAACGAAGGCTACACGGGATCACTTCTGGTTTTGTTTTTATGCTTTTTTTTC TAGAAGGTATCTACATCTGCATTATTTTACAGCCTTGGTATTTACACAGTCAAGATACAGTGTTA GAAACACAAAGTGTTGAGAAAAAAACTTCTCAAAATT[G/A]GTTCCAGACTTCAGGAAAATGATT TCCACATGGTAAGGCAGAGTCTCCAGTGTTGGTCATCCGAAGCAGCTTG
WI-6238	175	G	A	GCATTTATTCA GGGAAAACTT TAA / CTGTTTTTGGA GAAGACAAAG AA	CTTGATTTAATCAGGGCTTTGGGGTCATAGGGGGATTAGTCACTGTCACAGTCATAATAATGCATTTA TTCAGGGAAAACTTTAAT[C/T]TTCTTTGTCTTCTCCAAAAACAGCTGCTGAACACCTCAAATTAA GGGATGTTCATCTAAAACACCTTTACTGAAACTTGATTCCTTGGGCCAGAGGAAGGTCTTTACTGTAG
WI-6272	86	C	T	CCCAGAGAAG CTCTGTCTGC / CAGCCATGGCT TTGCAG	CAGAGGGACTTAATGCAATGCCTATTCGGGCAATAAATGAATACTTGATGCATTCATACAGGCAAGAA TCCCAGCATCCCAGAGAAGCTCTCGCCCGATTCCCTGCGC[G/A]CTGCAAAGCCATGGCTGCAGACATCAGGGAAGCT GGTGCCAGTTGCAGTTCTAGTCTCCGCCTCTCCAGTCTTCTCCTCTCTCCATTCTTCTGCGCCC TCTG
WI-6303	96	G	A	...	ATGCTTTTGCATGATTCTAATTATTGCCTTTTCAGAGCTCTGCTGGTAAAAGTGGGGTGCCATACA AACAGTCCCTTTCCAGCCCAGCGTGTCATGCATCCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAACTGCTGATAGTAGTGTT[C/T]CTGGTT CTTCCCTTTTACATTCTTTTGGGGGA
WI-6315b	193	C	T	...	ATGCTTTTGCATGATGATTCTAATTATTGCCTTTTCAGAGCTCTGCTGGTAAAAGTGGGGTGCCATACA AACAGTCCCTTTCCAGCCCAGCGTGTCATGCATCCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAACTGCTGATAG[T/C]AGTGTCCTGGTT CTTCCCTTTTACATTCTTTTGGGGGA
WI-6315	187	T	C	...	

Clone	Pos.					Sequence
WI-6375	28	A	G	GGTTTATTGCA TATGGAAATC AA	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAAATCATTAG[A/G]TATCTTTACAAAAAAAGGTTAGAATAAAGATCTC ACATTTGAAAGGCACATATGAAACATTTATAGCAAGCAAGGGCAGTGAGCATCAACAA
WI-6409b	112	T	A	---	---	TTGTGTCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCCTCCCACCCCTATATTTAA[T/A]GCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73	A	T	---	---	TTGTGTCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAATTCAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGCTCCCCTCCCACCCCTATATTTAATGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6523	165	G	T	GCTAATCCAGT AGAGACTGAA GCTG	AGATGCTTAGG GAAGGTTGATA CAGC	CTAATATAATCCTGGGCACATGGATTCCAAGAGAGATTTGCAGCAGATTTCATTATAGTTACTTAA CAGCTAAATAATAAGGTGTATTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTGAAGTG[G/T]TATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6554	195	C	G	---		TCTCCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTCATGAGAGCAAGGGAAACAGGAAGATGGGC TCCTGGAGTCCAAACAGGATGTGGACGTCCCTGGTAGTTCTCTCTTTCACACAACTTTTCCCTGAGA ACTGTCCCAGTCAGGTGGACCTTCACAACAACAGCTAAAACTCTGAGAGAAAAC[C/G]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAA
WI-6558b	68	C	T	---		ATTGTAATTAAAATTTACATGGGCCTATTTATTAAGGACATTGTGTAATGTTCCACTTGTTTTAAA [C/T]AATTACAAACATGTGGCTTAAAATAATGTACAGATCAATGTAACAAGTTTGAAAAATGGGCG
WI-6558a	42	G	C	---		ATTGTAATTAAAATTTACATGGGCCTATTTATTAAGGACATT[G/C]TGTAATGTTCCACTTGTTTT AAACAATTACAAACATGTGGCTTAAAATAATGTACAGATCAATGTAACAAGTTTGAAAAATGGGCG
WI-6629	75	T	C	TCTTTTCAGAG AATAAAAGTT GTCATA	TGACACAGCAT CCATTGCT	AACCAAACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAATAAA AGTTGTCATA[T/C]AGCAATGGATGCTGTGTCAGAAGCTACTGCCAATAAACTTAAGAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCAGGGATGTAAGAGTTAATGGAAGAT ATCGTGAGCCAAAAC
WI-6644	134	T	C	---		CTGCCCTGAACCCAATCAGATTTAGTTAAATCAATCAATCAAAACTCCAGTCTGTTTCTCTGTCTTT TTACTTAGCAAAGGAAAACTTTAGTGAATGCTACTTGACAAGAAGAAAGTCATTTCTCAAGCACA[T/C]ACCCAAACTTGAAGGTGATTGAACCCAAAATAATGGGTGGGAAACCACCAAATGAGGTGGAGGA ATGAGAAAGATGTGTGGGCCAAGCTACTGTTTATTTTGATGTTGCCAAT
WI-6690b	106	C	T	ACATAAAAATA TTGCAGTGTAT TAGCC	CAGACTCTGG AGCCACAGC	TGCTAAACACCACCATTATTAAGGAGTACTAGGAAAAACTACCAAACACAGCATGTGAAACAGT TGGGCACGGTGGTAAAGGCACAGACTCTGGAGCCACAGC[C/T]GGCTAATACACTGCAATATTTTA TGTTTAGCAAGATTATAGCTGGTCTGTGTATAACCAGAAGAGAGCGGGTATCTGG

Marker	Pos	Allele		Fragment A	Fragment B	Full Sequence
WI-6690a	28	T	C	AAACACCACC ATTATTAAGG AGAG	GCTGTGTTTGG TAGTTTTTCCT	TGCTAAACACCACCATTATTAAGGAGAGAGT[T/C]ACTAGGAAAAACTACCAAACACAGCATGTGAAAC AGTTGGGCACGGTGGTAAAGGGCACAGACTCTGGAGCCACGCCGGCTAATACACTGCAATATTTA TGTTTAGCAAATTATAGCTGGTCTGTGTATAACCAGAGAGCGGTATCTGG
WI-6770	53	A	G	CAAACCCCAA AACATCACA	GCTTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTAATGACACAGATCTTCCCAAAGTAATCCAAACCCCAAAACATCACA[A/G]AATTATTCAT ACTATTATACACTCCAAAAGCAAAATACTTCAACTGCAATCC
WI-6686	151	A	G	GCATTCTTCCA AAACAAAGA A	CCTTGTAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAATCAGCTAGCACTAATCTTGACCAAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTAATTTAATTTAGATGAAATTTCACATTAAAACATGGTAACTCCAAGCATTCT TCCAAAAACAAAGAAT[A/G]AACATTGGAATAGTAGTCACTTACAAGGAC
WI-6761	32	C A	G	GATCTAACAG CTGCAGGAATG G	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAATGG[C/A]CTTCTTCCTTCCCAGCTTTTGTGAACAAAAC AATTCTCCTAAGGCATCAGAAAAGCACTGAGTGCAAAATGGGTTGTTCAGGTACAAGGTCTC
WI-6844	225	T	C	...	...	TAAAATACTGCCAACTAGCATTACGTCCACTCTTGCATCATTAAAAACAAAGGGTATTCCTCCTTG GTATTTTCAAATGATGCCATTATACAATAAACGAAGTTAGAACTTAAAATGCACCCTGATTAATATG TAAACTGGTAATTTGTTTAAAAAGCATAATAATTTGGTTCCTTTCTTCATAAAATGGAAATTTAAA TATTTCTTCTGATAGTCTTGAGGT[T/C]ATCATTATGAGTAGTGCAAAGTGTG CGGTTTGCTACACTTTAATGTGGTTTTTTTAAGGGATTTTTTTCAGGTCTTGTCGTCAGCAACATCAA ACAAAAGGTACTGAGTACTCCACAGGGTACAGAGTGCTGCCAA[A/G]CACCTTAGAAAAATTACAT GACACGGAGAAAATGCGCCCTCGTCCTTGCTCCTTGAAGAGCTTACAGTCTAGGGATTGACAACTCACAGT CTTAGGAACTGGGCAAAGTAAGGCAAATTCTTCATCCCCCTAGAGCTATTGTG
WI-6824	112	A	G	GAAAAATGAG ATGCAGTTAA ATGCAGTTAA TCAATTC	TCACTTTGTGG CTTTAATTAT TCT	GTACAAAAAAGCTGAGAAGAGCCAACATTCTGATAGGTACGGACAA AAGAGCTCCTCAATCAAGGAGTTACATATTAGTTCTCACCATGTGAGAAAAATGAGATGCAGTTA AAATTC[T/C]AGAATAATTAAAAGCCACAAAGTGAAACTGTTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6889	139	T	C	AATTC		TCCCCAGCTCATATTTATTTGGGCACAGAGTGGGCACTCAAATATCTGATGAACTGAA AAGAGGTCTCCTTAAACAAGTATCATCTCCCGAAGAGAGAAGTCCAACCATATAAAATGTATGAT CAAGTCCCAGAAAACTTTGCCTTCCCCAGGAATGTGTTTCTAATTGGTTCAAAGCACACTGGTTCC CACTTTTACCACTT[T/C]CATGACATTGGACAATAGTACTACTCTTTCTAC
WI-6911	216	T	C	...		GCCAGTCTCTAGTAAGTCTCTAGGGACATGACCAGAAGCCCCTGTTCTATATGAAGACAAAC AGGTGGCCATACTTGGGTGGAGGGATACCGCTGCTATTCCCAGAT[G/C]AAGATTTGGTGGAAGGAG ACCATGACAGATGACAAACGGAAACAGTTTCTCAAAAACAGAGAGGTATGA
WI-9413	112	G	C	...		AAAAGCTTTAAAAAAAAAGTGGTGCTATCTTTAGAAACACTTTCAGCAAGATCAAGTAGCCCAGCT
WI-9557	74	C	T	...		ACAGCCCT[C/T]GGTGCATCTTAACCCTCTCCTCCCTTT

ID	Pos			Flanking	Sequence
WI-9617	37	G	T	---	TGCTCTTTTATTCACGTTCACAACACACGCCGTG[G/T]TGGCACAGTCTACCAAAGTGCCCGCAG CGCCACGCTTGGGCCGGAAGGTCTCATTCTGTTCGTCTCTATGGACTGATTGAATTTGGGATGGCCAG CTCCAGAATGTTCCACGTGGGGGCACTCTGTGGGCAGAGGCTGAGCCCTGCCCACACTGGCACCA AAGAGGTTGCACGATGCAGCTTGCCAGTGCAGTGGGTCCAAGCCGGGGTGTGCTGTG
WI-9657	121	T	G	---	AATGCTGGAGAAAACATCAACATTGAGTTGACATTTGTTTGCTGAAGTATAGCTACCATCCACTAT CATGAATTTTTGTTTCATTACAAATGATAGAAAAGCCAGATTCTCAAAATAAAG[T/G]ATAATTCTT TGTATTAAATAAATGTTTATAAATGTTTATGAAGCTCATTACATTATCTTTTTAAAAAGTAAAA TTTTAGAACATATGACGCTTTTCATATTAATTAATGCTTTTGATATAGATTTGAGG
WI-13119b	114	G	C	AAAAATTAAC CCTCCCAAGTA CAGGTGTGGTG T GCTGGGA	CAGGGTCTTGCTCTGTCTCCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTG[G/C]ACACCACCACCTGGTTAA TTTTTTAATTTTTTTGTAAAGATAGGGGTCTCACTATGTTGCCCGTCTCAAAAAACAAACCAACTAAC
WI-13119a	51	C	G	---	CAGGGTCTTGCTCTGTCTCCCAGGCTAGAGTGAGGTGGGGACTGGGACTACAGGCATGTGACCACCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACCACCACCTGGTTA ATTTTTTAATTTTTTGTAAAGATAGGGGTCTCACTATGTTGCCCGTCTGTTCCCAAAAACAAACCAACTAA C
WI-13112	71	C	T	TTAGAAATTTT GTGTATTATAT GGAAAAAG TCATAAAGAC TACAGACTTA AGCTTTTT	ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTAGGGATCATAAAGACTACAGACTTAAGCTT TTTT[C/T]CTTCTTTTCCATATAATACACAAAATTTCTAAATATCCTAAAAAAGAAAATATAAATAGT TTCAGTATGTATGTAGAGTCACATACTGTTGCCCGTGTTATTAATTGAGGGAATAGGCCAAT TT
WI-12988	36	C	A	CAAAGTGTACA TGGTACGTGCT CTACTGATGCT GTTT	TGTTAACATTTTTATTGGTACGTGCTCTCAGTACAA[C/A]AAACAGCATCAGTAGTGTACACTTTGAT AAAAAGGAATTTTAGCTTAGTAGAAAGAAAGCCCAAAGGTACAGAAGTATAATGAATATGTACAT CTTTATGGAAACTGTTTGTGTGACCATCTTATCTTCCCGTGGATGAGATGTATGCACACAAGT AAA
WI-13020a	108	G	A	CTAATAGTGG AACCCTGAGA CTTT CATTATTAAAC CCCTTTGCAGA	TGCTATTCATGACGACACGTGAGACAAATATTCTTATTTACAGATGGAAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGGAACCCTGAGACTTTA[G/A]ATCTGCAAAGGGGTTTAATAAT GCAAATATCACATATTTCCATTTTAACACCATATTTAAGTTTTCCATTTTCTTAATAGAAAATGA TAAAAAATGTTTCCCCAATAT
WI-12837	87	A	G	CCATATACAT ATATCAAGGT AAAGTCCA GCCATAGGAA ATGCTGTTTTT	TGTATAAAAATCCAACTTGTTCCACAAGTACATATGTCCTATGATTTTATGCATCACATCCATATAC ATATATCAAGGTAAAGTCCA[A/G]TACAAAAAAACAGCATTTCCTATGGCCAGTGTTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAAATGAGTATTGCACACTAAGCAGGAGGACGAGAAGCA AGTTGTGTCCA

Marker	No.			Primer 1	Primer 2	Sequence
L42611b	50	G	C	---		GTCCTCAGGCCCTTCTCTGGCTGCGAGAGCCGGTCTTCTCAGGTTGCCTGCTG[C/G]C]TCTCCTGCCTCTAGTCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACTTCTCTGTCTATACCTGCCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTCACATCAATGTATTCACCACTGGAGCTTCACTTTGTTAC
L42611	34	T	C	---		GTCCTCAGGCCCTTCTCTGGCTGCGAGAGCCGGTCT[T/C]CTCAGGTTGCCTGCTGCGTCTCCTGGCCTCTAGTCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACTTCTCTGTCTATACCTGCCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTCACATCAATGTATTCACCACTGGAGCTTCACTTTGTTAC
WI-1172b	179	C	T	A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG	TGAACGTGTGGTTAAAACTAGGCAATTGGTTAAAAATCAATTTAAAAAACAGGCCTAGAAACAGTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAAATACCATTTCTGCTTTCAAAAGAAAGACATGAGGGCTTCTGAAGAAATGGCTGATACCAAG[C/T]CTGCAGTGAAAAATGCACATGATGAGCCTGGAACATGTTGT
WI-1172a	17	C	A	---		TGAACGTGTGGTTAAAA[C/A]TAGGCAATTGGTTAAAAATCAATTTAAAAAACAGGCCTAGAAACAGTGGTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAAATACCATTTCTGCTTTCAAAAGAAAGACATGAGGGCTTCTGAAGAAATGGCTGATACCAAGTGAAAAATGCACATGATGAGCCTGGAACATGTTGT
WI-1177	35	G	A	GCAGATTGGA AGTGTGAAAA A	CACTTACATTT CTGAATATTTA GACTCTTT	AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAGAGTCTAAATATTCAGAAATGTAAGTGCTGCCCTCAACTGTTCTTTACCCACTAATTCTGCAATTTGAAAACTAGATTGAATTCCTTTGCAAAACCCTTGCAAATCATGGATAACCCGAGTTAATTAAAAGACATTAAACATGGCCTGGTG
WI-1231b	141	G	A	---		TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCCATATTCCAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTC[G/A]TTATTCCCTGAACGCGCCCTTCTTCCTTCGTAGTGACATTTAAAATCCACTTTACACATTCGGACC
WI-1231a	126	T	C	A	GGCTCTTTATT CTCCTTCTTTC	CGTTCAGGGTG AGGGAATAA	TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCCATATTCCAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTTATTCTCCTTCTTTCA[T/C]TAATTTTAAAATCCACTTTACACTTACCATTCGGACC
WI-472	114	G	C	ACATACATAT CCATTATACA ACAGAAAAG	GACCTTTCTT TCCAGCCC	GAAGGCAGGACTGTGTTTGGAGGACAAAAAGTAAAATCTTTTATATCTTTATTTTTAATTTTATTTTTTTCAGGCATATAGACATATCCATTATACAACAGAAAAG[G/C]GGGCTGGAAAAGAAAGGTCAAGTGAGATTTCAGATATTCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT

WI-478	46	C	T	GCATGTCTGTG TTACTCTATTT TGTTC	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGTCTGTGTTACTCTATTTGTTC[C/T]AGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATACTGCTTAAACACAAATAGAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAGGCTACCATCCAGTACCTTAGCACATTTAAAAATAAAAACCAAC ACTGCCCA
WI-533	29	T	C	ATCACAGCAG AGTACCTTTCT AACT	CCTTCCAACCT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTTCTCTAACT[T/C]ATAAGATTGTGTAGAGGTTGGAAGGAGGAGGACAGGA CTGTTCTGTTGGTATAATGACCCGTGTCCAGTTAATCCA
WI-601b	112	T	A	...	...	TCACTTATCTCTTTTTGTGGTGAGAACACTTAAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGGCGAACAGAAGAGGTTTCATTGACTCCTAAACTGAGTAC[T/A]CAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74	C	T	...	...	TCACTTATCTCTTTTTGTGGTGAGAACACTTAAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAG[C/T]GAACAGAAGAGGTTTCATTGACTCCTAAACTGAGTACTCAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107	A	G	CTCCTTCACAA CCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAAACAGACACCCTCGGCTTCTTCTCCACAGTCCCACATGGGTGCCAAACAATCCCACATTCCT ACATCCTCCCCACTGGGCTCGCCTCCTCCTCCACAACCTCACCA[A/G]ACTTGGCTTACCGGGAAGCATAAA GCCAAAGCATTTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36	G	A	ACTGCTTGCTT GTTGATTTAAT C	TTATTCTAATC CCACATGACAG C	ACTCACTGCTTGCTTGTTGATTTAATCAACCTAGCC[G/A]GCTGTCATGTGGGATTAGAATAAAATA AACACAAAATGAAAACACGATTGCTAACAAAGCAGATTCTTTTTCAAGGCACACGTAAAGAT AATAACTTCAA
WI-991	37	A	T	...	...	TGCATTCATTATGCACCAAATAATAACTTCTGTACAT[A/T]CATTATTGTATTTCATTATCACAAAAT TATGAGTGAGGGATGATTGTTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TCCCAAAGTCACAAAGTTAGTGACAGAGCCGGGATTCGAATCCATCAACTGAATCCAGAGAAAAT GTTCTGCATCACTGTACAACACTGACTCCTTTCTCCTTGAAAACAGGC
WI-1011	70	G	C	CAGTATCTGA AGTTTTTGTCT CCCA	AGGAACACCTA CAAAATGACTT CT	CTTCCTGACCTGTTTGCAGTGGGATACTGTGTTTTGAAGGCTCGTCTGCTCAGTATCTGCTTCCATTTCTCTAATACACTGC A[G/C]AGAAGTCATTTGTAGGTGTCCTGGCGTTTCTGCTACGTTTCATTATCAGATGGCTGTTTGCTGCATTCTGTGCACTGAAG CGTCTTAAGGGAGGGCTTGCAGAGCATTTATCAGATGGCTGCAGAGCGAGGGAACAGCATGGAGAGA TTCATGCAGAAGGTCCATGAGTTTACAGAATCTCAAGGAAGAAAGGCCCCTAGAGATGACACCAGAA ATGAGAGTGGCTTGCTCATGAAAATTGGACAGCAGCATGTTCCAAGCAGAGGGAACAGCATGGAGAGA AAAATCATACTCTATCCACGTGCAGAAAACTGGCAATTAGTTTGT[A/T]TTACTAAAACACAAATGT TTAACTTGGGGGTCCACAAACAAGGATATGTTGGCAAATGGTATTCTGTGATG
WI-5381	178	A	T	...	...	CTATGTATTCCATCTAGCAAAGCAAGACTATTTGGATAAGTTCACAAAGATGAGAACAGGTCCTA GAACCTCAG[G/A]ATCGAAAGAAAGAAGTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAAGGTA AAAAAATAAAAAATAAAGAAGTAAAGAACTTACATCCAGATTGTGCATTTCTTATTTGCACCCTGTTTGT
WI-5791b	76	G	A	...	...	TAGGAA

WI-5791a	44	C	G	---		CTATGTGATTCCATCTAGCAAAAGCAAGAGACTATTTGGATAAGTTT[C/G]ACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAGGTA AAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTCTTCTTATTTGCCACCCTGTTTGT TAGGAA
WI-5406c	120	C	T	---		CACTCTGCTGTTGTCCATGGGTGCCACAGAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACC[C/T]TTATGAGCCCAC ACTTCTCATTTCCTTAGAATTCTTGGACTCTGTGAAGAGGAAGGAAGAAAAAGAGAGGAGGCAA GG
WI-5406b	118	C	A	CCAGGATGTC AAGGTGAGAA A	AATGAGAAGT GTGGGCTCAT	CACTCTGCTGTTGTCCATGGGTGCCACAGAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAA[C/A]CCTATGAGCCCAC ACTTCTCATTTCCTTAGAATTCTTGGACTCTGTGAAGAGGAAGGAAGAAAAAGAGAGGAGGCAA GG
WI-5406a	42	A	G	---		CACTCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAG[A/G]GCCACTTCCACAGATGCAACAG GCCTTTGAAGGAGCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCTATGAGCCCAC ACTTCTCATTTCCTTAGAATTCTTGGACTCTGTGAAGAGGAAGGAAGAAAAAGAGAGGAGGCAA GG
WI-5798	48	G	C	TTTATTCTCCC TTGTTTTCTTT TG	ACTGTTAGAAA ACCAGTATTTT TCAAT	CCATTCCTTCTTCCTCCCTCTCCCTTATTCTCCCTGTTTTCTTTTG[G/C]ATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTATAAACATGCATAGTTCTATATGGGTATCA
WI-5415	54	T	A	TCTTCATGAAT TCATCTTTCAG TTT	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTTAAGCACGATTTGTCTTCATGAATTCATCTTTCAGTTT[T/A]TAGATCGGAT CATGAATTAGTCCAGGCTTTAGTTGTAATCGAAATTGGA
WI-5437	41	C	T	TCCCAGAGAA AAATCCAAGA G	AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGCAGACCTCCCAGAGAAAAATCCAAGAG[C/T]CTTAAACCATATTTGTGTTTA GAAACTCCTGTGCCAACCACTCTGATGTGAGTGAC
WI-5481b	131	A	G	TGTCATTTATG CTGCAGTCG	TTACTTCCAGG CTCCAAGTATT	AAGCCAATTCACATTAGTGTGATGAATTTACAGTATCTAATGCAGTATCTATTTGTCATTTATGCTCGTGTTCAAC TCTCTGTTTTCAAGAGGCTGGAAGTAAAGACTTGGCTATTTCACAATTA ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTCACAATTA
WI-5481a	29	G	A	CCAATTTCAC ATTAGTTGATG AATTT	CCCATGCATTA GATACTGTAAA ATT	AAGCCAATTTCACATTAGTTGATGAATTT[G/A]AATTTACAGTATCTAATGCAGTATCTATTTGTCATTTATGCTCGTGTTCAAC AACTCTCTGTTTTCAAGAGGTAGTAAAATCTATTTGTCATTTATGCTCGTGTTCACAATTA ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTCACAATTA
WI-5492	38	T	C	---		TCATGAGTCTTCTTCAAAGATGCTTGTTAAAGTCCCA[T/C]CAAAGAAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA

ID	Pos			Flanking	Sequence
WI-5826	134	T	C	---	TATTTTTTTTCTCAATTCCTGGAGCACACCATGTCTTTCTATTTCATGTGCTTCACATTTATTTTTTTTCACTTAGTTAAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATTCTTTAG[T/C]TTTCAAATTAAATGCCACCATAGAAATAAITTTCTAACCAACCAGCCAAACAGCCTCACTCTTCCTTCCTTGGTGCATTTACTCTTTACAC
WI-5546	40	C	T	CCCAATACTTTTCAGGTGAA CCTGTATTTA GCAAACATGGG A	CCTTATAAACCCAATACTTTTCAGGTGAAAAAAAGGGAAAA[C/T]ACCCATGTTGCTAAAATACAGGAGTATAAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAAATTCTGATGTGGGAAATAT
WI-5552	97	C	T	GGCACCAGCCT TTTTTAGAGT CCCAGG	TGTTTGTTCTGCACCTCCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTGATTGAGCGGGGTATGGGTGGGGTATCGGCACCAGCCTTTTTAGAGT[C/T]CCTGGGCAATTGTGCACTAGTGTCAGA
WI-5836b	161	C	T	---	TAAGTTGATTTAAACACTCTGTGCCTCAATTTCTCACCTATAAAATAAAGATAATAAGTATCTAAAAAAAAGAGAGAGAATTAAAAGTGGATAGACATGAATAACTCTGATGATACTGGTTGTATCCCTGAATCCTGCAATATACACATGATTCAATGAT[C/T]CCATTTGAAAATTAAGCTTTTGAATTGTTTTCCAATG
WI-5573	58	C	T	TGAACAGTTGG GTTCATAAGG AGGTGGGGA TC	TCGGGTATTAGGATGCGTTCACCCTCGATGATGATGGGGCGTTCATAAGGAGGTGGGGA[C/T]GACACATTACTCTCCAACTGTTCATCAGAACACTTCAACAGCG
WI-5850b	134	G	A	---	CAGGACCTTGGAGCCTTGCTGTCGTTGTCCTTCCACCCTCACTCTTTCTGCCTGCCCATGGGTGGGAGCCTCTCTCAGGCTTCCTCTATGCACGCGTCTATCTTCTATATGGGGCAATATCCAATTC[G/A][TTTTGCCATTTCCTGTATATCAAACAGAGAAGCAGAGGGTGG
WI-5850a	92	C	T	---	CAGGACCTTGGAGCCTTGCTGTCGTTGTCCTTCCACCCTCACTCTTTCTGCCTGCCCATGGGTGGGAGCCTCTCTCAGGCTTCCTCTATGCA[C/T]GCGTCTATCTTCTATATGGGGCAATATCCAATGTCCCATTCGTTTTGCCATTTCCTGTATATCAAACAGAGAAGCAGAGGGTGG
WI-5612b	125	A	T	CTATTAATGA TTCTCTTGAGA GCATCGTGTCA AACCTAAAAC TTC ACTG	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATTCTAACATCACAAATATCTTATTTCTGCCTGTCACAACTAATTTGCAAAGCATTCAATTGACTATTAATGAGCATCGTGTCATTC[A/T]CAGTGTTTTAGGTTTCTCAAGAGAATTATGCTGTTCCTGTAACTCAAGTA
WI-5612a	44	T	A	---	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATTCTAACA[T/A]CACAAATATCTTATTTCTGCCTGTCACACTAATTTGACTATTAATGAGCATCGTGTCATTCATTCACAGTGTTTTAGGTTTCTCAAGAGAATTATGCTGTTCTTCCTGTAACTCAAGTA
WI-5636	26	A	C	GCCAATTTTTAT CCGCAATAAA CATCGGAGGACT TTGGGAA	TGAGAGCCAATTTTTATCCGCAATAAA[A/C]TTCCCAAAGTCCTCGATGGAGGCATTTCAGAATCGGGGCAGGGGGAGGCAGAAGGTGAGACGATGTGAAGAAC

ID	No.	Allele 1	Allele 2	Left flank	Right flank	Sequence
WI-5865c	103	C	G	---		TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAGAATCTTTTTTTTCATTTATGCATTC ACTGACTCACTTGCTCTATCAAAAATAAA[C/G]AAATATAATAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCTTCA GAGAAGAGACAGACAACTAAATAAATTCCAGG
WI-5865b	99	T	A	---		TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAGAATCTTTTTTTTCATTTATGCATTC ACTGACTCACTTGCTCTATCAAAAATT[T/A]AAACAAATATAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCCTCCATCTTCAAAAGGTCACAGTCCTTCA GAGAAGAGACAGACAACTAAATAAATTCCAGG
WI-5865	165	T	A	---		TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAGAATCTTTTTTTTCATTTATGCATTC ACTGACTCACTTGCTCTATCAAAAATTAAACAAATATAATATTTTATTTACAGAGGAACTC AGAAGCCAGAAAAAATGACCAAGACACAGT[T/A]CCAGTCTCCATCTTCAAAAGGTCACAGTCCTTC AGAGAAGAGACAGACAACTAAATAAATTCCAGG
WI-5874	76	T	G	CATAGCATGG ATAATATTAT ACAGAAAAA	CCTAGTAAGTT TCAGTCATTG ATATGT	CTCAGACATTCATTTCATTAGTTGTTAATTTTGTGTATTCATAGCATGGATAATATTATACAGAA AAAAATT[T/G]TACATATCAAATGACTGAAACTTACTAGGTAGCAATTGTTGTCAATTTGCT
WI-5752	36	A	T	CAGCCTCTCAG TTTTTCCATC	GACAGAAAAG AGAGTAAATT ATGAAAAA	CATGGAGCCGACGTTCAGCCTCTCAGTTTTTCCATC[A/T]TTTTTCATAATTACTCTCTTTTCTGTC ACAATGTTCTGCTTCGTATTCAACTCTCATTGCTGATGGTAGTCATAAAATATGGGGTGATTC AGAAAATAAGTAAATG
WI-5760b	61	C	G	---		TTAGCAGAAACAACAACAAAAAATGTCACACACTGCAGTAAAGAAGTGTTTCCCGATAAATA[C/G]C CATTAGGTATTAGATAAGCATCCCATAAACATTGTTGAAAACGAAGCCGAGTTTCGATTCACACA GTTGTCTGTTTTAACCTCTCTAAATCCGATAAATAGCCATTAGGTATTAGATAAGCGGTCCCACGAAA CATTGTTGAAAACGAAGCCACGTTTCCGATTCACACAGTTAGTTGTCTGTT
WI-5760	187	G	A	---		TTAGCAGAAACAACAACAAAAAATGTCACAACAACTGCAGTAAAGAAGTGTTTGAAAAACGAAGCCGAGTTTCGATTCACACAGTT TAGGTATTAGATAAGCATCCCATAAACATTGTTAACCTCTCTAAATCCGATAAATAGCCATTAGGTATTAGATAAGC[G/A]TCCCACGAA GTCTGTTTTAACCTCTCTAAATCCGATAAATAGCCACGTTTCCGATTCACACAGTTAGTTGTCTGTT ACATTGTTGAAAACGAAGCCACGTTTCCGATTCACACAGTTAGTTGTCTGTT
WI-5944	52	A	G	TTCTCACCATG GGGTGGGATCT	GGAATCTTG AACTTGCA	AATATCTGGCCTTTTCTTCTTAGGAGGAGATTTCTCACCATGGAATCTTGCTAAAGTGTAAAGACTACTCATTTCTCAGTCTTCCTTGCTG CCCACCCTCACTATTGAGAAGCTAAAGTGTAAAGACTACTCATTTCTCAGTCTTCCTTGCTG
WI-5967b	148	C	T	---		GAGTTTAATGAATCCTGTTCCCTCCTAAAAACCTCCTGTTCCCCCAACTTCACATTCAGCAGATATT CTTTCATGGGTTATTTTGCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTCAAGAGTGTGAG TAATGCTTGGTA[C/T]TTGCTCGTGTGCCGTATCTGCTCCAATCACCCATTCCACTTTATTTCCTATTAT GCTGAATGAAACGGTTATATTACAG

ID	Pos			Primer/Flank	Sequence
WI-5967	165	C	T	---	GAGTTTAATGAATCCTGTTCCCCTCCTAAAAACCTCCTGTTCCCCCAACTTCACATTCAGCAGATATTCTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTCAAGAGTGTGAGTAATGCTTGGTCACTTGCTCTGTGCCGTAT[C/T]TGCTCCAATCACCATTCCACTTATTTCCTATTAT GCTGAATGAAACGGTTATATTACAG
WI-6093	53	G	C	---	GGGTAAGATCCAGAGCCACAGGTGAACTCGCCGGTATTGAAGTCTTTGGGCCA[G/C]GTCTGTGTAATGATCTGACTTCTCCCAGAACCCCCTCTCTCTGGAAGTTCCAACTGTGCACTGAGCCCATTGTAGGGAGCATTTGAACCAAAACCCAGCGACACTGCTGACACTGCTGACAAACCTTGATTGACGGTGACACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80	T	C	CTTCTTAATTA AGCATCTACA AGGTACTT / TGAAAACCCCA GAACAGTG	GACTCTGTCTCAAGAAAAAAAAAATTGAATAATTATTAAGCACTTCTTAATTAAGCATCTACAAGTGACTTA[T/C]CACTGTTCTGTGGGGTTTCAATCCTCTCACCTTTAGACTTCAGGAAATTCAGAAAAATGCATGAAAACACAGGATTGTTACATGCAGAGAAATAGGGGGAGAAAAATTGTCTTTCTC
WI-6450	45	T	G	CCAATGACTT ATTCTATATCT GTGTCACA / TTGTTTGAAAT GTGTGGTACTT CT	ATAGGACACAGTTTTCTTCCAATGACTTATTCTATATCTTGTCACA[T/G]GAGAAGTACCACACATTCAAACAAGAGCCAGGCTATGCCCAGGGTGGGATTATTTTCACGGTCATGGTAATATGCATGTAAGACTATTTTTACTGGCCTTCTTTATGCATAAAACAAGGTATTGGTCTATTCAACAAACATGTGTCAATACAG
WI-6461	88	C	T	---	CAGTTGTCATGTCCCTCTGGTACTAGAATATAGTCTTTATAGAATATGTGGTTTAGAATAAAGCCACAAATTATTCTATAAAACAACA[C/T]AAGGAACGAACGGAGGCTCAAAAGTGGAACAAAACGGCCTTAGTTTCTAAGTGGAAGACTAAGACGATATAGGGAAAAATAATCCGTGACCTCTTA
WI-7466c	141	G	A	TTTTCACAGTC TTTGTCCTGG / AGTCGCATGCC AATTTATAATT	GAAACTATCCTTAGTGGTGCCACATTTCTATTTCTGATTCTTGGTCACACAGGACGTTCTGGGGCTATGAAATAGTCTATTCAGTGAACTAGTTATCATAAAAGACATGCAAAAACCTTTCACAGTCTTTGTCCTGG[G/A]AATATCTCACAAAATTAATTAAAAATTGGCATGCGACTTTCTGATTTAGCCTGACAGGATTGTTCCTTT
WI-7466b	80	T	C	GACTTTCTGGG CTATGAAATA / TGTCTTTTATG ATAACTAGTTC ACTGAA	GAAACTATCCTTAGTGGTGCCACATTTCTATTTCTGATTCTTGGTCACACAGGGACTTTCTGGGCTATGAAATAGTC[T/C]ATTCAGTGAACTAGTTATCATAAAAGACATGCAAAAACCTTTCACAGTCTTTGTCCTGGGAATATCTCACAAAATTAATTATAAAATTGGCATGCGACTTTCTGATTTAGCCTGACAGGATTGTTCCTTT
WI-9814	104	C	A	---	TGCTTTTTAAAAATAACAATGACCACCACCTGACACCATAGTCGTGTCTCCATTGCCAGTCTTCCTCAGTAGAATAAGACAGGGACTTTGCTGGCTGCTATCT[C/A]TTCTCCTTCCAGAAGAGCACTTGGCCCCTCATAGGCATTCCATAGATATTTGTTGAATGAATGTGCTCTTTTTGCATATTGATTCCTACATTTGATACATTCTCAGGAGGGACATTTGGCCTAT
WI-9720b	55	A	G	---	CCTCTAACAAGAAGAAACTTGACTTCCTCAACTCAAAATACCCTTCTCAACTAATAATT[A/G]AGTAACCAAAATATTCCTTCAAATAAATTAATCTTTAATTAGAAGAAGCAACAGTGTTAGAGGTAGTACATTCACCACC

ID	Pos			Sequence
WI-9720a	47	A G	---	CCTCTAACAAGAAAAACTTGACTTCCTCCAACTCAAAATACCCTTCTCT[A/G]ATAAATTAAGTAACCA AAATATTCCTTCAAATAAATTAATCTTTAATTAGAAGAAGCAACAGTGTTAGAGGTAGTACATTCA CCACC
WI-9825	123	A T	---	CACGCTCTAAGGCAGGATGGCTTATGAGATACTTTGCATTGTCGTGTCTGCACACCTTGAATCTGCC TGCTGGCTGGCTCCCTTACTTTACCTCTCTGTCGTGTGCAGATGAAGGCTCAGGGTGCT[A/T]GAGGATTAG TAAGATCTCTTCTAAAGACAGGAGAGATTATTTACAAGAAGAACTCACCAGGGTTTAGTTTGCATT TAAGAATTGCCAGTCTTTTGTCCTGCATCATCTTGAACATTAATCCACATG
WI-9748	74	C G	---	CCACTTCAGTAAATCAATTGTAGCACTTATTTCTAAAGATTTCTAATTTTTATATGTTTACCCTTT GTCATT[C/G]TCAGACCAAGTACACATGTTTTCACACAGCCATCTTCTTTCCTGGAATCTTTCAGAAT TACAGTTATGATGTCCTTTATATTCCCCA
WI-9943	91	T C	---	TGAGGCTATGATTGCAGATTTGTAGTGACTAATACTTATTAAGCAATTTCAATGTGTGGGCACTGTT CGTTGTGTTTTATATCCATCTTC[T/C]ATTTAATTTTCTACTGAGCAGAAAAAAATGTATACATT AACCTTTGCTCCCTATTTGTACCTTTTAATATTGCATTTCACACCTTCTCTTTGTCATTTAGGGA
WI-9891	39	T C	---	AGGGGCCTTCACAGATCCGTCAGCTCAACACTGCCTCCT[T/C]AGTGAGCCTGTGAACCACCCAAGAC GGCTGGTCATCAGTGTCATCCTCTTCCTTTCCGGACAACTATCTTTAAAGAAAAAAAAGAGTGT CTTTGAATGTATCCATTTATCCCCAAATAATCTTGTTTAATAAATTCCTTATTAGGCCAAATCCAAT GTGCTGAAATATCTGCCAAGCATGTCATTCTACACAAAAGGGATTTGCAAA
WI-9897b	84	C T	---	CTCAGAATTATTCAGATCTTCCCCAAAATGTCATGATTCGTTCTCAAACATCCTATTTTCCTCAAAC ATTTATCTAGCCTGTA[C/T]AAGTCATCCAGTGAGGCTGTGTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTTGTACCCACATTA
WI-9897a	83	A T	---	CTCAGAATTATTCAGATCTTCCCCAAAATGTCATGATTCGTTCTCAAACATCCTATTTTCCTCAAAC ATTTATCTAGCCTGT[A/T]CAAGTCATCCAGTGAGGCTGTGTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTTGTACCCACATTA
WI-9935b	115	C A	---	AGATAACCCTGGAAAACTAGAAGAAATTAATAAACGTGTTGCACACCTCCACCAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGGTGCTTGGACTGGCAGGGGAGTTCAGACA[C/A]AGCCAAGAAAAAGCC TGATATTAAGAGGCACTTGCATTAA
WI-9935a	42	C T	---	AGATAACCCTGGAAAACTAGAAGAAATTAATAACGTGTTGCA[C/T]ACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGGTGCTTGGACTGGCAGGGGAGTTCAGACACAGCCAAGAAAAAGCC TGATATTAAGAGGCACTTGCATTAA
WI-9983	146	C T	---	CCTGTTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCGCTGCCTCCCCATTCCTTTGTCTTGA TTCCCCAAACCCAAGGTTCTCACCCAATCTGATCAAATGCTGACTAGGTCATGGCTGGTCAGGGTAA AGCATTATGA[C/T]AGACACAAGAACAAAGACAAAGAGGTAAAGTTGCTGTCCTCAAGAGAGAGACATAA AACAAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

ID	Pos			Seq 1	Seq 2	Sequence
WI-10019	139	A	T	TGATGTAATGC TATGTAGCAA ATCT	TTGATTACTGT GCTTAGGGGA	ATATCAGTAGTGGGTTGAGTATACAGCAATCTATTTTGTTTATTATGTGTGCTATAAATCAATGGTTCTA ACATTCAAATAAGATCTTTTGCTTCTCTGCTCAGATGCTTCAGTGATGTAATGCTATGTAGCAAAT CTA[A/T]TCCCCTAAGCACAGTAATCAAGGCCTTCTACCCCA
WI-10020b	122	T	A	GCGAGAAAAG AAATCATGAC TTT	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAATTTAGGC ATGCATAGAGAAATAGCAGTGTTTTATTGGCGAGAAAAGAAATCATGACTTTT[T/A]AAAAATACC AGACTAATGATTAAATAACAGTCCTAGGGTTCCGGAAGTGGCCTAAAGCACGTAGTAGCCCT CCTTAGA
WI-10020a	39	T	C	TGTCATCTTGA CTCGTATTAA ATAAATT	AAATTCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTA[T/C]GTTAACTGGCTCTGAAAAGAATTTA GGCATGCATAGAGAATAGCAGTGTTTTATTGGGAGAAAAGAAATCATGACTTTTTTAAAAATACC AGACTAATGATTAAATAACAGTCCTAGGGTTCCGGAAGTGGCCTAAAGCACGTAGTAGCCCT CCTTAGA
WI-10064b	170	C	T	CCTTTAGATAT ATTGTGATTGT TTTTACATG	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGGTAGCAGGATCAGGGAAGGCATTATAATAAAT ATAATTTGCAGAGCATCTCTCCTCCTATGCACCAGATATTGTGGTGACACTCTGTTAATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTTTACATG[C/T]GAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10064a	54	C	A	GTAGCAGGAT CAGGGGAAGG	GAGATGCTCTG CAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGGTAGCAGGATCAGGGAAGG[C/A]ATTATAATA AATATAATTTGCAGAGCATCTCTCCTCCTATGCACCAGATATTGTGGTGACACTCTGTTAATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10289	29	T	C	TCTCCTGTCCC CAAACTCTT	ATTCTTGTTGT ATTGAATGGAA TTAA	CCAGGGGATTCTCCTGTCCCCAAACTCTTA[T/C]TTAATTCCATTCAATACAACAAGAATTTATAGAA TATGCACCACATGCCACAAAGACACCCTTATATTAGT
WI-1319	40	A	T	TGGCACTTAG AACATAGTTT ATTCTTT	GCCACACACC CTATGGT	AAGAAAAATCCTTGTGGCACTTAGAACATAGTTTATTCTTT[A/T]ACCATAGGGGTGTGTGGCTTATCT TTTACCTGGCATGGCTTTAGGTCCTGTTTATAATTGGTATCTTTTGCCACAAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTAACATTAACACTGGTCAGATGTGTTTAAAACTTGTTGAACCTGCAGC
WI-10316	104	T	C	CTGTTGATTTT CTACCTCTATT CTCTT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACTTAGTGAGGTGTAAATCAGAAGCATCTATATTATTCACCAGTCACCACCCTG GACTATAGTAGTCGTTGTTGATTTTCTACCTCTATT[T/C]TAAACTTTTGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTATGAAAGGATGTTTAAAAGCCCAGCC
WI-2572	61	C	T	...	...	AGTGAGTTGTGCACACTTCAGTTACCAGGTGATGATTGAGCAGA AAAGTTAACACTTCAGTTCTCCCACA[C/T]AC

WI-10368	31	C	T	TGAAGCAACC AGGTCTTGTT	CAAGATATTAT ATTTATTCTCT AAGAGGGG T	GAGGGAACTGCCTGAAGCAACCAGGTCTTGTT[C/T]CTACCCCTCTTAGAGAGAATAAATAATATATCTT GAGATAGGGAGGGAGGCAGCCTGAGGACAGTCTGGGTTTGTTTCTACCCACTGGAAGCAGAATATCC TTCAAAGCTTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCTGATTGGCCTTTCAGGG
WI-10391	32	A	G	CTGTCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CCTCCCGTTCTCTGTCTCAGGTATGACTCCCA[A/G]TCAACTTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTTCCCAGGGGACGCCATCTGACACAGCCTTTTGCTTGTGTGACAAACAGAACATTGCAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-105567c	146	A	C	GTTACCCAGA GTCTTCTAATA GCAA	TGCCGCTTCCA GTAGCT	AGCGGATGAAATTTATATGTTATGCCTGACTTAGCGGGGTGCTCAATAAATATTATTCTTTTTCATATT TTCCAATTATTAATACTACTAGAATTTCACCAACAGAATTTTTAAACATTTTAAGTTACCCAGAGTCTT CTAATAGCCAA[A/C]AGCTACTGGAAGCGGCAAGAATTTAACCCT
WI-105567b	82	A	C	...	...	AGCGGATGAAATTTATATGTTATGCCTGACTTAGCGGGGTGCTCAATAAATATTATTCTTTTTCATATT TTCCAATTATTAAT[A/C]CTAGAATTTCACCAACAGAATTTTTAAACATTTTAAGTTACCCAGAG TCTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAATTTAACCCT
WI-105567a	60	T	C	GGGTGCTCAAT AAATATTATT CTTTT	AAAATTCTGTT GGTGAAAATTC TAG	AGCGGATGAAATTTATATGTTATGCCTGACTTAGCGGGGTGCTCAATAAATATTCTTT[T/C]TCAT ATTTTCCAATTATTATTAATACTAGAATTTCACCAACAGAATTTTTAAACATTTTAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAATTTAACCCT
WI-111153b	84	C	G	CAAACTTCAA ATTGCTTAAG TACTTTA	AAATCCAACA GTCAAGGTCTT C	CGTTGGGAATATTCTCTATCTCACCTAAATTATG[C/G]AGTGATTAAAAATATACATTTAACAAACTTCAA TTGCTTAAGTACTTTA[C/G]GAAGACCTTGACTGTTGGATTTTGAGTTTTTTCTTTATTCTTAATA AAAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-111153a	33	C	A	GGGAATATTTC TATCTCACCTA AATTATG	GCAATTTGAAG TTTGTTAAAAT GTAT	CGTTGGGAATATTCTCTATCTCACCTAAATTATG[C/A]GTGATTAAAAATATACATTTAACAAACTTC AAATTGCTTAAGTACTTTACGAAGACCTTGACTGTTGGATTTTGAGTTTTTTCTTTATTCTTAATA AAAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125	T	C	CACAAATGTA ACAAGAATTG ATCC	CCATGGCTGTA GTCCCAGT	GTTGTGAAACTCCAGTATCATTCCCTCAAACCACGCTTAAATCACAAATCACTTTTCTTTCCTGTA GAGCTCAAACTCAGTCGTGAATGAAATTGCTGCACAAATGTAACAAGAATTGATCCTTA[T/C]ACTGGG ACTACAGCCATGGCAGAGAAAAAGCAATGTAGTCAGCAAAATGTAACAG
WI-11163	58	C	T	CAAGTGAATT ATGACCAAAA TGAGA	TGTCTCTTTCA TTTGAGGTTTT T	TGACTCAAAGGAAAACACACAACCACCAAAAGTTCACCAAGTGAATTATGACCAAAATGAGA[C/T]AAAT TTGTTAAAAAAAAACCTCAAATGAAAGGAAATCAAATAGTTCAAAGATTCAGGTTCAATATTTGT
WI-10656	59	T	G	...	...	ACCTACAAAAATAGGGATAGTAGTCATGGTGTTGTTGGCAGACTTTTCTTTTCCTTTTTCTTTTTGT[T/G]CTCTTA GAATCCCATTTGCTTTTGGCCAGCATTCCCTCTCCCCATATTTTAAGGAGAGAATTCACCTTTTTCT CTGTTGGATGATCACAGGTTCTGCTCTTCCCAATCCAGAGCAGGTACTATTCACCCCATGGGGGTCAT AGAGAGAGGATTAAACAGGGTGATGCTGCAATGGGAATATTTGAAACC

Marker	No.	A1	A2	Seq 1	Seq 2	Seq 3	Sequence
WI-11169b	154	T	G	TTTTT	GTTTTTCATTC ATCCTCATTCA AAATATAA	TTAACCAAGA CTAACTTAAAA	CAGCATAGAGAGGCTGTTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAAAAATTAAGCCTAAAGTAGTGCTTTTAAACCAAGA[T/G]TTTATCATGTGTTCTGATAATTTTTTATATTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95	A	G	TTGAAAAA	AATAAGTGAA AGTAACTGAC TAAAAGCAC TACTT	AAACTCTTGGT	CAGCATAGAGAGGCTGTTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAAAAATTAAGCCT[A/G]AAGTAGTGCTTTTCATTCTT TTTTTAAAAAAGAGCAGCAGACATTTTATCATGTGTTCTGATAATTTTTTATATTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25	A	G	---	...		CAAGTGCTTGGACCTTGGATAGGTC[A/G]ACCGGCTGAAGGTTGGACAGTGTTGGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTAATATAGATCTTGTTCCTTTGGGTTACCACTAGGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTTGTCTAAATAATTCCAAAATAGCCATGGGGTTTGGACAAAATAC AAGGTTAGTGTCTCTCTAACTTTAATGGGCATA
WI-10686	133	C	T	AAGG	TGCCCCTGTCC	CAATCTCTAAA TTCATGTGTAG ACACA	AATAACCCTGTGGCACATAAAGGCAAATACTGAGCCCCATACAGAGTGTTTATGTTAATATTATGAAA AAAGTCAAGAGAACAAGATGATATAGTTCTGCTAGAATACTTGAAATCTGATGCCCCTGTCCAAGG[C/T]TGTGTCTCACACATGAATTTAGAGATTGAATGAAAATGGCAAAATTCAGAAAAGGG
WI-11175	77	T	A	A	AAATGATTCTT TCTGCTCAAAG TTCTTTTTGAA AA	CTGTTCTCACA	GGTAGGATGATTCTCTAGAATGCCACTTACAGCCACTGAAATATTGCCTCCCAAATGATTCTTTCTG CTCAAAGAG[T/A]TTTTTTAAGTTATCTACTATTATATTCTGCTTTTTCAAAAGAATGTGAGA ACAGTACAAAAATGTGTTCAGTATAGCAAATTAAAATTAAATTAAAAGTAAGAAAAAGAAGCCAATT TGGGC
WI-10694	144	A	G	TATGAGTTTTC	TGCAAATGCTT AAGGAGAAA	GGCATTTGTA	TAGAGAGGTCTTTCAGTTTCAGGGTTGGAGGGGGTGGAGGGTGAGATTCACTTCTTAGAAGCACTGGC TATGTACAGAAGAGATAAACTCTGAGAAGAACTCAGTTCTCAAAGTGTTCAGTTCTTTGCAAATGCTTTA TGAGTTTTC[A/G]TTCCTCCTTTACAAAATGCCATCAATTCCTCAAGGAAAAAAAAGCTTTCT T
WI-2716	23	T	C	C	GTGAATTCATCC AGAAAAACAG TTC	TCTCTTTTCTC TCTTGTTGTCA	GTGAATTCATCCAGAAAAACAGC[T/C]GAATGACAACAAGAGAGAAAGAGAATAAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCCCAGTGCATGGGAGCAGTG
WI-10719	115	T	C	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC AGCC	TCTCTTTTTCTC	CAGGCCCAACTCTGTCATTAAGTGTTTAGAACAGACACCTCAGTCACACAAAGTTTCTCTTGTATGT GCCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCTAGT[T/C]CGGCTGCTGGCAGTGCTT TTCCAGCCTGCTGCCCATAACTAA
WI-10721	40	A	G	CTTGCCA	TGGCTCTGCTA ATAAATAAAT CTCA	GAAACTCCCAC	CAACCAATTCAGATTAATTTTTGGCTCTGCTACTTGCCA[A/G]ATGAGATTATTTATGTGGGAGTT TCTGAAGATTCCCATGGTAAATAGTATTCCTCTTCCCTGCTTAGGTTTTGAAGAAGTTGAA

Marker	Pos				Sequence
WI-11204b	88	T	C	---	GCACACGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGGAGAACAGGGAGGTTGAGGTAAAAAGGGTG AAAAGAAAAACTTTCACCTTT[T/C]ATTTTAAAGTAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTAATTGGGAAGAGATTTAGTGAATCAGAAAATAAGTCTGAGGAAATTATTCAGAAAG GCAACATC
WI-11204a	80	T	A	GTAAAAAGGG TGAAAAGAAA AACTT	GCACACGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGGAGAACAGGGAGGTTGAGGTAAAAAGGGTG AAAAGAAAAACTT[T/A]CACCTTTTATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAATTGGGAAGAGATTTAGTGAATCAGAAAATAAGTCTGAGGAAATTATTCAGAAAG GCAACATC
WI-10732	80	C	A	GCTGTGTCTTC CATAACAGAA ATTGGTTCACT CTTTAA	ACATGTATTTCCTTAGTGGTCAGCCTTCCTTACCCCAAGAATATCCCTGGTTATTGCTGTGTCTTC AGGAACAATG ACATGTATTTCCTTAGTGGTCAGCCTTCCTTACCCCAAGAATATCCCTGGTTATTGCTGTGTCTTC ATTGGTTCACT[C/A]TTAAAGTTCTGTTATGCATTGTCTTGAGTCCACATAGGTGTTAATCATTCCA CACCACTCTGTTAAACTGTC
WI-11206	127	A	T	GGTTGTGTTTT CTGTATGTACA ACTC	TAGTCTTTCTTTGTACGAGTGTCATAAAGAATTACCACTCTGTCACATTTGTAAAAGATAGCACAG AGAGAAGCATTACACAGGGCACACAGCACAAACATGAGGTTGTGTTTTCTGTATGTACAACTC[A/T]CCAA CCATTAGGATTGTCACTCTCATATAGACAGAATTCAGTGGTGGTGATTTGAATTCCACACATGGA GAGTGACAATC ATAAGTCTA
WI-11215	68	C	T	CTAATGGTTGG ---	GAAAAAAAGTTTAATTGGGATTGCTTAGTTTGTCTAAATTTGACCTACTTTCAGATTTATTTTAGT [C/T]ATTTTTTCTATAATATTTCTTGTAAGTGATGAGTTTTCTATAAATTAAGGAAACAGATATTT ACACAGAGAAGACACAGGATTTGCTTGAATTAGTATAACATTCTTTATTCCAAGCCCCATTCCACCATGT TTT
WI-11219b	89	G	A	GAGAGAATAT TCCAAAAAGT AGAGAAA	ATGAAAAATGCATTAGAAGAATTGGAGGATAAAATTGGAGGATATTCCAAAAAGTAGAGAAAA GAGACAAAGAGAGATGAAAAATAGGA[G/A]AGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAGAGGCAAGAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
WI-11219a	18	G	A	---	ATGAAAAATGCATTAGAAGA[G/A]AATTGGAGGATAAAAATTGAGAGAATATTCCAAAAAGTAGAGAA AAAGAGACAAAGAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAGAGGCAAGAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
WI-11222b	136	G	A	CATACCACTGC GGCTGG CCTGGTAGCCA AGTTGTGA	AGCCACAGTGGAATCATTTACACTACCGAAATCAGCAAATGCTAAAATTGTTAAACATTTGAATTGGGGCTTTGGATTTTTGT TTTGTTTTTCCATAGACCCCACGTTGAACTATTGTTAACATTTACCAGCATACCACTGCGGCTGG G[G/A]TCACAACTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTGCTTCACAGGCTACTGG AAAGCC

WI-	Pos					
WI-11222a	25	C	T	GCCACAGTGG AATCATTTAC A	TTTTAGCATTT GCTGATTTCG	AGCCACAGTGGAATCATTTACACTA[C/T]CGAAATCAGCAAATGCTAAAATTGGGGCTTTGGATTTT TGTTTTGTTTTTCCATAGACCCCACCGTTGAACTATTGTAAACATTTACCAGCATACCACTGCGG CTGGGTCACAACTTGGCTACCAGGAGAGAACCTGACACAGACTTCGTAATTGCTTTCACAGGCTACTGGA AAGCC
WI-10775	39	C	T	TTTATGCCATA TTAATTCATTA CACTC	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTTTTATGCCATATTAATTCATTACACTC[C/T]ACATCATATTTCTTAGCAAATACA TCTAGACACCTGGCACTCAGTAGATATTCCTGGCACGATAATCATTGTTATCATTAGACATTGCA GGAACCACCATATGGATAAATGTGTTGTTTAATGAAGGCAAGCAATTA
WI-11226	165	A	C	...	...	TTGCATGCATTTATACGAAAGGAATTAAAATATCTTCCTTATAGTTGAATTTTAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATTAGAAAATTGTCAGTGGTTGC TAGTACAGGAATCAAATTTGGACTATGAACA[A/C]GACATAGTTGCTAAGGATATTCCACAAATTAT TTCATGA
WI-10778	62	A	G	GCAAGGGGAGG AACATTTACA G	CTGGTGACATC AGAGATGGAC	CAGTGGCTGGCTACTGACAAAACGTAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG[A/G]G TCCATCTCTGATGTCACCAGCAGGGCCAGGAAGGGTTGATCTGGAG
WI-10789	21	C	T	GGGACACACT GCTCTAGACC	TTGAGGGACCC TGGGA	TGGGACACACTGCTCTAGACC[C/T]TCCCAGGGTCCCTCCAAAGGTGGGTGTAGAGGCCCTACTGCCCT GCCCTGGGGACGCAGAGGCATCAGGGCCTTAGTCCTCCTGGGGACAGTGAAAGGGCCACCACC
WI-10810	58	C	T	CATCTTCATGG GCAGGAATT	CAAACCCTAAG AAACACAGAA ATG	ACAGAAAAAATGCCTAGGTCTTGTAGCAGAGAGAAAGCATCTTCATGGGCCAGGAATT[C/T]CATTT CTGTGTTTCTTAGGGTTTGTGGCTGGCCATCAGTTCAACTCAGCCCCTGTCCCCTGATCCAGCAACATT TCCGTAACTACCCTCTAGAAGTCATGCAAAGAGAAATGATGA
WI-10828	23	T	C	...	...	GGACCAAACAGAATTACTTGGCA[T/C]AGGGTTCTTAAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATAATTCTTTAGTAGAG GACTTCTAAAAGTCTATAAATCTGATTTCTCATTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10832	91	G	C	CATTAATCTGC AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	TATGCCTTCCCAAGCAGCCATCCACGCTGCTCTTAGCACAAAAAAATAGAATACATCATTCTGAATG GGCACATTAATCTGCAGGCTCTCC[G/C]TTTCTAAGTCACTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGCAGATGAGAGAAGGGGCTGCTCCGTGAAATAC TAGTTCGG
WI-10834	96	C	T	AGAATTAACT GTTCAAAAGT GTGTTAAT	TGGCCCTATAA AATTGGTATTA AG	GATTTGAGTATTATCAAAAATTGCCCAAAGACCATTAACAAGATTTAATAGTTAAAGCCAAAACTATA AAGAATTAACTGTTCAAAAGTGTGTTAAT[C/T]TCTTAATACCAATTTTATAGGGCCACCATTAACTT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-2287	24	T	C	...	...	GGATGATGTTCTCGCTCACCTGGTCCCTTTA[T/C]AAAGCCTCTTGCATCCCAAATGTGTAAATTATTTATTCT TGGTATTTCTCGCTACCCATAGTCACCTGTCACGTGTTCCACCCT

ID	Pos	A1	A2	Fragment 1	Fragment 2	Sequence
WI-2296	81	A	G	TGTTACTTTGA TTCTTTGCTCT GA	GCAAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAGGTCTCAGGCCTTTAGAATAAGTTGTTACTTTGA TTCTTTGCTCTGAC[A/G]CCAGTTAGCTGTGTGATTTGCAGAAGGTTACATTGTTTGTTG
WI-2300	77	G	T	GGCACAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGTCTTCCCTGGAAATTTCCTTATTGAGCGGGGCAGGTGGTAGGCACAGAAGC CAGTCATAC[G/T]TGCTTTAAAATTGACCCAACCATTACTAAGAATAGCATTCA
WI-2371	55	G	T	GTCTTGTTCTT CCCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGGAAAGGTCTGGTCTTGTTCTTCCCAGCTTCT[G/T]GTGGTGGCT GTCAATCTTTGACATCCTTGCTTGCGCAGCTGTATAATTCCAATCCTTGCCTCCAGCTTTACATGATGT TCTCTCCGTGTGTCGTG
WI-2395	122	A	C	GAACATATTT GTAGAAAAAT TACTATCCAA	TCACCTTTCTA TTTATTCTGAA TTCA	GGGGGCACAATTTAGCTACAGTGCATATTAAAAAGATAACATAGAATATCATAATAACTTGGTTTAC TGAAATCTGAAAACTTAGGATGAGTGAACATATTTGTAGAAAAAT[A/C]CTGAATTC AGAATAAATAGAAAGGTGAATCATCTTATATCATAAAGAAGCTAAATTATTAGTAACAATCTTTA CATTTACACAAACCCA
WI-2437c	192	G	A	---	---	CACCAGCCACCACCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTGGGGACAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACACAACTTTCTAAATAATAGACACCAAAAATTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179	G	A	---	---	CACCAGCCACCACCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTGGGGACAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACACAACTTTCTAAATAATAGACACCAAAAATTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128	G	A	---	---	CACCAGCCACCACCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTGGGGACAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACACAACTTTCTAAATAATAGACACCAAAAATTCCCAAT[G/A]CTC TAAATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71	G	A	GCAACCTACT GACAATTTAA TTTTAGTT	AACAACTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTTCTTCCTTAGACCCTCCAGAAAATAATGCAACCTACTGACAATTTAATTTTA GTTG[G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCGAGAACT
WI-1356	123	T	C	TGTTTAGGAA ATAATGACAA GAAAAA	TGGTTACAACT GTACCAAACAT G	CTGTAACCTACACACATCCTCCTGTAACCTCTAGGTTACTTGTAATACAAAACACAATGTAAATGCT ACATAAATAATTGTCATACTATTGTTAGGAAATAATGACAAGAAAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCAGCCATTTCCCCCAATATTTCAATCCACAGTTGGTTTAATCCACAG
WI-2886	46	C	A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGGAGAAGA[C/A]AACGAGATAAAGCATG GCAAAGACCACGCTGAAAGTATCCCAGGGTGCTGTATGTGCACATAGGAAGAGATCACTTACCTCAGCA TAGGAGGAGGGGCTAGGCAAGGAAAAGGTGTCAGAGAAGAAACAGAGAGGAGCGTT

Clone	#					Sequence
WI-2906b	77	T	A	...		CCTGAACACCTGGAGCACTTCCCTCCCTTGGACACCTTCATTCTTGCTGGAATGCTC TTTCCCTCT[T/A]GAGCTTTGCTGGCTTACTTTTCTTTTTCCTTAGGTTTCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTTGCTGACCAACAAA
WI-2906a	50	A	C	GACACCTTCAT TCTTGCTGG	AGAGCATTCCA GGCAAAGT	CCTGAACACCTGGAGCACTTCCCTCCCTTGGACACCTTCATTCTTGCTGG[A/C]ACTTTGCCTGGAAT GTCTTTCCCTCTGAGCTTTGCTGGCTTACTTTTCTTTTTCCTTAGGTTTCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTTGCTGACCAACAAA
WI-1736	175	C	T	...		TACTCCTCATTCCTCATGTCCCTAGACGTACTCAGATTTCCATGCCCTGAAACATTTATTTCCTAAAT TAGATTTCCCACCCCAGCACTATTTACACAGAAACAGCATGGAGCAGTTGGAGTCTGGCTCTTAGA GAACTTACTTAAGGACAGTGGTTTCCATCTGTCTTCCCA[C/T]AGAGGATCTAGGGTGTCTTTGGAACC ACCTTGG
WI-1851	136	G	A	GCATTGAATT AACTATAGAT GTGTTAAGTA TTG	CACTAGCAATG TTAAACTGAAG TTG	AATACCCCAGTCCTCTAACACCATCCACACTGATCAATCAGGTTTAACATATTAATCTGGGGAGG ACACAAACAATTTAGACCATAGTGAATTAACTATAGATGTGTTAAGTAATTAATTATTAACATGGTA CA[G/A]ACAACTTCAGTTTAACATTGCTAGTGATTCCATGTGGATACCATGTACCTTCTTACACATG TGA
WI-3000	62	G	A	CCCAAAAACAC AGAGACCCC	GCCACTATAGG ATTGACTAAGA CTCA	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTCAGCACCCAAAACAGAGACCCC[G/A]T GAGTCTTAGTCAATCCTATAGTGGCAGTAATCAGTGCCTGGTGCATAGTAGACACT
WI-1754	177	G	A	TTTTCTCCCTT CTTAAAGAGA TAGTC	AAAGTCGAATT GCCTCTGG	ATGGATCTGCTCAATTATAGTCCCAGATAAACAGCCCTTCTCCCCGCCACCCCGGATTATTTACT TAAGGGTTTAGCAAATTCACCTGACAAAGAGTTAGGTTTCAACATTGACCCTCATAAAGTGATTTT TTCTCTTCTGTTTGTTTTCTCCCTTCTTAAAGAGATAGTC[G/A]ACCAGAGGCAATTGGACTTTCTGT AGCCACAAGATT
WI-3167	37	T	A	AAATTCAACC ACAGATCTAT TAGATTC	TGTGATAGTTT TGAGATGGGTG	ACAACACAGCAAATTCAACCACCAGATCTATTAGATTC[T/A]ACACCCATCTCAAAACTATCACATCAA AGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-3208	140	G	A	GTGGAGTGGGC AGATAAAGA	TCACTCAAACT AGGGCTTGG	CAAGCACACATTCAGGCAGTGGGCAGTAGGGAAGGTGGGCAACTTGCGCAGCAGAGAGGAGGAAG AAGTTCAGACGCGTTGGGTAGGATAAGTGGATCCAACCCCTTTGTAGGGCAGGTGGTGGGGATTCAAG ATAAAGA[G/A]G[A/A]CCAAGCCCTAGTGTTTGAGTGACACTGTGGGGATTCAAG
WI-1775	47	C	T	CCTGCATGGTC TTTTCTCTG	AGTTGAGATTT ATGACAATGAT GTAAA	ACTCCACCAACAGTTTTGTGAGCCAACCCTGCATGGTCTCTTTTCTCTG[C/T]TTTACATCATTGTCATA AATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55	G	A	AGCATATTCA TTGATTTCCTT ACAT	GAGGACTTAAA AAGGAGCATTT G	CTGCCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCATTGATTTCCTTACAT[G/A]ACAAATGCTC CTTTTTAAGTCTCAACTTTAAAGCGGAAGTTGAGACACTGTGGGGAATAGATTTCCTTAGGA

ID	Pos					Sequence
WI-3416	33	C	T	CCAAGTTGTA GCATTCAGAA GTC	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCCTCCAAGTTGTAGCATTCAGAAGTC[C/T]CTCTTAGAGGTAGTTGTGCTCGTCGTTAAAA TATGTTTTCAAGATAGTAGTATCTCCCTGTTGTCACTTCCTCCAAACAACAAGTGTACCAACAGCATTGTTAAG GAAATGTGCAATGCTTGCTACCTCTGACGCACAACATAATTAAATCCCATTGCCTAAAAAGACCAGG
WI-3453	70	C	T	TTCTTAGGCCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCCTACAACAACAGAAATTTAACAAATTGAAAATCAGCTACTCTTCTTAGGCCCATCAGAG AAT[C/T]GAAGTCATGGGGAAAATTGATGCCATGTGAATTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109	G	A	---	---	CATGCTAGGTAGATCTGATCATGAAGTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTCCCTAATTTTAGCACACAGTATTTTAATGAGGTGGT[G/A]TGGGAGAAAATTGATGGTTGCG TAGTTGAGTTTTCTGTGTCCACC
WI-3474a	90	A	G	AGTCAGTTCC CTAATTTTAGC AC	CAACCATCAAT TTTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTCCCTAATTTTAGCAC[A/G]GTATTTTAATGAGGTGGTGTGGGAGAAAATTGATGGTTGCG TAGTTGAGTTTTCTGTGTCCACC
WI-3502	79	C	T	CCTGGGGTTCT GGATGTCT	GGGTGACCCTG TCCTCA	TTTGACCCCATACATGAGAATAAAACCATAAGAAATGGTGGAAAAATAAAACGGGAGAGACCTGGG TTTCTGGATGTCT[C/T]TGAGGACAGGGTCACCCCAC
WI-3600b	146	G	C	GGTTTCTAACC TGGATATAAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCCTGCCTGTTTCCGAGTCTGATTATCCATGCCCCTG ATAGTTCTGTGAGCCACCTAAACTCGTTTCCTGCTTAAGTTATCCAGAGGTGGTTCTAACCTGGATA TAAACATCT[G/C]ATGGAAGGCTGCACTGAGGTCACAAA
WI-3600a	78	T	G	CCATGCCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCAGCAGTGTCCTGCCTGTTTCCGAGTCTGATTATCCATGCCCCTG ATAGTTCTG[T/G]GAGCCACCTAAACTCGTTTCCTGCTTAAGTTATCCAGAGGTGGTTCTAACCTGG ATATAAACATCTGATGGAAGGCTGCACTGAGGTCACAAA
WI-3678	125	G	T	---	---	TAAAATCATGCTTATTTTTCACAAGGTAATCCACTCACAATAGGCAATTGATGTGATCTCTTCTGTAA GAAAAGCTCTCATCCTTCCTGAACCTTCTACTTACTGTGCTGTGTATGATGCACCT[G/T]CCTTTTGG ATAGATGGTTGATAGGAGATGGGTTGTTAAAGACACAATTACCTTGTGTGTTTCAGGCAGAAATAG ACTCTCTCTGTGTAATCACTGAATGAGTCCAAAAGCCTTTATGTCTTAC
WI-3687	67	A	C	---	---	AAAGGCGATGTTGAGATACCACATTCCATGAAAGAAGTAAAAACACACACAAAAATATGACATAAAA T[A/C]AAAAACTACTATAGTTTATGAAAATGACTTCCAAAATTCAGAGAAAGTCACTTAAAACAGG ATTCTCAATTCATTCCAGAATACTCCTCTGTCATTCTTAACTTTGACTGCACAG
WI-3735	72	T	C	CCTCAGTTATG TATCAAATGA C AAAAC	GGCTCACCAAT CATTGTTTT	TCTAAAAATGTGAAACCAAAGAATCCTGACACGACCTAACCTGCCAGTCCTCAGTTATGTATCAAATGA AAAAC[T/C]CACACCGGTTCAATGAAAAAACAATGATTGGTGAGCCATGTCCCCTTATTTAATGAAAA GATCTTGGGCAATTAACTC

Marker	Pos			Primer	Sequence
WI-1819	51	C	T	...	GAAAAGCAGGAAGCCAGGCAGGACAAACTTTGAAAAAGTCTTTCAGCAC[C/T]TTCGTGTGGATCCG AATTTTAGTGTGTGATTGGCAGGCAATGCGGGGTAACATGTTCCAGTGTTTAACTTGCACAGAATTGC CAGATTAGCGGATTGTTGACTGTGTCCAATTAATGAAATGTGAAAAAAAAAAGGGTGGTAACTGTT AAGCCTGCTGCTGCAATGTTTAGACACGAGTGGGGGGAGGTGGAATACC
WI-3746	116	G	A	...	GGCCTATTCACATGACACTGGGCCAGATCTTGCTTCCCTTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCCTGGCCCAGGAAGATGGTTGTCTTCATCATCTCGTCTCTGC[G/A]GCCCCAGGATAAAGCA GGCA
WI-3867	49	T	C	ACAGTCATTT AGTCTTCCTGA CAA / TAAGATAACC ATACTAGGTAC ATCCG	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCCTGACAA[T/C]CGGATGTACCTAGT ATGGTTATCTATCTGACAGACAAAGGACACTGTGACACAGAGATTGTACTTGAACAAAGACACAGT CATTAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCTTCTGCTATAG CATC
WI-3898	25	A	C	TCGTCGGTGTC TTTAGAAGCA G / CTCTCC	CAATGACCAATGTCTTTAGAAGCAGCAG[A/C]GGAGAGGACACCGACGAGACACAGGAAGGAGTGAG GTGAAGATGAAAGCAGTGTGACGCAGCCACAAGGTGAGGAAGAGCAAGGGTTGCTGGCCACT
WI-3901	114	A	G	...	GGACCATTGTCCCTCAGAAGTACATTCAAGCCCTGACCGGTGTCTCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCCTGAACCTGGCTTCCTCACCTGACAAGTGG[A/G]TATCATGTGCTACACTGC AGTGTTTATAATGCTGCAT
WI-3914	99	C	T	TGATTCTTCTC AAGACTCACA GC / TCTAGAAGCAA TGAAGGATGG	CTGAGGAGATTGATGCTACTTTACCTGAGGAAACTTTTATTACCTCCCCTGAGTTTGTTGCCTTGCAA GACATTGCTGATTCTTCTCAAGACTCACAGC[C/T]ACCATCCTTCATTGCTTCTAGACCTATAACTAG ACTCAAGTCCCAGCAGCCCCTTAAAGGTAAGGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	G	A	CCAAGAGCGT CCTATGAATC A / AACAGCAATA ACAGGAACAA ATG	CCACTCCCAGGCCAAGAGCGTCCTATGAATCAT[G/A]CATTTGTTCCTGTTATTGCTGTTCACAGAGT GGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC
WI-4091	84	A	T	TTGAGGTCTTA GTCATTGCATG / TGAGTTCCTAT TAAGTGACAAT ATTGTT	TAATTCACATTGCTCTTGTTGTGCATG[A/T]TGTATAAACAATTGTCACTTAATAGGAACTCAAGCATAGTTATGTGT TCTTAGTCATTGCAAT ACATTTATTGCTAACAGCAG
WI-4160	117	A	G	CCTATAATTTA GCAACAATAT CAACAGAA / TGCAGGTAGAA TTTTCTAATAT AGCC	TCCTCTTCTGTAATAGGAAGTCTGATTAGATGCCTTTGAGGTTAGGTTGGCTTCTAAGATGGTAATT ATCTGTGCCAAGTTTTTGTTCCTATAATTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT
WI-4168	32	A	G	GGTGAGAGTC AAATTGATAC AAAACA / ATTGCCAAACA GATTTTCAGA	CGTTGCTGGTGGTGAGAGTCAAATTGATACAAAACA[A/G]TCTGAAAATCTGTTTGGCAATCTATTAAAGG CAAATATATACCAGCAGTGTGGTCTAGCAATTCACTGCTGGCATTACCTAACATAAATGAT

Marker	Pos	Allele 1	Allele 2	Flank 1	Flank 2	Sequence
WI-4177	68	T	C	TGAATAAGCACGTATTAAATTTACCTA	AAGGCAGCAAATCATGATG	ATGCCTGCGATATACTTTCCAAATGACTAGTATGAATAAGCACGTATTAAATTACCTATTATATTA[T/C]CATCATGATTTGCTGCCTTCTTCCAAATTACTACAAATTGTATTGTCACATGAGGCACATGATCCCATTAACCCAAATAG
WI-4199	51	A	C	CTCCCCAAGTTAGTCAATATAAAAA	ATATGTTGATTAGGTATAACAATATGTGTG	GCCATGAGCACAGAGGCTGAAACCACTCCCCAAGTTAGTCAATATAAAAAA[A/C]CACACATATTGTTATACCTAATCAACATCAAAATGTATAGATTAAACAGTCCACAGCAAACAA
WI-5163	24	C	T	CTGTCACTGGTCTGCCTGT	AAAGGAACACAGGAACAGACC	TTCTGCTGTCACTGGTCTGCCTGT[C/T]GGTCTGTGTTCCTTCAATGTTCAACTGCTTGTATCTGTGCCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGGCTTTGTAGACCAGAGTTTCTTGGAAATTGCAACATTTGGGCAT
WI-4250b	117	A	G	---		TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTTCCACCAAGTGCTAAAGCAGTTTAATAACAGGTTCAATATGAGTCTTGTGAAACAGGGGTGGGAAGGATCCTGTAAAAGG[A/G]TAAATATTGTTTTCCATAATATTGAAGATGTG
WI-4250a	94	G	T	TCAATATGAGTCTTGTGAAACAGG	CTTTTACAGGATCCTTCCCAC	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTTCCACCAAGTGCTAAAGCAGTTTAATAACAGGTTCAATATGAGTCTTGTGAAACAGG[G/T]GTGGGAAGGATCCTGTAAAAGGATAAATATTGTTTTCCATAATATTGAAGATGTG
WI-4255	68	G	C	TGCTCCCCCATCACCT	GGCCTACTTCAAGTTGTGTAAGG	TAAATGTCTGGGGAGATAATAGGAAAGGTCCATCCTCTGATACCTTGGTTGCTCCCCATCACCT[G/C]CCTTACACACTTGAAGTGAGGCCCCATCCAAACACTGGTCAGAAGAGTAATACTGTCGAC
WI-4256	57	C	T	---		ACAGCCTCTTCAAATGGCACAATCAAAAGCACCAGTAAAAGCAGAGGCAAAAATCTGG[C/T]CTCACCATTGGAAAAGTCTTCTGAAGGATAAGGGAGTGAATGACTGCTAGAAGAATGATTGGCCT
WI-4325b	71	C	T	---		AGTTCACTGCCTAGATGAGTAGACCATGTTGTCTTTGTAAATGTACATGGGCAGGAC[C/T]GGAAAGATG[C/T]TACTATAGATAAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCACCCAGGACACTGCCATATCT
WI-4325a	58	C	T	---		TGGGCAGAAGTCGGGTATGGCAAGTCAGGGTGGGTTAACTTGGATGCCCACTTCTGCCTGTCACCTTCTCTAGACTCTTGACCCTGCAGGAGGATCCCTGCCTCCACGGCTCCACAACTGTCGTCAGGGCCC[A/G]GAATCGTGGGGAGGTAGGAATGACGAG
WI-4347	158	A	G	---		CCAGTCTAGGCTGCAAGGACTTCAATTCTGGGGCAAGTCCTGGCGTGGTGTGTAGGGTCAGAGGCAGGCGACCTGAGGGAGGACACAAACCAGTGGGACACCAGGGGTACTTGTATCACC[T/C]CTCCCGCAACCCCAAGCAGCAGCAGCTGCAGCTCCAGGAAAGACTCCTTACTTCCACTTGAGAAAGGAGAGGGGAAGAGAG
WI-1936	117	T	C	---		AAAGAGGACTTTGACACACAACTTGGA

ID	Pos	Allele 1	Allele 2	5' flank	3' flank	Sequence
WI-5204	54	C	T	...	...	TAGATTTTGATTGATGACAATAGGGAAGCCTTTGTTAAATTGGGTTTTGAAGAGAA[C/T]GAAGAGAAAA TGGAAAGGGAAGAATTGACAGAAACCAAGAGAGTGTTGAGGGAGCAGCAAATCCCAGTTTGACTGGA ATATAGAGTGATGTGTCAGGGTTG
WI-5215	70	A	G	GGACCTTAAT ATTTAACAGA CTCAAAAA	AGATAATTTG TAAAGATAGTT TTCGC	TTTCCCTTATTTATTTAGGAAGCAAAAATGTTCATACAGGACCTTAATATTAACAGACTCAAAAA TAT[A/G]GCGAAAACTATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTAGCACATTTCCT GTAGTCAAGGTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112	T	G	TTGTATCAAA GAGATGGGGT ATATAA	AATTAAAGAA ATCTTTACATG GTTCTTT	CCCTGAAATGTGCTTGCTTCTCCTCCAACTCTCTAGGGAACTTTTCCATGTCAGGTGAAGGTTTGA AGAGTACTTAATTAACTTGTATCAAAGAGATGGGGTATATAA[T/G]AAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTTCATCAGGGCTCTTCCACTGTCTATCAGTAAA
WI-4456	49	C	T	AGTTGAATTA TTCAGAAAAT TATAGTTCC	TTTCCTGTTAT GCATGAACTTG	ACACATTTCATTTGCTTAAGTTGAATTATTCAGAAAATTATAGTTCC[C/T]CAAGTTCATGCATAA CAGGAAACACCAGGTTGGGGCAATTGATTGAATTGT
WI-4461	49	A	G	TCACTGTTATT TTAAAATTAT CCTTCC	TTTGACCTTTC ACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTTAAAATTATCCTTCC[A/G]TGAAATTGGTGAAA GGTCAAAGAATGAAATTCCCACTTTTAGATTTCTGGAAATTTATTGCGATGATAATGCAATGGGC
WI-4465b	75	G	A	...	...	CTACTGGATTTTACTTTGCTCAAGCCAGCAACACGAAAGTATATAAAGAAAACAGTTAGTAATCTT TCAACCTTT[G/A]TATTTCTCTTCTACCTCAGGGAATC
WI-4465a	41	A	G	AAGCCAGACA ACACGAAAGT	GGTGAAAGATT ACTAACTGTTT TCTTT	CTACTGGATTTTACTTTGCTCAAGCCAGCAACACGAAAGT[A/G]TATAAAGAAAACAGTTAGTAAT CTTTCAACCTTTGTATTTCTCTTCTACCTCAGGGAATC
WI-1949b	160	T	C	GAGTGAATAA ATGAATGCCA TAATC	TGAGAGGTGGG GACAAAAA	GGGGTTAGGACCTCGAGATCTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTTCAAGGCTGCTGACATGGTCATGGTTTTGTCCCCACCTCTCCACCTTTCCCTGG GGAGTGAATAAATGAATGCCATAATC[T/C][T/G]CTGTGTTTTTGTCCCCACCTCTCCACCTTTCCCTGG CACA
WI-1949a	86	T	G	CAGTGGTGAG ATGCTCTGAGT	CCATGTCAGCA GCCTTG	GGGGTTAGGACCTCGAGATCTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGT[T/G]CAAGGCTGCTGACATGGTCATGGTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCCCCACCTCTCCACCTTTCCCTGG CACA
WI-4529	64	T	C	CCAAGTAAGT CTATCATTCTG AAGATG	TTCTAAAAATA ACACTTCCTGA AAAA	TGAGAGAGTTTTGGATTATTCATCCTCTGCAACACTCCAAGTAAGTCTATCATTCTGAAGATGT[T/C] GAGTTCTTCTTTTATATCCTATGATTATTTTTCAGGAAGTGTTATTTTAGAATATAAACTCCTGGGT CCCATCCAGGTCTAGGGTCAATGGCATCCATGGGTCGCTGCGGACAAGATGGCCCTAGGGATCATTTT

WI-4540	110	A G	GCACCATGTGG CATCC GACAATGCAGC	AGCTTTCCTTTCTTAAAAATTGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTAACAGTACTTGCAATAAGCACCATGTGGCATCC[A/G]TGCATGGCTGCATTGTCCAGTC AAATGAGACAACTTCCTAT
WI-4582	226	T C	---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACAATTAAATTCACCAAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATGAGAGACAGCTCCAGTAGCATTCAAGGCCAGTTAACTTATTCCTGTACACA AATAACTTTATGGGAGACAGCAGCATTGTAATTCAAATCAATAAATGACTCGGTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGT[T/C]CCTCCTTGCTAGAAACCATTTGAT
WI-1965	105	G C	GCCATTGAGG AAGTGTTTAA AG	CAAAGGTTAGTTTAACTTGGGGGGCAAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGCCATTGAGGAAGTGTTTAAAG[G/C]AGAGAGATGACCCATCCATTCCTGG GCTTCTTATATGACACCATACTATTCCACACAGATGTGGAGTCATTTATTGGTGGTGTATGACAGT CATGG
WI-5248b	99	C T	CACTGTTTTCT ATTGACCGTAC TTG	TGTTTAAAAACCATACAGTTGTGTCTGCTACGTTGTTAGAGCAACCCCAGAAAATTAAAACGCCTAC CATTTTTCACTGTTTTCTATTGACCGTACTTG[C/T]TTGCTTTTTGCTTTTTCCCTTCTCTCTTTTCTG CCCTCTTTAACTATT
WI-5248a	38	G C	AGTTTGTGCTG CTACGTTGTT	TGTTTAAAAACCATACAGTTGTGTCTGCTACGTTGTTA[G/C]AGCAACCCCAGAAAATTAAAACGCC TACCATTTTTCACTGTTTTCTATTGACCGTACTTGCTTTTTCCCTTCTCTCTTTTCTG CCCTCTTTAACTATT
WI-4596	69	T A	TGAAGCAGAA AGCACTGTGA	CATTGGTGGGTCCAACTTCTCGGTGACATTACTCTGTTGACTTGCTCTGAAGCAGAAAGCACTGTGA C[T/A]CATTATTAGGCCCATCTCCTGCCTGAAGCCTACAGCAATTTGTAACATATGGCATTGGG ACATATCTCTGAGCCCATCAACTATTGACAAGATTCTCCTTTTTAACAA
WI-5252	119	A C	CAGGAGATGGG CCTAATAATG ---	GAAATAGGGCAAATTAAGACTTCAATAATTAAGAAGTCTTGGGAAAAGGATTTGTGATGATCATTG AATCTGTTTAAATACAGAATTAATACTGAATACCTGTGTGAATCATTGCTTT[A/C]TACCATGTACA TATTATATGAATTAACAATGTAAAATAGTACTAAGAAATATTGGCCCT
WI-4606	61	A C	GCAATGCTAG AAAATTATGC CT	TGCAAAAAGGAGAAAATGATAACCAGGACTGTGTTGTTCAAGCAATGCTAGAAAATTATGCCTA[A/G]C CAAGTAGCAACTTAAGCACCTAAGGCAGAATGAAAGTTTCTCTCTTGTCATTAAGTCCTCTATTCA ATTACCATTTATCGGGGTAATTAAACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGTCTTTGCTATGCT
WI-5257	77	C A	GAGGCATGAA GCAAAGAGG	CAATGAGAAGTTACCAGATGCGGGCAAATTAAGCATATGAAAATACCAAGTGTTGGCAGAGGCATG AAGCAAAGAGG[C/A]CTTTCATCTGCCCCTGGTGGGTTTTTCAGTAACTGCAACATGTCTTTGCCTCC ATTACCATTTATCGGGGTAATTAAACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT CGGATGAAAAGATACCCTTCTCTATGACTCAGCAATTCAGCATTCTTCCACTCTAGGTATGCACCCTAAACATGGGTG GCAAAT
WI-4649	50	C T	TGTACTAGGTG TACTTACACAGA	TCACTGTTTAGAAAATTTCTTCTTCCCTCAGTGAGCACCATTCTTTCCGAATG[C/T]GATGATTTCTTGTA GAGACCATTCT TTCCGAATG TACTTACACAGA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGCTACCTGAATTTGTATTTTTTTAA AAAAATCCTCCCAATATTG

ID	No.					Sequence
WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT GTCTCTT	CTGAAGTGTTA AACTGGATTTG G	AACTGTGTGGTATGTATGTTGTTGTGTATTTTCTGGAGAGTCAGTTACTCTCACTAGATCATAAAGGG GACTTGGGAACCAAAGTATCTCAAGACATTAATCCTAGAAGCACAAAGAAAGTATAAGTTGTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTAACACTTCAGTAACGTT
WI-4677	82	T	C	TCCAAAGTG ATTAGGTGAA AAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTGAACATACGTCGACATTTGGAAAAATTGTCAAAAGTGATTAGGTGAAAAAT GAGTTGAAATAAATG[T/C]AAGTTGAATAATGACACTGTTGAAAATGATGAATCTGCTTTCAATTCA CATGGAAAGGAGGACTAGAACACAGCAGGTTTTTATAGGGGAATACTCAT
WI-4698	135	C	G	---	---	ATGATGTCTATCATGAGGAATTCTGTAGAAAATTTCACCTGGCAATTGATTCAAATAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTCTTTCTTTGACGGAAGAAAACTTCAA[C/G]TTCGAGAAGGCTTAGATTATATCGCTGAAGCCCATTCTG
WI-4722	88	G	A	TGCACTATGG AACACCACAC	AATATGGAATC TGCATTCAGTT G	CTTCCCATTCTGCCCAGTTAGATGACTGCCTCTCCACCAGCCTAGAAAAAGATGGGAGAGATTTATTTTC TGCACTATGGAACACCACAC[G/A]CAACTGAATGCAGATTCCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAAGAGGAAAATGGAGCCATGTAACAGAGGAGAGCTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAGTAAATCACTTTGATGGTTGAGATTTCAGAAAACGTGAAATTATTGAGTAACCATGGG TCAACTATGAT[C/A]CCAAAAACAGCAGTGTTGTCTAAAAAAATATGATAGTTTCTTCTCCTGTCCACC GCAATGAAAGGAGTT
WI-2028	176	T	C	TGTTTACGTTC CCTGTCTCATC	GGTTGGAAACT CAAATTACCTA GAA	GACTACAGCGGCACAGACAGGCATTGTGTGGCCTTGCACAGGTGTTGGTTTGTTGTTAAGTTAGATT TGAATCCTTTAAAGAAGAAAAGTGGCTCTTCAGTTACTACAGACCTCATCATCCTCGGTTCTCTTG CACCCAGTCCACTTCACCTGTTTACGTTCCCTGTCTCATC[T/C]TTCTAGGTAATTGAGTTCCAACC TGTGG
WI-2033	183	T	C	GGGTGCTAGA ACTAATCCCTC A	CAGTGGTTCCA CGTTCTCC	ATGTGTATGAGCTCCACATTCGCAGATTCAACCAACTATGGATAGAAAATATAGTATTCCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAATTTCCAAGGTTATACAGGACCAGTGTTGGAATTT AGCATTCTGGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA[T/C]GGAGAACGTGGAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTTCTGGTGGAAGGACAAGAGTTGAAGCAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCCACCAGCCTCCTTCCCACCATTCTCCATCCTCTACTCTTTCTACTCTGA[T/C] AGGCAGACTTATATGGAAAAAAGGGA
WI-2034	150	T	C	CCACAGTGCA CCAAGGAC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGTCTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTGAGGACCATGTGGCGCCAAGA CCTCCTTCTGCGCGTTCAGTGAAAAGACGATGAACTCCTTCATCTTCTACAGCGAGCTTGACTTCACCA CAGTGCACCAAGGAC[T/C]CGGACCTGCACCAAGGACT[T/C]CGGACCTGCGCACTCTATCTTCTTTACCCCTTCCGCGACACCAGATGCTGAGATGCC ACACTCTGAGTG

Marker	Pos	A1	A2	Sequence col 1	Sequence col 2	Sequence col 3
WI-2038	155	C	T	TGTGTCTTAAAG GTGTGTAAGT ATTAATTAG	ATTTCCTCTTG AAAGAAACAT CA	TCAGGTGACAAGAGAAAAGTCACATTTCTTCAATCACTCACCATTGTCTGTTATTGTCTCTTGCAGTGT ATCCAAGGATGTCACTTTGGAACTCTGTAGATCAGAAAAACTGTGCTTAAAGTGTGTAAGTATTA
WI-4782	113	C	T	GATGCAGAAG ATAACTAGAA AATGC	GAACTCTTCTG GTTATTTTCT GTTC	ATTAGATTTCTATTTGATA[C/T]TGATGTTTCTTCAAGAGGAAATTTGTGTAAGAGGATTCCATT TGCATTTCCATTGGC TCATTGACTTTTAGAGTTCCTTCAGTCTTATGTCTTATTTCTTTAGGAAAAACTAGGCTAGGGAGAA CACAATTCAGGTTCTCTCCAGATGCAGAAGATAACTAGAAAATGC[C/T]GAACAGAAAAATAACCA GAAGAGTTCATTATGGTTTTTTTCCAGAACGATTAC
WI-4788	65	A	G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAATT AAAAATTTTGGC ATAA	AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAATTCAGTGCATAGAATCATCTGCTAAGTTCC[A/G] TTGAAAAAAATTATGCCAAAATTTAATTTATCCAAACTTAAGTCGAGATTATAATTGATATTT AAAAAACTATATTGAGTCTTTCTAAAAAGATGGCGTATCACTCTA
WI-5300	38	T	C	TCCCAGAGAC CACTTCATTC	CTACTCTTCT ATTTCATAATC CAAAAA	CTTACTTCCAAAGTGTTTCCCAGAGACCACCTTCATTC[T/C]TTTTGGATTATGAAATAGAAAGAGT AGGTGTTATTATTCCTCTTTTACCAAGGTGAAATTGAGGCTCAGAGACAAGGTAGTAGATGAGCCCA AGGTCAGTGACAGAGCCA
WI-4818b	121	G	T	TGATAATGGG GCCCTGTT	CCTTCCTTTA TATGTATGCCA GA	TATAATGTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAAACAATCTTATATA ATAATTTATTCAAGAAGGAAAAATATACATATGGGGTGATAATGGGCCCTGTT[G/T]CTCTGGCATA CATATAAAAAGGAAGGCTAA
WI-4818a	43	A	G	TTGCCATAGAC TAGGTTATGTC C	CATATGTATAT TTTCCTCTTG AATAAATT	TATAATGTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCC[A/G]CACATGAATAAACAATCTTAT ATAATAATTTATTCAAGAAGGAAAAATATACATATGGGGTGATAATGGGCCCTGTTGCTCTGGCATA CATATAAAAAGGAAGGCTAA
WI-5317	139	T	C	TTCCATTTCTG GTAGCAGGT	GATGCAAAGA AGAAATGAGTC C	TTTTCCATTTGTTGATTCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAATAATGATGTTTATATATTACAATTCAACAGGAATTCCATTCTGGTAGCAGGT ATA[T/C]GGACTCATTTCTTCTTGCATCTATTTCTAGGTTATTTGCAGCCCCGAGATCTACCCAGG
WI-4888	56	G	A	GCAAGATATA AAGATTAAGA AAAGATAACA	CAATTCCACTA CCTCATTTATT CA	AAATGAGTAACCCAAGTTACTCGGCAAGATATAAAGATTAAGAAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAATTGCTTGATAACTGGAGTAGTGCCTT
WI-5328	44	A	G	---		AACATTTTTAACCATGCTACATTACAAACACTGAAAAGAACAG[A/G]AAAAAAAAGAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAAGAAAATATGAATCAGAAAAGGAAAGAAAT AGAAACACGTGATACTGGAGGAG
WI-4897	93	A	G	---		GCCTTTTTGAGTTTAAGTCTTTTGAGTGGTGTCTTTTTTTCCCCCACTAGTGTACTCTCGGCCCAAAT CCCCAAAAGAAAATAAGCGCCTTGG[A/G]GATAAAACACATCTTC
WI-5345	29	G	A	---		CCCTGCTATAGGTCAGTTTGTCTGCATTTCTATATCACTCAGCTTCAGATCCATCAGTTTGCTTGTTGAAGCCACATCCACT GAGGTATATTCTGTGTCTGCATTTCTATATCACTCAGCTTCAGATCCATCAACTTGCAG

				AATAAGATGG TACCTTAACTA CATAAAACAA	CAAAGTTGGTA CAGAGAATTTC AAA	
WI-5370	143	T	C			TGCATGTTACTTCTTGGAAATCATAAAGGGATCTGAGAGCCTACAGTATATGGCAACATTAACCAAT CTTTTGAAAATTTACCTGTATCCCATCATGGTTCATTTGCAAAAAATAAGATGGTACCTTAACTA ATAAAACAA[T/C]TTTGAAATTCTCTGTACCAACTTTGCTTTTC
WI-9711b	423	T	A	---		GATCTCCTTCATCCCTCTCCAGAGAGGAGAAGAGGAAACACAAGAGAAGAAACGCCTGGTGCAGAGCC CCAATTCCTACTTCACTCATGGATGTGAAATGCCCAGGTGAGGAGGACGGGCTTGCTGTGAGTGGGGAAAGCAC TGGACCTCAACAGTTGGAAAAATGTTGTAGTGTTAGCTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTTCTTCGCCTGTGGAAAATATTTCCCTGATACTCTTAAAATTTGAATG
WI-9711a	390	C	A	---		GATCTCCTTCATCCCTCTCCAGAGAGGAGAAGAGGAAACACAAGAGAAGAAACGCCTGGTGCAGAGCC CCAATTCCTACTTCACTCATGGATGTGAAATGCCCAGGTGAGGAGGACGGGCTTGCTGTAGTGGGGAAAGCAC TGGACCTCAACAGTTGGAAAAATGTTGTAGTGTTAGCTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTTCTTCGCCTGTGGAAAATATTTCCCTGATACTCTTAAAATTTGAATG
WI-9702c	345	G	A	---		GGAGGAATTTCAGGGTGAATGGACTGCTCCCGGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTCTACAGGTGCCCTCTGTGCCTATTCAGCAATTCCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTTGCAACTTCTCAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTCATTCCAGTGTGCTACAGCATCTGATAG
WI-9702b	344	C	T	---		GGAGGAATTTCAGGGTGAATGGACTGCTCCCGGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTCAGCAATTCCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTTGCAACTTCTCAGTTTATT[C/T]TAACTTTAATGATCTCTGTGA CTTTATACTAGCTTTAAGAGGTTTCATTCCAGTGTGCTACAGCATCTG
WI-9702a	179	C	T	---		TATAGTATTTAACGAAGCCTAGAAGCACGGCTGTGGGTGGTGATTGGTC[C/A]GCATATCTTAGGT ATATAATAACTTGAAGCCATAACTTTAACTGGAGTGGTTTGATTTCTTTTTATTTATTGGGA GGGTTTGGATTTTAACTTTTAATGTTGTTAAATATTAAGTTTTGTAAAGGAAAACCATCTCTG TGATTACCTCTCAATCTATTTGT
TIGR-A003N21	49	C	A	---		AGAAATGGCTACTTCATAGGGCAGCAGCCACTTTGGCTAATTTTAACATCCAAAGCTAATAAAT AATCAAGAAGAAATAGAGAACATTAACAAAATAAATTATGTTCTATTTGGGAATACCTAATATCAG ATACTAACAACAAGTCAGTGATAAGAATAAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAAG[C/G,T]CTTCTAGGTTAGTAGAAAGTT
TIGR-A004V30	203		G			

ID	Pos					Sequence
TIGR-A004W22	232	C	A		---	GGATAAAATCAGTACAATAATGGGGACCTTAAAACTGCTGTGATGCAGGAGGTGGAGGGGCTGGGCAGTG CCCGGAGGCAGGGGAGGAGCAGTGGGACAGGGATGCTCAGTGGTGGAGCAGCCCAGCCCTGGGCTCTGGA TGGGGCATGGGAATGACCCAGGTTCCCACATCATGCACAGCAGGGGCCTGTGAGCTTGAGTGCAGACAG GCCTGCCCCACATTGGTGCTGCCCCCCGCCTA[C/A]CTGGAGATGTCTCTAAAA
TIGR-A005D24 b	138	C	T		---	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAAAATTCTCTTGAGATAATTGATTTCATATTC TGTGGCTTCAACCTCCATTTACCTCTTGTCATTCCAACATCTTTATAGAGAAATAAAAACCCAATTT CTC[C/T]TTTCACCATTAGTTGATTATCATCTGGATTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTAAATTCATAAACTCCTTCACCTTTAATAATTAAGGAAACAAT
TIGR-A005D24 a	123	A	G		---	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAAAATTCTCTTGAGATAATTGATTTCATATTC TGTGGCTTCAACCTCCATTTACCTCTTGTCATTCCAACATCTTTATAGAGAAAT[A/G]AAAACCCAA TTTCTCTTTCACCATTAGTTGATTATCATCTGGATTTCACTCAAGATGCAGCTCCTAAGATTATTG TTATGTAAATTCATAAACTCCTTCACCTTTAATAATTAAGGAAACAAT
U03735	74	C	G		---	TGAGTCTGAGCACGAGTTGCAGCCAGGCCAGTGGGAGGGGTCTGGGCCAGTGCCACCTTCCGGGGGCC GCATCC[C/G]TTAGTTCCACTGCCTCCTGTGACGTGAGCCCATTCTCCACTCTTGAAGCGAGCAG TCAGCATTCTTAGTAGTGGGTTTCTGTCTGTTGGATGACTTGAGATTATTCTTGTTCCTGTTGGA GTTGTTCAAATGTCCTTTAA
U39840b	42	T	C		---	GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAAT[T/C]CAACAGCAAACAAAACCACA CAAACCAAACCGTCAACAGCATAATAAAATCCAACACTATTTTCATTTTCATGCACAACC TTGCCCCAGTGCAAAGACTGTTACTTTATTATTGTGTATTATTACTACAAA GACGGGCCCCAAACCAATTTTTCC
U39840	56	A	C		---	GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAATCAACAGCAAA[A/C]ACCACA CAAACCAAACCGTCAACAGCATAATAAAATCCAACACTATTTTCATTTTCATGCACAACC TTGCCCCAGTGCAAAGACTGTTACTTTATTATTGTATTATTACTACAAA GACGGGCCCCAAACCAATTTTTCC
WI-8997	41	G	A	GCCCACTTGCT CCCC	TGTTTGTACGC AGTGCTCA	GTGGCCCACATCGGACCTGGACCGTCCCCTGCCCACTTGCTCCCCC[G/A]TGAGCACTGCGTACAAACATCCA AAGTTCAACAACACCAGAACTGTGTGTCCATGGT
WI-7008	180	A	G		---	TATACCACTTCCATTTGATGATGAATGCTGCTGTTCATGACCAACTTTATGGCTAGATGGGTCAGAA AGCACCCAGTTCATGATAGGCAGTCAGGTCATATGGTGACTTGATGACCCAGAGTCAAACATTCAG TTTCCACCAAAGCCCAGTAACAGCCCAAGAGCTGTCTCTCAAAAG[A/G]AGAGTAGTTATCTGCAGA AGATGGCAGGGCCTTGCTCCGAAAGCCTAGAGACGCCACTGTGATTCACCT
WI-9005	26	C	T	CGAATTTGCTG GGGAATCT	TCCCAAAAGTC TTAAGAAGAA AAA	GGTCCCACGAATTGCTGGGGAATCTC[C/T]GTTTTCTTCTTAAGACTTTTGGGACATGGTTTGACTCC CGAACATCACCGACGCGGTCTCCTGTTTCTGTTTTCTGGGGTGG

ID	Pos	Allele 1	Allele 2	Sequence A	Sequence B	Sequence C
WI-7593	46	G	A		---	TTTTTGTTTGCTCTGGACACCCACTGCTCCCAGGATGAAAGGAGAG[G/A]AATGAGATCAGTTTTGGACACTTCCTCTCTTGAAATATAAAGAATCAACAAGTTACAGTCATGTTGGGGACTCTT
WI-6962	78	A	G		---	AGTTGCATCTTGGGGGAAAGGGCTCCAGTGTTATCTGGACGGTGTTATCTGGACGTGTATAATCCAAGACAGAACCCAAGTCTCCGATCCAGAGA[A/G]GACAAAGCTCCTCCTCTATCCATCATAGATAACCATTCTCCACAGCCTCCACTTCATTCCACTGACTCCTGGCCTTCTGAAAATATTCCCTGAGAGAGAACAGAGAGATTTAGATAAGA
WI-7059	43	C	G	AAGGCACCCA GCCATC	GCTCCTCGCTG GGTCA	GCAGAGAAGAGAACCATGCCAGGGAGAAGGCACCCAGCCATC[C/G]TGACCCAGCCAGCGAGGAGCCAACTATCCCAAATATACCTGGGTGAAATATACCAAATTCTGCATCTCCAGGAGAAAATAAAGAAATAAA
WI-9063	53	A	C	CACTTCACTGA AGACACCAT TT	TCTACTTCTG CCCTTGGGT	AGCAGCCATCACACATGATCTGTTTTCACCACTTCACTGAAAGACACCATTAT[A/C]TACCCAAGGGCAGAAAGTAGAACTTACTATTCATTAAATGTTGACACAATTGGAATTGTC
WI-7079	293	T	G		---	AAGGGGCATTGAGACTATAAAGCAGTAGACAATCCCACATACCATCTGTAGAGTTGGAACTGCATTCTTTAAAGTTTATATGCATATATTTAGGGCTGCTAGACTTACTTTCCTATTTCTTTTCCATTGCTTATTCTTGAGCACAAAAATGATAATCAATTACATTTATACATCACCTTTTGACTTTTCCAAGCCCTTTTTACAGTCTCTTGGCATTTCCTGCCTAGCCTTGTGAGGTAACTGGGAT
WI-9074	38	A	G	GGTAAAAGTT CTTTTGCTCT AAAAG	GACAGATTTT GACCTAGTTCC TT	TGGATGCCGAGGTAAAAGTTCTTTTGCTCTAAAAGAA[A/G]AAGGAACTAGGTCAAAAATCTGTCCGTGACCTATCAGTTATTAATTTTAAGGATGTTGCCACTGCAAATGTAACTGT
WI-7104b	249	C	T		---	GGAGTTTGCCCCTTCCTAAGGGAAGGAGATCTTTATCTTTCTGGTTGGCTTGACCAGTCACGTTGGGAGAAGAGAGAGTGCCAGGAGAACCCTGAGGGACCGGTTCCTACTTTGGACTGAGAGAAGGGAGCCCCAGGCTGGAGCCATGGAGGGCCCAGCAAGAAGGGCTTGGGTTCTGAGGAAGCAGATGTTTCATGCTGTGAGGGCCTTGCACCAGGTGGGGGCCACCAGCAGCAGCATCTTTG(C/T)T
WI-7104	157	C	A		---	GGAGTTTGCCCCTTCCTAAGGGAAGGAGACCCTGAGGGACCGGTTCCTACTTTGGACTGAGAGAAGGGAGCCCCAGGCTGGAGCCATGAGGGCC[C/A]CAGCAAGAAGGGCCACCAGCAGCAGCATCTTTGCTGCTGTGAGGGCCTTGCACCAGGTGGGGGCCACCAGTTTCCACC
WI-8974	34	C	T	CCTGAGCCCTC AAGAACTCA CCTGGC	TGTAGGGCTGA GCTGGC	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA[C/T]GCCAGCTCAGCCCTACACCAGTTTCCACCTGGAGTTCATGCAAGGGCAAAAGGCAGTGCCATGCAAGCTGTTTAA
WI-9161	61	C	T	CCTAAGCATTG CCTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTTAGCATTACCCCCAACCTCATTTTAGTTGCCTAAGCATTGCCTGGC[C/T]TTCCCAGAGAGGTGGGGCTGGATCTGTCTAGTCTCTCGTGAACCTGTGTTTCCTCCCCCAGTCATCTTTCCTGCTGTTCCAGAGAGGTGGGGCTGGAT
WI-9014c	93	T	C		---	CCCTGTTCCCATCTCTGTCTGCAACTTAT[T/C]GTGCACTGAGCTGCAACTTCTGTCTCCATCTCTGTCTGCAACTTAT[T/C]GTGCACTGAGCTGCAACTTCT

ID	Pos					Sequence
WI-9014b	44	C	T		...	CCCTGTTCCCATGCTGACCTGTGTTCCTCCCCAGTCATCTTTC[C/T]TTGTTCCAGAGAGAGGTGGGCTG GATGTCTCCATCTCTGTCTCAACTTTATGTGCACTGAGCTGCAACTTCT
WI-7023b	206	C	A		...	TCTGAGAGAAATGACTTGTGGGAGACACCCTGCAGATCCTCATGGGTTTGTGACAGACCCTGCGTGCT CAGTGCCCTTAAGTGCATCCCGCTGCTGACTTGAGTGGGATCAACATCTGTCCTTCCCCATTCAACAC TCTTTTTTGGGCCCCAGTATTCATGCTCTCTACCCAAAGCTCTGGCTGGCAGCACTAA A[C/A]ACACACACATTCTTGCTCTACCCAAAGCTCTGGCTGGCAG[A/C]CCCTGCGT
WI-7023a	56	A	C		...	TCTGAGAGAAATGACTTGTGGGAGACACCCTGCAGATCCTCATGGGTTTGTGACAG[A/C]CCCTGCGT GCTCAGTGCCCTTAAGTGCATCCCGCTGTGTGACTTTGAGTGGGATCAACATCTGTCCTTACGGGGTC CCCTCTTTTTGGCCCCAGTATTCATGGCCAGGGTTTGTTGGACACCTGAGCAGCACTAA CACACACACACATTCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54	C	T		...	CTGAAATCCCCTCTCTGCCCTGGCTCGGGGACCCCTTTGCCCTTCCCT[C/T]GGCTCCCAGCC CTACAGACTTGCTGTGTGACCTCAGCCCAGTGTGCCGACCTCTCTGGGCCTCAGTTTTCCCAGCTATG AAAACAGCTATCTCACAAAGTTGTGTGAAGCAGAGAGAAAGCTGGAGGAAGGCCGTGGGCCAAT GGGGAGCTCTGTTGTTATTATTAATATTGTTGCCGCTGGTGTTGTGTTA
WI-9171	62	G	A		...	ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGAATAAAAGTAGAGATAATAATCA[G/A] TTCTTTACAACCGATGGTAATTAAGCTTGTATTCACAAGACTTCATGC
WI-9171		CTAGGACCCC ATTCTCCTATT CT	TCTAGAGGGTA TATAGGACAGG ACTG			GTGTGAGACCATCATCATGGTGCCAGTCTAGGACCCCATTCTCCTATTA[T/C]CAGTCCTGTCCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAAATTGAG
WI-9174	47	T C T	CAGAGGTCTTG			AAGGCCAGATGCACATCCCTGGAAGGACACTCCATGTCCGAGAAGAACAGATA[A/G]ATCCCTGTATT TCAAGACCTCTGTGACCTATTTATGAACCTGCCCCCAGAACACACAGCAATTCCTCAGGCTA AGCTGCCGGTTCTTAAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-7753	52	A G GAAGAACAGA	CCATGTTCCGA AAATACAGGG A			AAAGAACTACAGAGGGACGATGTCCAAAAACAAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCCGCA[G/A]ACCTAGGTCAGACTTTCCCTTTCATCTT
WI-9186	76	G A CGCA	AAAGGGAAAG CCACTTCTCCC TCTGACCTAGG T			TTGGACAAACCTAGAATTTTCTCCCTTTATGTATCTCTATCGATTGTGTAGCAATTGACAGAGAATAA CTCAGAATATTGTCTGCCTTAAAGCA[G/A]TACCCCCTACCACACACACCCCTGTCCTC
WI-9193	94	G A CA	AGAATATTGT CTGCCTTAAAG GGTGTGTGTGG TAGGGGG			TTTGGATTGATATCGTGAAAGATAAACACAAAATCCATTCCAGGTAGCTCGGCACCAACTAAGAA CTTTCCCTAAAGAAGAAGATAAACACAAAATCCATTCCAGGTAGCTCGGCACCAACTAAGAA
WI-9015	48	C	T		...	GGAGCCAGGAGGACAGCAGGGTCTGAGAGAGGGTCTGAGACTGGGGAAGAGTCCAAGGAGGAGCAGCCAC[A/G]GTCCCTAATGACACCACCCACTCCTAGCC
WI-7254	37	A G AGGAGCCAC	GGTCTGAGAG CATTAGGGA GGAGTGGGTGT			CTGAGGGCTCGTGCCCCTCAGACTGGGGAAGAGTCCAAGGAGGAGGAGCAGCCACTCCTCAATGC TCAATGGCTCCCCTGAAATCAAGACAGG

Clone	Pos	Allele		Fragment	Fragment	Sequence
WI-9231	32	G	C	CAGGTCCCCCA GATTGA	CACTTGCCCAC ACTCAGAC	GTGACCCTGCTGTGAGGTCAGGTCCCCCAGATTGA[G/C]GTCTGAGTGTGGGCAAGTGTGTCAAAAGGGGC TGCCCCCCAGGAGGATGAGGCTGAGAGCAGGAGGGAGTTGAGGCCGAAGAAGTCA
WI-7836	120	T	C	CAAATAAACA ATGCAACGTTC	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTTGGGAAATAGAGAGTTGAGATAAACACTCTCATTCAGTAGTTACTGAAAGAAAACTCTGCTA GAATGATAAATGTCATGGTCATCTATAAACTCCAAATAAACAATGCAACGTTCC[T/C]GATTTCTAAT CTTGGTTCTGAGAGCCATTGGTTCAGTTGTAGCAATCCCCATACCAGCT
			C	CAGCTTCAGCT TAACTGACAG	AAACAATCTA	TCCATTCCTTTGGCCCTGCCCAGCATGTCATGCTCCCAGAATTCAGCTTCAGCTTAACTGACAGA[T/C]
WI-7286	65	T	C A			GTTAAAGCTTTCTGGTTAGATTGTTTCACTGGTGATCATCGTCTTTCCATGTGTACCTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91	T G	TAAAT	CTAAGCATGT ACGTGAATTTT TTAAAAGTTTA CATCTAT	CCCAATTTTA	CAAATTCTTGGAAATATCTCAAATGTTAATAACAATGAAATTTTCTCATGCATACTATTACTACT AAGCATGTACGTGAATTTAAAT[T/G]TATAGATGTAAACTTTAATAAAAATTGGGGTGTGG
WI-7860	50	C G	...	A		GAAGATTAAGGGAGGGTGTGCTCTGTGTCTCCTCCCTGCCCTCTCCCCA[C/A,G]TGGGGAGAGACC TGTGATTTGCCAAGTCCCTGGACCAGTCACCTGGCCTTATGGGTTGGGGGTGGTAGGCAGG TGAGCGTAAGTGGGGAGGGAAATGGGTAAGAAGTCTACTCCAAACCTAGGTCTCTATGTCAGACCAG ACCTAGGTGCTTCTCTCTAGGAGGGAAACAGGGAGGACCTGGGGTCCTGTGGAT
WI-9064	29	A G	TTC	CGTACCTCCAA ACATAATTGA	GCTTGAGTGTA AGTCTCGCGAGA	CAAGGCGTACCTCCAAACATAATTGATTC[A/G]TATCTGCGAGACTTACACTCAAGCAATCCTGAGG AATACTGAGGGAGGGCCTGGCTACTGTCTCTCTGCGACTCTGCTTTG CACACTTGTCTGTTCTTCAGTGCTGGAGGTCTGGCAGGGTCTGGCCCCCAGAGGTCCTCCCTCAG[G/T]AACT GGGCCCAGCCCTGCGCAGGGGTCTGGCCCCCAGGTAGGGCGGGAGAGCAGTCCCTCGCCAGCCTCCAGT GGAGGAGGGGACTCCAGGAATGGGAAATGTGACACCACCATCCTGAAGCCAGCTTGCACCTCCAGT TTGCACAGGGGATTGTCTCTGGGGGCTGAGGGGCCCTGTCCCCACCCCCGCCCCC
WI-7307	128	G T	...	GAAATGTGAC TTCACTTGGT	CAGGTAGAATT TTCTGTCCATT	GAGGAAATGTGACTTCACTTGGTG[C/T]CAATGGACAGAGAAAATTCTACCTGTGCTACATAGGAGAA GTTTGGAATGCACTTAATAGCTGGTTTTTACACCTTGATTTCGAGGTGGAAA
WI-9274	25	C T	G			AATTCCTTTCTGGTAATCAGGCACATGATGAACTTTGATTAGTAGGTCTGTGATTAAGTTCTTAAAT TGTTTGCAGTCTTTATGTTTATTATCATAGGTAGGTGGACCTAAATTCCTTATCTCATATCTTTATT AATTCAGCCAGTGTATCCACCAGTTTTTGTTTTATGTTTTATGTCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTTTGTTAAACTGAATTGTATAGCGATGA
WI-7313e	266	T C	...			AATTCCTTTCTGGTAATCAGGCACATGATGAACTTTGATTAGTAGGTCTGTGATTAAGTTCTTAAAT TGTTTGCAGTCTTTATGTTTATTATCATAGGTGGACCTAAATTCCTTATCTCATATCTTTATT AATTCAGCCAGTGTATCCACCAGTTTTTGTTTTATGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTTTGTTAAACTGAATTGTATAGCGATGA
WI-7313c	256	C T	...			AAGGTGTAATATCGTTTTTGTTAAACTGAATTGTATAGCGATGA

Clone	Pos	Allele 1	Allele 2	Fragment		Sequence
WI-9281	68	G	A		...	ACTGGTGGGAGACTGTGAGGATCCCAGGATTCAGTATCCTGGCCGTATTCCTGGCCCAGAGGGCCTTGCTGGCTACTGG[G/A]TGTTAGTTTGCAGTCCTGGTGTCCTCTATGACTGTGTCCC
WI-7848	142	A	G	GCTAACACTT TTAAAACCGT CTC	CATTTATTTG AAAGCTATTCA GACA	TTCTGAAAATATAACCAGCCATTGAGCTATTTAAAACTTGTAATTTTTAATTTTTACAAAAATATAA AATATGAAGACACATAAACCCAGTTGCCATCTGCGTGACAATAAAACATTAATGCTAACACTTTTTAAA ACCGTCTC[A/G]TGTCTGAATAGCTTTCAAAATAAATGTGAAATGGT
WI-9304	70	G	A	GTATATTACA ATGATCACCG ACTGA	CCCACAGAAC TATTGTAAAAC AA	TCACGTTTGGTGCTTCTCAGATTCTGAGGAAATTGCTTTGTATTGTATATTACAATGATCACCGACT GA[G/A]AATATTGTTTACAATAGTTCTGTGGGCGTGTTTTTTGT
WI-7933b	314	C	A		...	TTACAGAAACTTGCCCTGTGCCTGTGCCCCATGCTAGGGGCGGAGGGGTCTTTCCTTCTTCTTTCC TACCTACCCCTTTCTTCTTGGCCAGGGGCCTCGTATCCTACCTTCCTTGTCCCCTGGGCTGGCTGCAC AGAGGATTGCCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTTGCACAA AGTCTAAGGGACCATGGCTGCCTGCCTCTGGGGAGGAACCATAGCTCCCT
WI-7933	96	G	C		...	TTACAGAAACTTGCCCTGCCCTGTGCCTGTGTCCCCATGCTAGGGGCGGAGGGGTCTTTCCTTCTTCTTTCC TACCTACCCCTTTCTTCTTGGCCAGGG[G/C]CCTCGTATCCTACCTTCCTTGTCCCCTGGGCTGGCTG CACAGAGGATTGCCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTTGCA CAAAGTCTAAGGGACCATGGCTGCCTGCCTCTGGGGAGGAACCATAGCT
WI-7374	182	T	A		AAATGAAACTT ACGTTTGTTG TG	CCCAGATGTGCCCATCACGTTTTTCTGAGGCTTTGTACTTTAGTAAATGCTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTTGACTTTGTTAAATATTTGAAATGTAAATGAAAGAAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTTCTAGCTGCTGTTGAAGAATATATTG[T/A]CAGAAAACACAAGGCTT GAT
WI-9343	78	C	T	CCAACAACAT CCTCTGCCA		GGTCTGCTCCTGCTACCTTGACCCTTCCCTTTCCTCGTCTCCTCATCATCCCAACAACAT CCTCTGCCA[C/T]ACACAACAAAAACGTAAGTTTCATTTGGGCAAA
WI-7386b	104	T	A		...	CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAATGTAAACAATTGTTA[T/A]GTGTTTAGAATCAGAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75	A	G		CTTTAGAAAA TCTGCTTTAAC CCTAGGGAACA CAATTAGAGGA	AAGAAGGAGCTCAGTTACGGGGGTTTTAAACCTTCATGAAAACCTGAAGAGTTCACTTTTGTTATTAT GCTCTTA[A/G]TGATTTACAGACTGATGCCAGACAAACCTTGGGAAGA
WI-9360	79	T	C	TTGG	A	TGAAGGGGTGTGGCATCTGTGTTTCTGATGCTTACTACAATATGTGAACCACTACTTTAGAAAATCTG CTTTAACTTGG[T/C]ATTCCTCTAATTGTGTTCCCTAGGAAATGACTGTCCCAAG
WI-7423	107	T	C	TGCTGGGGCTGT GGTCCAGAAGA GCCCG		TGCTCCCTGTCCCATCTGCAGTGGACCCAGGACCGCATTGTGACACTGCATTGCGGCTCTGTGTTCCT[T/C]CGGCCTCTTCTCTGGACCTTGCGACCGTG GATACCAGGCCAGGCCATGTGCCATGTGATTTGGGCTGGTGGGTGAAATAAAGGCATACTGTCT

Marker	Pos.					Sequence
WI-7424	131	T	A	CAAGAGAGAG AGAGGAAAGA A AAAA	TGCAAAGAAA GAATGAAAGT G	CCAGGAGCACTAGAGAGGGAGGGGGAAGAGCAGAAGTTAGAGAAAAAAGCCACGGAGGGAAGG AAAAAACATCGGCCAACCTAGAAACGTTTCATTCGTCATTCCAAGAGAGAGAGAGAGAAGAAAAAAA [T/A]ACAACTTTCATTCTTCTTGCACGTTCATAAACATTCTACATA
X86400	118	A	C	---		TCCTGCAAGAAGTTCTCAAGCCTTTTGATTTTGTGCAATAAAGTACAGCTTTGCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACTTTCTTCTTCTAATTTAAGTGAGA[A/C]TCTTTAAACACCT GTTAAATTTAATGTAGCAGTCTGAGAAATCTAAAATTATGTACCACTCGTTTATTGTTCATTCATCCA TCCCTTTTCCCATGAATATTTCA
WI-8053	242	T	A	---		GTGGCCACTACATGTTATAGAAACCATCATCTTGTCACACAGCACAGTCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAGAAAAAGCATTAAAAGTGTCCCATTAAAAGGGACTTTAATCAACCTAA TAAACTCTAATTCTGCTGACTTTTAAAGATCTAAGGTCATTTTAATACATGCTGAAAAGGGTCACA ATTAATTCTTGATCTTTTTACTCACTGTTAACTTATATATAAAA[T/A]TTCAGAAC
WI-6190	165	G	A	---		TACACAATGAATTGCTTTTATTCGGTATGCATCCACATTTCAGCATTTAGTGGTCCTGAACAGCAAG TGGAAAGACGCAGCAATTTGCCAGGAGGTCAAGCCCAACCAATTTCGGGGATCTGCTGTGCACCGG GTTCCTTCTTAATCCCTGCTGAGGATCTTG[G/A]GAAGCAGCAGCACCAAAACCAAGGCATGCA CCGGATTCAAGGTGTCTTTTTGTTCCAGTTGTGTCAGATTCCAAACTAGACCCCA
WI-6275	148	G	C	---		AACAGTCACCACCAACCACATGACCAACTCGCCCAGGCAAGGCCTTGCTTCCCTCCCCCTTTGCGTCCC ATGTGCCAGTGTCAGCGAAGGTCGGGGAGGCACCGATGTTAGCTTCGCGCCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAAA[G/C]GGAAGGAAACCTGGACAGGCTTTCAGCACTGAGAAATCACTTAAAACTG ATTTGCTTTCAGTAACTGGTATGTCTGAA
WI-6421	41	G	T	---		ACCAAGAGATCAGCTGTCTAAAACAGCAGCTTTTTGATTGT[G/T]GGGCTTCCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGAGCCGTACCTGAGAGGGGATGGGGCTCTCTCACAAAA GAATATTTGGGGCAGAACCCTGGAACTGGCCACCAGGGACATCCCAAATATCCCCTCCTCCTCCAGGG CTCACCCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215	T	A	---		GGGTGAGACGGGGTTATTGTGCACATTTACACAGCGTCGGGGCTGGGGCAGCGGCCATGCTC CTGTGGTCGGGCTGCTCTACAAGGGCGTTCACTTTTCTTCACCACTACTATGTACAGTGCTCCAA GGTGATGGGCTACAGTGCTGCATCAGTGAGTCTGTACACACATTTTACATAAATTACACGACTC ATACATGAAAAA[T/A]AGAGCCTAAGGGCCCTGTATATTTAATGAGAAAAAAA
WI-9420	202	G	A	---		AACTTGTTTACAAAATAGGCTTTGCAAACTTCATTACTGAATTGTAAAGTCAATGACTGTGTTGTTTT TAAAATATGTACCAAGGAAAATACAAATTGGATAATGGATGATCATCATTTTCATGCTCAGGAGAACAGCAC AGAAAATAAAGGATACTGCACAAGGTGCAAGGAAACCGGAACCCATTGTGTACAGTCTTCTTCACACAG [G/A]GCATTCTTTCACCTTAACTGCAGCTGTGCAAGATGCCTCAGTGTG

WI-9448	184	G	A	TGGGGCTGCTTTAGACTTCATTCTAGAGCAGAGCACCTAGTGAGAGGAGAGAGAC TGCCTTGCCCATGGTGGTTAAAACTACATGAGGGGACTGAAATCTCTTGGATGCCAGTCCAGATCCC TTTTAAGAAAAATGGCTTGTGGTTCCAAGGCTGGCCACCAC[G/A]CACTGGTTTCTAAA TCTCTGGCTTGGATTTTATCCAAGCGCATGTTCCTAACGTGCCCGTGAGCAG
WI-9470	204	G	A	ATGTCAGAAGAGACACAGACAAGAGGAGTTTTTCCCTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAAATCAGATTCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCACGAATATGATCTCCCTAAAGCCCAGATTCCTACTAGAGCCGCTGGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCTCCAAGCTCACCAGGGCTCACCTTCCCAAG
WI-1245b	201	G	T	GATGATTTCTGAAGTCCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCCTGATGCAGATCTGCTGTGAGCCATGTGCTGCGGCATCACAGGGGT TTATTAATTTCATTTATCATCTGGACAGCCCCTTCTTATAACGTACATCCTTGCCTCTCTTCTGAGGC T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T	C	GATGATTTCTGAAGTCCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGG[t/C]GCCTGATGCAGATCTGCTGTGAGCCATGTGCTGCGGCATCACAGGGGT GGTTTATTAATTTCATTTATCATCTGGACAGCCCCTTCTTATAACGTACATCCTTGCCTCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G	A	TTCAGTGATAAGGACAGGTCTAGAAACAAGCGGTTCCCAACCCTGGCACCAATGACAGTTTGGACCAAA TAACTCTTTGTTTCAGGGGACTGTCCTACACATTGTGGGATGTTTAGCAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACACAACCCCTCCCCAACAATCATGACAATGTCTTTAGACATT GCCAAATATACCTTGTGTGGGACAAAATGGCCCCTGATTGAGAACCACTGGTT
WI-5385	110	G	A	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAATGGTGGGATTGAAGAGG GAAGTCTCGATAATTTAACATATGGTTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTAA TTCTTTATCAACAGACTCTTTGAATCAATTTAGAGAGATACTCAGTGAGCCCCATGGCTAGAGTTCCTGAC CCCTGCTACGGGGAAACATTGAATGCA
WI-5403	199	T	G	ACCAAAACGTTGGCCAAAGGCTCCCCAAGACTCACCACCCCAACTTGGTGCTTACCCTATGCCGGGTG GGATTGAAGAAATAACCATAAAATAATTGCTACAATTTTCCAGTAGTAGTTACCAGGCACCAGCCTAT TGGAAGAAATCATAAATGTAACCCTACAATGTATTGCTCTCTGGCTTGGTGCCAGGCATAGAGTT[T/G]]GGCCTACAACCCATTTTATCCTTTATCATTGAACCCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	G	A	TGGTATTTTCCTTTTCCTAAAATGTTATGATTAATTAGTGTCTTTGTAGAAATTGAAAAAATGTAAA TCAGAGAACAGAAAGAAAATAAAGTATAGTTGAAACCTCTAACAATTTGAAACCTCTAACAATTTTAGATTTTTAAGGCCTAG GGAAAGAAAGAAGAGCCTGGAA[G/A]AGGGAAATGAACAAACCAGAAAAAAAGTGTGT GGCTTAAGGGGAAGCCAAGGAAGAAAGTTAAGT

Marker	Pos			Sequence
WI-5801a	48	A	G	TGGTATTTTCCTTTCCTAAAAATGTTATGATTAATTAGTGTCTTGT[A/G]GAATTTGAAAAAATGT AAATCAGAGAACAGAAAGAAAATAAAGTATAGTTGAAACCTCTAACAAATTTGAATTTTTAAGGCC TAGGGAAAGAAGAAAGAAGAGCCTGGGAAGGGAATGAGAAAAGCACAACCAGAAAAAAAGTGTGT GGCTTAAGGGAAGCCAAGGAAAGTTAAGT
WI-5696	61	C	A	TTCTATTTAAATCCTGTGCCCCATTGCAAGACTGCATTCAGTCTGCAAGCCTTAGTTTC[C/A]TAA AAGCCCCCTCACACCGAGGGACAATGTTCAGAACTAAATGACTGCAGGTGAGCAATTCTCTGTATTA TACAAACTGGGACCAAAGATGACTTTATAATAGTGCAAGAGACAATCAGGCAGCAGACTGGGAGGACC TTATAAATAGATTATATAAGGCTGTGGTGTGAGTTTATTTAACTT
WI-7461	153	C	T	TATTACTTAGGTTCATAGAGCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCCC AATTCTTAACGCTCCCTCACTTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCCTG TGGGCAGGGACTGTGTC[C/T]GTTCCCTGTTGGGTCCCCGGAACCCAGTGTGTGCCTGGCCACAGAG GAGGCCCTGAGTAGCATGTGCTGCA
WI-9716	221	G	A	AGAAGACAGAGGAGCACTGGGATCAAGGACTGATAAACTGCTTAATGGTCCCTTGTCTCTCTAAC GCTTTGGTATACTTTCTCTTTCTGAAGACCAACCCTTCAAACTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTTCAGATGTGTACTTCCTACATTCTGGAAAACTAGATGAGTTAGGCTCTCTTCATCT CAATTGAAAATTCTAGAA[G/A]AAAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49	C	T	TTTTCGTTAAGTCTGTGAAGCCACACAGAAGTGATCTACTCCTTTAC[C/T]AAGTGTTACTTTGCA TATATTTTATGGGGATGATTCTATCCCTACTTAAGATTTCTCTCTCCAGGTTAAATATTCCATTCCT TGTTCAGGAGTTTCTTATTTGGCCTTCTTCTTTTTCTAAAACCCTTAACCATTCTGCTTCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31	A	C	GAAAACCTCGTTGGCTCAAAGGAAAACTGTAG[A/C]AAATTCTTTTTTTTATTTTGTTTTTAACTC AAAGAGTGGAGTTTGCATTGCAGCCACGCTGCTCTTTGTTTTGGTGTAAATCCTCTAGT GGGCACTTTGCAAAAGCAATTTTAGAGCCAAAGGTGGTGCATGGGAAGGTTGTGGAGGTTGCTGAAAAG TAGCAAATGGAAGAAAGGGTAATGGA
WI-10312	41	A	G	AAGGCCCAGTGTGGGAAAAAGCAGAACAAAAACACTCCAAGAATAC[A/G]AGATATAAAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTCATGCTGATGAGGGCATGTCAGACCAAAAGACATTTGGGTCT TGAGGGGTTGAATAGGGAGTTTGTCTGGTGAGTCTTGCCCAGTCCCATAGTAGGTGTTCCATAAATAAAC AGTGACTAAACTGAGGTAGAGTCACAGAGAGAAATTTCA
WI-11152	179	C	T	GATTCTTTGCGACATGCGAGAGCAGCAGATACGGCAAGGCATCTTGGGCATTGGAAGGAAACGAGCCCTA ATTCATAGAAACAGACTCTACAAAGGACCAGTTAAAGGTCTCGCACCAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGGACAAGTGGGACAAAAGGCTTGTCA[C/T]TCTGTCAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167	A	G	TGGTGAGGAGCTGTAAGGCTGAAAGAATAGTCTCTGCTCGTGCTCTCGGTCTTCGTTGGAAATGGATGGAGTGCCT TTTACAAAATTTTCCTCTTGCCATGGGTGTTGTTATGTTAGAATCATGGAGTTGGAAGACTTAGAATTCA ATTTGGGCTGGTACAGTTTACTGGAAGTTGT[A/G]TGAACTTGAGCAAGTGTCTTAATGTCTCTCA GCCTCAATGCCCTTCCCTGTAA
WI-4701	198	G	A	GGGTTCATTTAACAGCCTTCCCCACTGGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGAGAGATAG AAAAATGGTGCCCACTATTGACTTGATAAACCAACAACACATTAAACTCCTCCCCCACTCTA CCCGCCAAAGTCTACCCTTTGGTTCTTTATTTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A] CCATGTCATTTTTCAGAAAAAGCAGTATA
WI-4823	164	C	A	TTTATCTTTCCAAACCATGTGTGTTTTCTTCACATACTTTACGTAATTTAAATCATGTCATTCATTTAATTA TGCACTTACTTGTTGGCTACCAGACATTGCTTCCAATTGTAAATTCCCTAACAACAGCAAGCATAACT GATGTGTGTCCATCTTGTATTCCTAAAA[C/A]AAAGAAAAGTGCTTTTGTGCATCTGCCCCTCTGT CTTCCCTCTGTTCACCTCCTGTATTCCCTATTCCAGCATTCAATGATTA
WI-4860	72	A	G	AAAAAAACAACTTCATTTGACATTCTAAGAAGATAAAGAAAAACAACGATCCACTGTGTGTTTGCTT GATTT[A/G]GGAGATAAAACCTGATCTCTAAGAAAATTAAACCAAGCAGTACACTAAAATAGCCT TTGTGTGTGGTTTTCAGGAAAGACAAGGCCAATCCAACTAAGTTGCTAAGAAAATAATGTTTCATATCA CTCTAACTTCCACATAGAGCATTAATATAGCA
WI-9705	111	C	A	TGAAAGGACCAGTTCGAATGCCTACCAAGGTAAAGTAAATCGGAGGGGCAGGAAGTAGGAGTTGCTT CCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGGTTCGGCTGCC[C/A]AAAATTGTTAACACTGATGC TGTCTACAAAGCACATAGAAATCGGTGGTAGATTGCGGTTCCTAGTAAGTAGCTAATGTTTAGATA TGATTGTTGAATTATTGTTGCTGTGTTCTTGGTG
TIGR-A004Z48	177	A	G	CAAAATAATCTCTGCTTAGAAGTTGCTCTAGGCCATGGATTCATGTAAGGGTGGGGCAGGGTGGGACTG AAGATCTGTTGGCAGGGCTCACAGAGACGGGGGTGAGGGGAGAGATCGTGGGTTCATGAGATCCCAT CTTGGGCAATACGGTTATCCCGTGTCTTCCATACGCCACAGA[A/G]TCCTCCAATTCAGGGGCTCCC GTGGGGATGGTGGAGCCAATGAAGACCAGGTAGATGATCGCCACCTAGAGATG
U17579	34	T	G	GGGGATTCAATGTGTCTGTCTCATCCAATAAGCAC[T/G]CATGACCTCAGCCCCATACTCTTCTTCCC TATGTTCCCAGAGACAGAGAATAGACCTGGCCCCCTCCTTCCTAGGGGATCACAATATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCCATGCCAAATAGAACGATGAGTGCTGGGATCAATTTCTCATGGGAGCC TGGGGAGAGGGATCCTTTCTAGTTGA
WI-7747b	88	T	G	GTGAGAGCGGAGGCTGAGCCTACAGATGAACTCTTTCGTGGCCTGCTTTCGTTAACTGTGTATGTACATA TATATATTTTAATTTGA[T/G]AAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAGTT ATTTCTTTGTTTGTTTGTTTGGGTATCCTGCCCAGTGTTGTTTGTAAATAAGAGATTTGGAGCACTCTGA GTTTACCATTTGTAATAAAGTATATAATAATTTTTATGTTTGTTTCTGA

					Sequence
WI-7747a	44	T	C	---	GTGAGAGGGAGGCTGAGCCTACAGATGAACTCTTCTTCTGGCCTGC[T/C][TCGTTAACTGTGTATGTAC ATATATATTTTGTTGATTAAATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAGTT ATTTCTTGTTGTTGTTGGGTATCGTCGCCCAGTGTTGTTGTTAAATAAGAGATTTGGAGCACTCTGA GTTTACCATTTGTAATAAAGTATATAATTTTTATGTTTTGTTTCTGA
WI-7189	197	T	C	---	TCCAGAATTTCCTTCTTCAGCTCATTTGTCTCTCTCACAATTAAGGGAGTAGGTTAAGTGAAAGGT CACATACCATTATTTCCCCTTCAAACAAATATATTTTACAGAAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTACAATGTGGTTATTTTTATATTAAGCCTACAACACATTT[T/C]AG TTTGCAAATAGAACTAATACTGGTGAAAATTACCTAAAACCTTGGTTATT
WI-7850	57	G	A	---	AGCCCCAGCTGGACTCATGGATGTGCACCCTTGCTCCCTGCTCTTTCTGCCTCTGG[G/A]CTCATGTA TCTGCGCAGCTCTGGTACCCTGTGTGGGTGCCATCTCTACCTCTGACACAGACTGCCTGCCTTGAAGCT GAGAAGGCACAGGGCCAAGGAGCCACAGAGCCTCAGCCCCAGCCCCAGGATCCGGTCCTCATTTT ATTGGTGATGATGAATGGGAATGAAATCAGGGGCGTGTCTACTAGAGCC
WI-7907	69	G	C	---	CTCTTCTTCATCCCATCACCCCCTAAATAGGTCAGGTGAGGGAGGCTGGGAAGGAGGTGGGAGGAGG G[G/C]AGAAGTGAAGGAAGATAGGAAGGATATTACCTCTTCTGTATTTTTTAAGAAACATTGTTT GGTGGCAGCAATCTCCCTGTCCCTATCCGTGTCAAGGTATCAAGGTAAAATTATTGTCAAAGTTTAAAT AGCAAGTCAAACTTGGATGTATCAAGTATCAAGGTAAAATTATTGTCAAAGTTTAAAT
WI-7919	242	T	C	---	GAAGGCAGCTGGATCACTTCCCGCAGTCCTTGGGCAGCGCTTTGCTGTGGAACACGAGAGCTCCTCCT CAGGGGCCTGGCACTCACCTTCTATTCTGTATGATGTATTGGTTAAACACTGTCAAATAATAGAGAT GTGCCAGATTAGATTTCTTACCCTAATCTGTTAATATTGTAACTTTATTCCATTGAAAGTGTCA AGCCCATTCAGATAAGCTATAAATCTGGTCTTTAAGGAA[T/C]ACAACTTT
WI-7928	101	T	G	---	CTCCCTTCCTATGTCTCTCAGCAGCACGTTGGGGCACGTTCATCTTCTGACGTTGCTGGGCTA TTCCCCTGCAGTGCAGACATCGTCAAAATTCA[T/G]ACAAGAGGAAATTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTTGCACTTAAAACTGAAATTCAACTCTTTATATAGGATTTTCTTT CTATCTCCATCTCCTCATTAAAAAATACGTACATTCGAGGTAATGGTA
WI-7936	131	T	A	---	TTTTGAGTCAAAGACTTAAAGGGCCCAATGAATTATATACATACTGCATCTTGGTTATTCTGAA GGTAGCATTCTTTGGAGTTAAAATGCACATATAGACACATACACCCAAACACTTACACCAAAC[T/A] ACTGAATGAAGAAGTATTTTGGTAACCAGCCATTTTGGTGGGAATCCAAGATTGGTCTCCCATATG CAGAAATAGACACAAAAAGTATATTAAACAAAGTTTCAGAAGTTTGTTGAA
WI-7944	99	T	C	---	TACACGTTCCAGCCCGTTGCCCCACTCATCTGCGCGGCTTTGCTTTGGTTGGGGGCAGATTGGGTTGG AATGCTTTCCATCTCCAGGAGACTTTCATG[T/C]AGCCCAAAGTACAGCCTGACCACCCTGGTGTG TGTAGCTAGTAAGATTACCCTGAGCTGCAGCTGAGCCTGAGCCAATGGGACAGTTACACTTGACAGA CAAAGATGGTGGGAGATTGGGAATGCCATTGGCATGCCATTGCAAACTAAGAGCTCTCAAGTCA

Marker	Position	Allele 1	Allele 2	Sequence
WI-7805	101	A	G	TTCTAGGCTGTACAGTCTGATGCATGATTTTTATAAATATTTCATACTCTTGTGAATTTGGATCTT TTACTTGAGCATATATTTTAGAATATGTGT[A/G]TGTTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGCAGGTTCATTGTGGAATAGTTTAACAGTCAGGAAGGCTAAACTGGTCAGTATTAAATGTGTAGC CCTACCAAAAATAGCCAGTAGTATCTGAAAATAAAATGAAGTAT
WI-7416	137	G	T	GGCCAGGAGATTAGCAACAAGGATTCATTCGTTACTTCTGTTACTGCCCTTTTATCTTCCCTCTTGCCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTGTCCTTGGCAGTGCT [G/T]CTACTCCTCCAGGTGCAGCATACATACCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAAATTGGCAAATGTCATCAG
WI-140	252	C	T	ATTTGAAGATTTGGAGGGCTTTGCCAGGAGAAAATAGATTTCAATTGGATCCCAAACTATAATGACA AGTTTTAATTAGGTGTGATCAAGGCTTCTAAAAGTGAAATGCAAGTTGTTACCAGTAAAGTTTATA TCTTCCATTCAGCCCAGCTCATTGCCAGAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAATTTTAGTTTAAAAATGTGTCATTGTCTGTATTGGCATTCCT[C/ GAGGTCTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCGAGTTCCCCGGATCAAGTGCTGGCACC CATGATGGAAACTCTTGCCATGGTTTTAGTACCCTGACCAAGTAGTCATTCCATCCTGACTTTAAAA TTCTAAACAGCCTTTGATGGGACAATCTCTGCTAAAGACTAACCACTCCTTATCTTATCTTCAGCTA CCTGCTTCCCTTTC[C/T]GTTTAACAAAGCATAGAAATATTCTGAACAACT
WI-198	218	C	T	TTCATGGTCCCAAGACAGATTTTAAAGAAGAAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTTG[T/C]CCAAAGGCTTGATGGGAAAATCTCAACATTGTTACCTAAGAGAAAGAGGATGT ATCTTACTTGTTTAAAAAAACTGCATATGCCTTTATTTTGTTTAGTTCCC
WI-205c	146	T	C	TTCATGGTCCCAAGACAGATTTTAAAGAAGAAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTTG[T/C]CCAAAGGCTTGATGGGAAAATCTCAACATTGTTACCTAAGAGAAAGAGGATGT ATCTTACTTGTTTAAAAAAACTGCATATGCCTTTATTTTGTTTAGTTCCC
WI-205b	146	T	C	GAAGACTGAGTTTCCAGGAGGTTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTGCAACCCAAGTNCTTCCAAGAGGTCTCAGACTACCTCCTCCCATCTCCCCCT CTCCCCCACAACACACAAATACAGAGATT[G/C]AATTCAGGAGCCAGTTTCTAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTGGTGTCTTAGTTTCTCAAATGGGAAATGG
WI-234	165	G	C	AGCTTTTTGAAATCCAAAAACCACATT[A/G]CTTGACTCTCTTATCCTCCTCTTGTTGTAACATCTATCC CTGAGGCAGAAAATACAGAACACACCCTGTGCCTGCCTGAACGAGGAAGGATGGGGGCGGGGAGACAT CGGTCAATGTATCAAAGCATCTCATCCCTGCCTGAAAGACCTCTCCTGATGACTGGGCAAA
WI-276b	25	A	G	---

WI-276	25	A G	AGCTTTTGAAATCCAAAAACCACAT[A/G]CTTGACTCTCTTATCCTCCTCTCTTGTTGTAACATCTATCCCTGAGGCAGAAAATACAGAACACCCTGCTGCTGCCTGAAACGGAGGAGGGATGGGCGCGGGGAGACATCGGTCAATGTATCAAAGCATCTCTCTGATCCTCCTTGCCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGCTCTGGCAAGGGCTTGTCTTATCCTCCTTGCTATCCTGATGACTGGGCAAA
WI-427	59	G A	TTTTCCCAATCCACAGGTAAAACTAATAATAATGGATGTATAGAATTTAGAACTACTTCC[G/A]GTTTTTCCCTGGGGAAAATATTCACAAAACATTGTGGTCTGCAATCAGGTTAAAAGACATAGTGTGCCATTTGTCATCAGACAGCAGGTAGAGGCCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGTATTCATTATTAGAGCCAGGGTCTTGCTCGTCTCTGTCACCCAGCTTTCAGTGCAGT
WI-562c	106	T C	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAGCCCAGAAAGGAAGCCTGTCTCAATACACTAGATATAGTTACTGTGATTATATATTTTAA[T/C]AAATGGTCCTTTATTAAAAAAAAAAAGNTATCTAAAGAGAAAAACCATAATAATCCTCAGGTAATTATGGCCACAGCCAAAACCAGTCTTTCTAAAGCCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106	T C	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAGCCCAGAAAGGAAGCCTGTCTCAATACACTAGATATAGTTACTGTGATTATATATTTT[T/C]AATAAATGGTCCTTTATTAAAAAAAAAAGNTATCTAAAGAGAAAAACCATAATAATCCTCAGGTAATTATGGCCACAGCCAAAACCAGTCTTTCTAAAGCCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103	T C	GTGTAATTGGTGGCTTGCAACTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAGGTAAGGATGAGGAAGAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCTGATACATG[A/G]TAATGACCCTCCATGAGCTCTGGTACCTCATCATTACCAATGTGAGAATTATTAACTTGATCTAATATTCTTCACAACTAATATAACCTGAGAGAAATAAGTCTATTTAAT
WI-597c	141	A G	GTGTAATTGGTGGCTTGCAACTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAGGTAAGGATGAGGAAGAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCTGATACATG[A/G]TAATGACCCTCCATGAGCTCTGGTACCTCATCATTACCAATGTGAGAATTATTAACTTGATCTAATATTCTTCACAACTAATATAACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141	A G	GTGTAATTGGTGGCTTGCAACTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAGGTAAGGATGAGGAAGAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCTGATACATG[A/G]TAATGACCCTCCATGAGCTCTGGTACCTCATCATTACCAATGTGAGAATTATTAACTTGATCTAATATTCTTCACAACTAATATAACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136	A G	GTGTAATTGGTGGCTTGCAACTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAGGTAAGGATGAGGAAGAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCTGAT[A/G]CATGATAATGACCCTCCATGAGCTCTGGTACCTCATCATTACCAATGTGAGAATTATTAACTTGATCTAATATTCTTCACAACTAATATAACCTGAGAGAAATAAGTCTATTTAAT

Clone	Pos			Sequence
WI-611	66	G	C	TTCAAATTTAACACCATTGGGTATATATAATTTTNGCTCTATCCATAGTTCTAACCCTCTTCTCT[G/C]ACAGTGAGACACCTGCCTTCTATTGTCCTTGACGTATTACCACCTGCGTATTCGATCAGTCACCCATCTGGAACCAAGGTTTCATTCTGCTGGCGTGTCCGCCCTCCTCCTGCTCCTCGCTTCCTTTCCTGGGCTGAACCCTTCTCTGTGTGGCGTGTCCGCCCTCCTTCCTCGCTCCTTTCCTGGGCTCCAATAC
WI-681b	156	A	G	TGAAGCCCTCTCTATACCCAAGTGTCTTTATCTTAAAATGCTGTGGTGCAAGTATCTACCCCCTTAGGGATATTGTGAGAATTCAATAAGTTCATACAGGGGAAGCACTTGTNCCTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[A/G]TTATACTATGGCACCATTGGGACACAGATTATATGTCAGACACCACGNATGTCCTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
WI-681	156	A	G	TGAAGCCCTCTCTATACCCAAGTGTCTTTATCTTAAAATGCTGTGGTGCAAGTATCTACCCCCTTAGGGATATTGTGAGAATTCAATAAGTTCATACAGGGGAAGCACTTGTNCCTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[A/G]TTATACTATGGCACCATTGGGACACAGATTATATGTCAGACACCACGNATGTCCTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
WI-867b	119	G	A	AATCTTAACAGCCTTTGATGCCAAAGCCACTTTCAGTCTTAATTCTTTTTGGAGCCTAAGATCAGTGCAACCCTCCAAGGCTCCCCAGTATCTGGCACATCTTTCCCTTTC[G/A]TTGTGTGTTGGCCAAATAATATCTCCCCCAGGGACGTCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGCAGTGCTATGTGGTTTGAATGTGTCCCCCACAAAGCACACATTAGAAACTTA
WI-867	113	A	G	AATCTTAACAGCCTTTGATGCCAAAGCCACTTTCAGTCTTAATTCTTTTTGGAGCCTAAGATCAGTGCAACCCTCCAAGGCTCCCCAGTATCTGGCACATCTTTCCCTTTC[A/G]TTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGCAGTGCTATGTGGTTTGAATGTGTCCCCCACAAAGCACACATTAGAAACTTA
WI-871b	119	G	A	AATCTTAACAGCCTTTGATGCCAAAGCCACTTTCAGTCTTAATTCTTTTTGGAGCCTAAGATCAGTGCAACCCTCCAAGGCTCCCCAGTATCTGGCACATCTTTCCCTTTCCTTTCCTCCTGAAACCTGAGAAAATGTATCCAAAATGTAACCTTGTCCAAAACGAATCTCAGTTTCTGCATATGTAAAATGTAACCTACCTCATG[C/G]AACTGTTGAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAATGCCTGAATTGTGTACCCTAAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTGTATTTGTACATAA
WI-871	123	C	G	TCATCAGACCTGAGATTCAGCATGAATGAAATCTACCAAAGGTACCACAAATGTAACCTTGTCCAAAACGAATCTCAGTTTCTGCATATGTAAAATGGGAATGATAAGAGCACCACCTACCTCATG[C/G]AACTGTTGAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAATGCCTGAATTGTGTACCCTAAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTGTATTTGTACATAA

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WI-884	198	T	C	---	AGGTTCTGGACTTGATGCTGGGAAACAATTGGGTNCTGGAGAATTCCTATTTTGAGTNTTCACAGAT CAGTAGAGCCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACTTTCCTGATCTATTGGGA ACTTCCTCCTAATAGATCAGGAAAATCCACCTCACTTAATCATGGACAACNNAAAAGGAATA[T/C]G ATCCCGCCATGCAACATTTATTCAGTGAAAAACATGATGAAAATGAACATAAT
WI-921b	205	G	A	---	CACTTCCCAAGGGCTCTGGGGGANGAGCGGTGGGGACGCCTGCCGGGAGCAGTTCGACACTGACTGA TGCTTTGCTGCGCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATACTGG CAGTGATGCCTCTCACGCCTGGCCCCCCAAGAAAAGTCTTNGCCAGGAAAAGCACGATCCATCTAC TCT[G/A]GGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCTTCCGAG
WI-921	205	G	A	---	CACTTCCCAAGGGCTCTGGGGGANGAGCGGTGGGGACGCCTGCCGGGAGCAGTTCGACACTGACTGA TGCTTTGCTGCGCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATACTGG CAGTGATGCCTCTCACGCCTGGCCCCCCAAGAAAAGTCTTNGCCAGGAAAAGCACGATCCATCTAC TCT[G/A]GGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCTTCCGAG
WI-945c	90	G	C	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTCACTGGCTGTGTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGCCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAAATGTCTCATGACCAAAACAAAGTTCAAACANTAGGTGCAGCACANNNGGGGTT TTCTCTGGTCATAGAATCTCTTAAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-945b	90	G	C	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTCACTGGCTGTGTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGCCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAAATGTCTCATGACCAAAACAAAGTTCAAACANTAGGTGCAGCACANNNGGGGTT TTCTCTGGTCATAGAATCTCTTAAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-960b	167	C	T	---	TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTTGAGTACAT ATCAAGCACACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTTTCTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCT[C/T]CTTAGAGGTATCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155	G	A	---	TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTTGAGTACAT ATCAAGCACACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTTTCTACC CTGAGGAATTTATCAAAGAT[G/A]TTAAGTTATCTCCTTAGAGGTATCATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181	T	C	---	TCCCACTGAGTATGGCTTTCAGTAGTTTTATTATGATGTGCCTAGGTACATTTGTTTTATTTGTTCTG CGAATTGTTGTATTACTTTGGGGAGAAATGCTCAACTATAAATATTGCTTCTGACCCTTTCTGTGTTC CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCCACTA[T/C]GCTGTTTTTACTCCTCCTCTG ATTTTTTTTCCATTATTTTATTGCTCTGGCTTCATTTGTAAATNTG

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WI-1147b	204	G	A	TTTGCCATTATTTGAAGAGATAACCCACACCTTGGTGTGTCCAGGGTTTTCACAGGTTATTAGTGGTCAGTCA CATAGGCATATAGTAGTACCTGTATGACTTCTATTCCAGCACCGCAAACTTCTCCTCTCCCTGCTGGCTC CTGAGCCAAAAACAGGCATTACCATAAATCACTTGTTAGGATGAACTTATCTGGCCAAACTGATA C[G/A]GCATGACCCGACCCTCAGGTATATAAAAACACTCTCAGGCAGA
WI-1158b	147	C	T	GCATTCAGAGGGTTCGTTAATGACATTCACTGAGGCCCTGTCTATGTCAGGCCCTTGGTGTTGAAGA CGCAATCATGAACAAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG[C/G]GCCAGGT GGCTAAGTGCTGGGGTCTGGGGTCAGGCTGCCTGGGTCACATCCTGGCTCCCAAACTGCTTTGCTATG GCT
WI-1158a	124	C	G	AAGTTTACAGAAAAAATACCAGAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTNCCCACAGACACACTTATCCCCTAGACAGCCATTCTTTTGAATGN[T/C]GNCANT AAAAATGATTTGAAATTGGAATAAAGCCCCTCCCTCTAATGATTGACAGTGTTAGACCTTGCCTAG GGC
WI-1304	124	T	C	TTCTCAATTCCAATCTGTGTGTTACTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAATTNACTCCACTNATGTCTNACAAAATNACACTGTTTTAANTGNNATATG[C GGC
WI-1305d	202	C	T	TTCTCAATTCCAATCTGTGTGTTACTTTATTTCTTTCTTTCCATT[C/T]TATGTTGGTAAATATAAAG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAATTNACTCCACTNATGTCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGGCGGANGTAATANGTATACAGNANTCATAAACAGCCCTGCCTACCA /T]AGGGCGGANGTAATANGTATACAGNANTCATAAACAGCCCTGCCTACCA
WI-1305c	46	C	T	TTCTCAATTCCAATCTGTGTGTTACTTTATTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAATTNACTCCACTNATGTCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGGCGGANGTAATANGTATACAGNANTCATAAACAGCCCTGCCTACCA
WI-1305b	153	T	C	TTCTCAATTCCAATCTGTGTGTTACTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAATTNACTCCACTNATGTCTNACAAAATNACACTGTTTTAANTGNNATATG[C TGCAGGGGCGGANGTAATANGTATACAGNANTCATAAACAGCCCTGCCTACCA /T]AGGGCGGANGTAATANGTATACAGNANTCATAAACAGCCCTGCCTACCA
WI-1305	202	C	T	TTCTCAATTCCAATCTGTGTGTTACTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAATTNACTCCACTNATGTCTNACAAAATNACACTGTTTTAANTGNNATATG[C /T]AGGGCGGANGTAATANGTATACAGNANTCATAAACAGCCCTGCCTACCA

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WI-1306b	248	A	G	⋮	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAAATGGACAATCTTGTNGNNNNTNG GGCTGGGTGACTGTGCCTGGGTCATTTAGAAGCCATAGAAGTGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAAGTGGCCCTNNTTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCTTA[A/G]GC
WI-1306	240	A	G	⋮	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAAATGGACAATCTTGTNGNNNNTNG GGCTGGGTGACTGTGCCTGGGTCATTTAGAAGCCATAGAAGTGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAAGTGGCCCTNNTTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTT[A/G]TCTTCCTAGC
WI-1307b	118	T	C	⋮	GACAAGGCTGGTACTAGTTCCAATTCCAAATCTATGTACACTTTCCTCTCCACTTTCTCAAGTGGACA GATTTTCTGCATTATACTGCTTGGGGGTTGGGGGAGCCAGTGGTGTAGGCAA[T/C]GTGAGATTGTCTTT CCTACCCTCTTAAATGTATCTTTNCTAATTATNATGCTAAAACCGGGTACTGTGATCTATCACTGGTT TCTTTTTGGTGTTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTT
WI-1307	118	T	C	⋮	GACAAGGCTGGTACTAGTTCCAATTCCAAATCTATGTACACTTTCCTCTCCACTTTCTCAAGTGGACA GATTTTCTGCATTATACTGCTTGGGGGTTGGGGGAGCCAGTGGTGTAGGCAA[T/C]GTGAGATTGTCTTT CCTACCCTCTTAAATGTATCTTTNCTAATTATNATGCTAAAACCGGGTACTGTGATCTATCACTGGTT TCTTTTTGGTGTTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTT
WI-1325b	169	T	C	⋮	GAGAGATGGCCAAGACAAAGCAGAGGGAGAGAAGCAACCNTCTGTGGTTTATCGCAGCAAGCN ATGTCTGTCTCCATACCCAGAAATGAGCATGTCGTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACACATTCCCACTTTACATCAGTGGGAATTTGCTCCTT[C/T]TCTTACCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATTCCCACTTTACATCAGTGGGAATTTGGGACTTGGTGAAGTTAGGTT
WI-1325	165	C	T	⋮	GAGAGATGGCCAAGACAAAGCAGAGGGAGAGAAGCAACCNTCTGTGGTTTATCGCAGCAAGCN ATGTCTGTCTCCATACCCAGAAATGAGCATGTCGTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACACAATGCTGCCTTGCTC[C/T]TCTTACCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATTCCCACTTTACATCAGTGGGAATTTGGGACTTGGTGAAGTTAGGTT
WI-1327b	162	T	C	⋮	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAAGTCCTGTTATTGTAAA ACACCAAGTGCGGGTTTAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGT[T/C]GAAGTTGGGTAGCTACCAGGCCTCCCCAAATGTAGT TCTTGNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAAG
WI-1327	175	C	G	⋮	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAAGTCCTGTTATTGTAAA ACACCAAGTGCGGGTTTAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGTGAAGTTGGGTAG[C/G]TACCAGGCCTCCCCAAATGTAGT TCTTGNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAAG

WI-1341b	136	G	A	TATCAGCATGATTGTGGCTGTGTTGGACACAAAGTCAATTTGTACTTTTGNTGCNNNTCCTTTTCTNTTT ACCTGATCCACTATCTTCTCTCAAGATCANGTTCAAATTTGGCTTNCTTTGTTNAATTATACCCAAGC [G/A]GGGATTGTGATGGATCTGTTTATTTCCTGTCTGTGTTTCCCCAGCCCACTTGCACTTAGCAAGTGT GTTTCAGGATTTGTCTCTGTTTCCCGAGCCCACTTGCACTTAGCAAGTGT
WI-1349e	192	G	C	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAATAGAAATTGTGAAGTACTAGATTTCAGAAAATA
WI-1349d	264	C	A	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAATAGAAATTGTGAAGTACTAGATTTCAGAAAATA
WI-1349c	192	G	C	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAATAGAAATTGTGAAGTACTAGATTTCAGAAAATA
WI-1349b	264	C	A	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAAATATGATAGAATAGAAATTGTGAAGTACTAGATTTCAGAAAATATGAT
WI-1349	264	C	A	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAAATATGATAGAATAGAAATTGTGAAGTACTAGATTTCAGAAAATATGAT
WI-1403b	57	C	T	TGGTATTTGGAATGGGGGTTCAGACTCCGGGTTCTGGCTTTGGTAAGTTG[C/T]TCCGAAT GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATACGT AAAGTTTACATCAACACATAATTCTTGCCCTGCATCATGCATTTGGCAATATGTCACATAGCTGTCCTCA TAATCCCCAAAGTGCCAAAAGGGGTTGTATCTGATTTGT
WI-1403	58	T	C	TGGTATTTGGAATGGGGGTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTGC[T/C]TCCGAA TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACACATAATTCTTGCCCTGCATCATGCATTTGGCAATATGTCACATAGCTGTCCTC ATAATCCCCAAAGTGCCAAAAGGGGTTGTATCTGATTTGT

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WI-1417c	31	C	T	CAGGCCGGAAGAGAATTCACGTGGAGAGATGT[C/T]TTGGCCAGGGCGGGGCAGATGTGAGCCCACGGG GGTGACAGCAGCATGCCTGCTGGCCATTTGGAGGGCCCCAGAAGGAATCCCAGTGGCCCTCTCAATGACTTG GGGTCCTCGGACTTCGGAAGTTTCAAAAGCTGGGTCCGGTTTTGAGGCGGGTTGC AGGCGAGGCGCCCTTAGGTCCGTATTTAATGTTTGCTTTTGTAGAAAAAGTCGC
WI-1417b	31	C	T	CAGGCCGGAAGAGAATTCACGTGGAGAGATGT[C/T]TTGGCCAGGGCGGGGCAGATGTGAGCCCACGGG GGTGACAGCAGCATGCCTGCTGGCCATTTGGAGGGCCCCAGAAGGAATCCCAGTGGCCCTCTCAATGACTTG GGGTCCTCGGACTTCGGAAGTTTAAGGGGCTCGGCTTCAAAAAGCTGGGTCCGGTTTTGAGGCGGGTTGC AGGCGAGGCGCCCTTAGGTCCGTATTTAATGTTTGCTTTTGTAGAAAAAGTCGC
WI-1729	172	A	---	CCATGAGCAAACAGCATGTTTCTACTCTGTGATGTGTATGTTAGGGGGCATGTATATCTGTATTTCTT TTTATTCTCTCCAAAAGAAATTTCATTATGCAAAAACATTATCAGGCAGTGCAGCTCGTAATAAAGA TGTTGGAGAACTGAAAAAAGAGAGCTTACATGCACCCCAATAGCAAAACTCTCCACACATTCCAGCA GATGTATGTGTCCTTCCGTGGTNACCTTCTCTCCCACCATCACCTGTTTT
WI-1732b	122	T	C	TGCCTTACTTCTTTGTTCATTCCCACCATTACATTTGTAAATTGGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGGTCAACCCTT[T/C]ATTCAGTCT CTGCCACATGTCTAGTAACTGTGAGTGATGGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACTACTATTCATCATCATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1732	114	C	T	TGCCTTACTTCTTTGTTCATTCCCACCATTACATTTGTAAATTGGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGGT[C/T]AACCCTTTATTCAGTCT CTGCCACATGTCTAGTAACTGTGAGTGATGGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACTACTATTCATCATCATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1750	97	A	G	GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTCCCCCAAAAAAGGTTTAAAATCTGTGTTGGA CATAATGTTTGAATTGCAGTTCACCTTGG[A/G]TTAAGGTGTGCTGTGTTTTCTGGCAAAGAGTCAG TGGGAGGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCAGTCCTGACTGAG CTACATTCACTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31	A	G	GGTACACAAAGAAATGCTTCTGGAAATCTAC[A/G]TAGGCGCCTTAACATTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCACCATGAAGCTGGGCAAAGAACAATTCCTAGGAAAAGTACAATTAC TGGGAAACTGTAGAACAAATAATTCTCATAGTTTACACATAGCTGGGAATCACTCATGTTCCCATCA ACTGGAGAGACCTTGTTGAGTACAGAGGACATTCAAGAATAATCATCATAAAAAT
WI-1803c	77	A	G	CCACTCAGTAATAATAGTGTTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGAT[A/G]AGTAGGGTAGAGCATCCACACTTGGGAGGACATATTCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATCTACTACAAAAGCATGACTTCTAGAAAATTACTTATTACTCTTGTCCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAATAACTGGAATCA

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WI-1803b	77	A	G	CCACTCAGTAATAATAGTGTTGGAGATAAGTATATGTGTAGGCACATAATAATTATTTTCAGGCAGAACCATTATGAT[A/G]AGTAGGGTAGAGCATCAAAGCATGACTTCTAGAAAATTACTTATTACTCTTGTCCTCAAGGTGCTAATTTCAAATATATCTACTAAATACAGTCTTATTGAGGAAATAACTGGAATCAGGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAATAACTGGAATCA
WI-1837b	112	C	T	TTTACTTGGGATTTTCATAGCTGATCATAATTACCATTGATAATTCACTTCTTTTCCCAGGCTCAAGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATAC[C/T]TCTGTCCCCAGTTTATTTTTAAGGTTTTTTCATTGCACCTGATGCCAAAACAAAACCTCAAAAGACCTTGAGTGAATTTTGAGCTCGTGTAACAACTGGGAAGTCTGGGGAACGTTTTAGCTTTCTGCTGTGGCT
WI-1837	112	C	T	TTTACTTGGGATTTTCATAGCTGATCATAATTACCATTGATAATTCACTTCTTTTCCCAGGCTCAAGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATAC[C/T]TCTGTCCCCAGTTTATTTTTAAGGTTTTTTCATTGCACCTGATGCCAAAACAAAACCTCAAAAGACCTTGAGTGAATTTTGAGCTCGTGTAACAACTGGGAAGTCTGGGGAACGTTTTAGCTTTCTGCTGTGGCT
WI-1840b	79	G	T	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAGACACCTCAGACCTATTGGATCAGGATCTTTCAGGTAGCACT[G/T]GAGAATCTGAATATTCAGCACACATACAAGTGTGACAACCACTGTTAGTATATTTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAATTATAAGACTATCGCA
WI-1840	79	G	T	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAGACACCTCAGACCTATTGGATCAGGATCTTTCAGGTAGCACT[G/T]GAGAATCTGAATATTCAGCACACATACAAGTGTGACAACCACTGTTAGTATATTTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAATTATAAGACTATCGCA
WI-1879b	110	C	T	GGGCTCACTTCATCAGAGCACATATCACGTGATAGTCTGTTCCTTCTTTTCATAACTTACTCCCCCGCACTGTAGGNTTCTTTTGAGGTNAAGGACCTGCCNTTTTA[C/T]TGTCTGCNAAATAAACTCCCAAAAAAGTGGTTAGTCCACAGGGTTTAATAGTTCTTGTTGAATTTCTGTGTGCGACCCTGTGCCTTCTCAAGAAAAAAAAAACATTGAAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110	C	T	GGGCTCACTTCATCAGAGCACATATCACGTGATAGTCTGTTCCTTCTTTTCATAACTTACTCCCCCGCACTGTAGGNTTCTTTTGAGGTNAAGGACCTGCCNTTTTA[C/T]TGTCTGCNAAATAAACTCCCAAAAAAGTGGTTAGTCCACAGGGTTTAATAGTTCTTGTTGAATTTCTGTGTGCGACCCTGTGCCTTCTCAAGAAAAAAAAAACATTGAAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119	C	T	TGTTCTCTGGTCCAGGCACCGGCTAAGTCTTGTCTGCATAATGAATAATCAACTGGACAACCCCNGCTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGTAAAGTGCCCTGCCCCAACGCGCACAACTAGAGACGAGCCAAACAGGTGTTGAACCCAGCTCGCCTGACTTCAGAGATCTGTGTGCTTAACTGCCATGAGAAAACCACTTTTCTTTGCTCC

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WI-1900	119	C	T	TGTTCTCTGGTCAGGCACCGGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGGC[C/T]GCTCTGAGAGGT AAAGTGCCCTGCCCCAACGCGCACAACTAGAGAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAACTGCCATGCCATGAGGAAAACCACTTTCTTTGCTCC
WI-1943c	165	C	T	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGTGAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAAGACCAGCC[C/T]CTCTGAANCTGGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCACTTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165	C	T	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGTGAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAAGACCAGCC[C/T]CTCTGAANCTGGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCACTTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164	C	T	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGTGAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAAGACCAGC[C/T]CTCTGAANCTGGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCACTTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1960c	270	A	T	CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTTGTGGAGTGAGGATTCTGGAGAAGCACCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960b	270	A	T	CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTTGTGGAGTGAGGATTCTGGAGAAGCACCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1977	203	T	C	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTTCTTCATAGAGTNTTGTTTTAGTCTCGTAATAATACTGTTGCCCTAGGAAGGTTGTT TTTCCTACTGCGTCTGTGTGAAAGCCTTCCCCATCGAGTGATACAGTACTTTCCAGTTTATGGAGATTT[T /C]TAACAATCAAACACTGGCTGAGGCTGTTGG
WI-2012	102	T	C	AAATTCTAGAAGCCAGAAGTCAGCTCACGATTTATAAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTCTTAATTCTGCACAAAAACTAGCTAAAAATC[T/C]TTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAGCACTCAAAAGTTATGTAGAGTAGCAGCTGTCTCTGAGTCACTTTTTCTACTCTCATT GGCTTCACCAATGCTTCCACTGGATC

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WI-2013	127	C	T	CTTTTAGAGGGTGGTCATTTCGGTTCCCTTCTGGAAAGTGATTCGTGTTTAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTAAACAGTCTCCAGAGATAAATGCTGATACTGACACT[C/T]CTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTGTTCAGTTATGCTCCCGGGTCC CCTTTCACTGGAGGGATATCTCAGCTTTCTGAGCCCCTGGTTACTGCAATCC
WI-2032c	166	G	A	ACCAGACATCCCATCAGGAGTTAGTCCTTCTGGCAAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAGCCAAACCTAACC ACATCACCCAACTGGTTTTCTAGATGTACAC[G/A]TGTGGGACCTCTGTCTCAACCTCCGACTTTCAC AGATCATTGGGTTAGGCTCACCTTCCTGTAATTGCTTCTGTTTTTCAAAGGG
WI-2032b	219	C	G	ACCAGACATCCCATCAGGAGTTAGTCCTTCTGGCAAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAGCCAAACCTAACC ACATCACCCAACTGGTTTTCTAGATGTACACGTGTGGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCA[C/G]CTTCCTGTAATTGCTTCTGTTTTTCAAAGGG
WI-2032	219	C	G	ACCAGACATCCCATCAGGAGTTAGTCCTTCTGGCAAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAGCCAAACCTAACC ACATCACCCAACTGGTTTTCTAGATGTACAC[C/G]TCTGTAATTGCTTCTGTTTTTCAAAGGG
WI-2054b	188	C	T	CGTTTTCTTCTACATCTTGGGGNACATAAAGANGAAAGAAAGNAGCTGTCTTTTTGTGGTAGTTTTGCT CAGAGCTGCCTAGAGCNAGGACNAGGACAAGACAGGTGACCTTCAAAATACCTTACAGATTAGGATTTGGA TTTTCATGGTGGTTGGCACAGCCCAGGCTCAACAGAACTAATACCTGCT[C/T]GTTCCTCTGCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGGGCTGTCTT
WI-2054	183	T	C	CGTTTTCTTCTACATCTTGGGGNACATAAAGANGAAAGAAAGNAGCTGTCTTTTTGTGGTAGTTTTGCT CAGAGCTGCCTAGAGCNAGGACNAGGACAAGACAGGTGACCTTCAAAATACCTTACAGATTAGGATTTGGA TTTTCATGGTGGTTGGCACAGCCCAGGCTCAACAGAACTAATACCTGC[T/C]GTTCCTCTGCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGGGCTGTCTT
WI-2573d	129	T	C	TGGGATTAAAACCCTGTTTCTTCCTTCCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTT[T/C]TGA TATCATCTGATCTTCCCAACCAGGGCTTATTTATGCCGCTTAGGTAAGGGGTAAGCAAACAGAGGCTGTGT GAAGTGAAATGATTTGCTTGCACAAGGTCATATGGGCTTGGGCTTGGACGAG
WI-2573c	165	A	C	TGGGATTAAAACCCTGTTTCTTCCTTCCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTTTTGATAT CATCTGATCTTCCCAACCAGGGCTTATT[A/C]TTGCCGCTTAGGTAAGGGGTAAGCAAACAGAGGCTGTG TGAAGTGAAATGATTTGCTTGCACAAGGTCATATGGGCTTGGGCTTGGACGAG

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WI-2573d	129	T	C	---	TGGGATTAAAACCCTGTTTCTTCCTTCCCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAAATAGCTCTTAAAAATGCACTTGCCGTTCACAAGGTGTTCCGTGCTT[T/C]TGA TATCATCTGATCTTCCCAACCAGGCCTTATTTATGCCTAGGTAAGCAAACAGAGGCTGTGT GAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165	A	C	---	TGGGATTAAAACCCTGTTTCTTCCTTCCCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAAATAGCTCTTAAAAATGCACTTGCCGTTCACAAGGTGTTCCGTGCTTTTGATAT CATCTGATCTTCCCAACCAGGCCTTATTT[A/C]TGCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTG TGAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573b	165	A	C	---	TGGGATTAAAACCCTGTTTCTTCCTTCCCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAAATAGCTCTTAAAAATGCACTTGCCGTTCACAAGGTGTTCCGTGCTTTTGATAT CATCTGATCTTCCCAACCAGGGCTTATTT[A/C]TGCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTGT GAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573a	129	T	C	---	TGGGATTAAAACCCTGTTTCTTCCTTCCCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAAATAGCTCTTAAAAATGCACTTGCCGTTCACAAGGTGTTCCGTGCTT[T/C]TGA TATCATCTGATCTTCCCAACCAGGGCTTATTTATGCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTGT GAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2868b	60	A	G	---	GACTTCATGCTCATGAACAAGCATTGTCTTAATTACAGACATTAAGAACAAGCTTCC[A/G]CTC CCACTTCCCTCCCCACTACTCATCACCTCAACCTCTTCATCCCACTTAAAGAGGTTTCTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTCTATTAACGCTTCCCAATGATGCAGCCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAAACAGCTGAAAAATGAAAATATCGATATAC
WI-2868	60	A	G	---	GACTTCATGCTCATGAACAAGCATTGTCTTAATTTACAGACATTAAGAACAAGCTTCC[A/G]CTC CCACTTCCCTCCCCACTATCACCTCAACCTCTTCATCCCACTTAAAGAGGTTTCTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTCTATTAACGCTTCCCAATGATGCAGCCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAAACAGCTGAAAAATGAAAATATCGATATAC
WI-2870b	131	T	C	---	CATGCTGTGTAACCTCTGTGCTGCTTGCTGTCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCATTTAAATTATATCACAGCTTTATGTCCACTTCCTGTTCCTGCCATCAC TGGGCTTTTTACAAAGGAGGGCTTT
WI-2870	131	T	C	---	CATGCTGTGTAACCTCTGTGCTGCTTGCTGTCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCATTTAAATTATATCACAGCTTTATGTCCACTTCCTGTTCCTGCCATCAC TGGGCTTTTTACAAAGGAGGGCTTT

WI-2954c	49	T A	TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAAGGCATAAAAAAA[T/A]CAGCACCTGGGGCACAGAGGGAGCTCTATGCATTTNAATTCCTCATACCTACCCCTCCTCTCTGGCCATCCATCAATGAGTCCTTTGAGTCCTTGGAAAGACTCTATTCCCTGGGCAACCCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCAGAG
WI-2954b	41	A G	TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAAGGC[A/G]TAAAAAAATCAGCACCTGGGGCACAGAGGGAGCTCTATGCATTTNAATTCCTCATACCTACCCCTCCTCTCTGGCCATCCATTCAATGAGTCCTTTGAGTCCTTGGAAAGACTCTATTCCCTGGGCAACCCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCAGAG
WI-2954a	38	G T	TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAA[G/T]GCATAAAAAATCAGCACCTGGGGCACAGAGGGAGCTCTATGCATTTNAATTCCTCATACCTACCCCTCCTCTCTGGCCATCCATTCAATGAGTCCTTTGAGTCCTTGGAAAGACTCTATTCCCTGGGCAACCCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCAGAG
WI-2971b	62	T C	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTTCTAAGA[T/C]GCTGCCAGCACCAATAAGCTTTCTTCAAAACAATTGTGTAACCTCCTCCTTAATAAACCTAACATTTCCTTGTTCCCCTGACATTCTGAAGGCCACGCTGGTCTAGATGTGTATGTCCCAGATTGCAATCCTAGTTCTTTAATGTTATTCTGAAAGAAAACCTTTTTACTTAGGGATTTGTCT
WI-2971	62	T C	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTTCTAAGA[T/C]GCTGCCAGCACCAATAAGCTTTCTTCAAAACAATTGTGTAACCTCCTCCTTAATAAACCTAACATTTCCTTGTTCCCCTGACATTCTGAAGGCCACGCTGGTCTAGATGTGTATGTCCCAGATTGCAATCCTAGTTCTTTAATGTTATTCTGAAAGAAAACCTTTTTACTTAGGGATTTGTCT
WI-2995d	133	A T	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCCTCCAGTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTTT[A/T]AAATCTTTCTTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151	G C	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCCTCCAGTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTTNAAATCTTTCTTTCTGGT[G/C]TTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A T	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCCTCCAGTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTTT[A/T]AAATCTTTCTTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT

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WI-2995c	151	G	C	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTTNATCAAGATAAAGACCTGGAAGACCCAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A	T	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTTNATCAAGATAAAGACCTGGAAGACCCAGCCAAAAGGAAGGAGCTGGANTTTTTTT[A /T]AAATCTTTCTTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151	G	C	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTTNATCAAGATAAAGACCTGGAAGACCCAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151	G	C	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTTNATCAAGATAAAGACCTGGAAGACCCAGCCAAAAGGAAGGAGCTGGANTTTTTTT[A /T]AAATCTTTCTTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133	A	T	GTGGTGCAGTTCAGTTCATCCTCTGGAGCTCCGTGTGAGATCAGACTGGAGGCCAGTCTCCAGCTTGAGACCAC ATCTCACTTAGCTCCTT[C/T]CCTGCCATATCCTGTTTCCTTACTCCTATCCTCGAGACTTCTTCCT GAATGAATTACATGCACTCAATCCCTGCCTCTCTGCTTTNAGGGAACTTGACCTAAGACAGAA ATCTTAGTACCAAATACTTTGCAAGG
WI-3147	85	C	T	ATTCTGTAATGTTTTCACTGCTTCCAGTAAAATTCTTATTGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAGCAAGAACAACAACAGAAAGCCTCGTTTGCAATCGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTTNATATCTTAT
WI-3234b	68	T	C	ATTCTGTAATGTTTTCACTGCTTCCAGTAAAATTCTTATTGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAGCAAGAACAACAACAGAAAGCCTCGTTTGCAATCGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTTNATATCTTAT
WI-3234	68	T	C	

WI-3292b	106	G	A	GTTTTGCTAGACTAGGAGTTCAGCTTCATCCAAATCCCTTAAGGATANTTAGCTCTGCACTCATCCTCCCTGTCCCCGTCCCAAGCCTATGTTACTGGTATGGCT[G/A]TGGTATTGGATTGGGATGGGATTACTTGCCATGAATATTTCCATTGTTCTCATTAATGTATTAATTAAGTAAAATATTATTTNCCATGAGACACAATTGGAAAAACATTCATGGAAAAAAACCCATTTCAATC
WI-3292	106	G	A	GTTTTGCTAGACTAGGAGTTCAGCTTCATCCAAATCCCTTAAGGATANTTAGCTCTGCACTCATCCTCCCTGTCCCCGTCCCAAGCCTATGTTACTGGTATGGCT[G/A]TGGTATTGGATTGGGATGGGATTACTTGCCATGAATATTTCCATTGTTCTCATTAATGTATTAATTAATTAAGTAAAATATTATTTNCCATGAGACACAATTGGAAAAACATTCATGGAAAAAAACCCATTTCAATC
WI-3355	19	G	C	CCATGAACCATGGGCTACA[G/C]ATATTCCTAAACTTCAGAGTCCTCCTTACTGGAGAGGGATCCACTTTTAAAATATGATTCTTGAAGTGGCTGCATACTATTCCTTCCAAGCACTTAAACTCATCAGAAAAAAATCATCAAAAAGTCGAAGTTAGTTTTNATTACCTTCACCTTTCAATGGAAAACTTTATAAACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3408	194	G	A	CCATGAAGAATGAGTTCCTCCCTCCCCTGGGTCACGTCTAAGAATAGCACACCCTTGAGAATTTNACTTAGCACGTGGCATTGTAATGGCTGGATTCCTCCGCTCTAAGACACACCTTATGCTTTCNAAGCTTTCTGGAATTGGGATGAATCTNACATTCAATGTGCACCCTTCGTGTGGGATCACTTCTCC[G/A]TGCCCCATCTCTGGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAAATCAGG
WI-3505b	131	G	A	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCCATTTGTCATCAGTGCACTTAAAAAATTATTTGAAAAAATTGCCATTTTAATATCTTTGGAACTTCCTAACACATTACCTATTTTTNAACCAAAC[G/A]AGGTGATTCCTTATGGGAAAATATATACAGCAAGAAAAAAANANNGGAAAAAATGTTGATGATACCTGTTTTAATTGGGAAATATGTTTGCATAT
WI-3505	131	G	A	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCCATTTGTCATCAGTGCACTTAAAAAATTATTTGAAAAAATTGCCATTTTAATATCTTTGGAACTTCCTAACACATTACCTATTTTTNAACCAAAC[G/A]AGGTGATTCCTTATGGGAAAATATATACAGCAAGAAAAAAANANNGGAAAAAATGTTGATGATACCTGTTTAATTGGGAAATATGTTTGCATAT
WI-3564b	177	C	T	GCTAGTAAGGTTCCACCTAAATGGTTCCAAGTCAGGAGAGTCACTAAATGTTTGAGAAATAAAAGTGAAAATCAATGTGTCTTCCCAGTGTATTCACATGGCACAGTGTCACAGAGGGCTTGAGCGTCTGAGCGTGGGACTTCACTGGTTGACTAACGTTAACATGCATGTCTGTT[C/T]AACAAGTGTTTGTTGGTGTCATCAGTGTCACACATGCTACCTTCCTTCACAAAACAAA
WI-3564	177	C	T	GCTAGTAAGGTTCCACCTAAATGGTTCCAAGTCAGGAGAGTCACTAAATGTTTGAGAAATAAAAGTGAAAATCAATGTGTCTTCCCAGTGTATTCACATGGCACAGTGTCACAGAGGGCTTGAGCGTCTGAGCGTGGGACTTCACTGGTTGACTAACGTTAACATGCATGTCTGTT[C/T]AACAAGTGTTTGTTGGTGTCATCAGTGTCACACATGCTACCTTCCTTCACAAAACAAA

ID	Pos	A1	A2		Sequence
WI-3649	64	A	G	---	AATGTCCATGCTGTGACTGACCTGTCTAACACCTTCCTAGTATTCCTTAGTGGAAGATTCAC[A/G]AGACCAGTTGCCTTCACTTAGTAGGGCCAATGATGAGACTTTTAGGTGCTACCACAAGGGTACCTGCACAGCCACATCATATGTCACAGTAATGATGACAGTAATGTGCAAAGGACCTGTCTTCTGCCTGGTCTTCCTGTTTTACCATATTA
WI-3674b	133	G	C	---	ACAGTACACATGGCCCCATTATGGAAACAATCATCTGACTTATGTTACCTGAGAAGTTCCCTCTCTAAATTTAACTACCAGGCGGAGTGCTTTATAGTAATTAAAATATGTTTATTTAGAAAATAACAAAAT[G/C]AAGAAAAAATGATAGTCAAGTTGTAGACACTATTAAAATTGTAACTGGTCAAATGATTGTTAATTCTTAATTAATTGTGTTTATGTTTNATTACTGCCAATCACAGCCAAG
WI-3674	133	G	C	---	ACAGTACACATGGCCCCATTATGGAAACAATCATCTGACTTATGTTACCTGAGAAGTTCCCTCTCTAAATTTAACTACCAGGCGGAGTGCTTTATAGTAATTAAAATATGTTTATTTAGAAAATAACAAAAT[G/C]AAGAAAAAATGATAGTCAAGTTGTAGACACTATTAAAATTGTAACTGGTCAAATGATTGTTAATTCTTAATTAATTGTGTTTATGTTTNATTACTGCCAATCACAGCCAAG
WI-3682	137	G	A	---	CAATATAGACCAAATGACTGCCACAAAGAGAAATTAGTGGATCTACATTAGAAACCACATGTTTTTATTGGCTCTTCTCTTCTCTCTTTTAATGCTCTCCAACACCAATTCACTTTATTCTTTTCAATT[G/A]AGCATTTGTCCAATTAAAGTCAATGAAAAATAATGTACATTTTCAACAAGTATACACATTAAGCCCTGCAAAAGTGCTTATATGCTAT
WI-3854b	194	G	A	---	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTGCCCTTGGACAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAATAACTCTGGTTCAGGAAGGCAAGGGCAGTTATGACCACTTTACAACTGAGGAAATCAAAGCAAC[G/A]AGAAGTTAAAATGGCCTGTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-3854	194	G	A	---	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTGCCCTTGGACAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAATAACTCTGGTTCAGGAAGGCAAGGGCAGTTATGACCACTTTACAACTGAGGAAATCAAAGCAAC[G/A]AGAAGTTAAAATGGCCTGTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-4039	210	G	A	---	AGCCAGCCACATCATGTTGAGTCCTGCTCATTCTTCCATCTCTATTTCTCTCTACTGCCTTCACCTTCCATTAACAGAGAACTCTGTGATTACATTGTATGTTGGTTACACTACAGAATCCAAGATGACCTCCCCATCTCAAGGTCAACTAATTAACACCTTATTTGCAATCTTTGTCAATTACCATAACATATTCATGG[G/A]TTCTGGGGATAAGGGGTAGACATTTTATGGGAGGCATTA
WI-4110b	130	T	C	---	GAAAAATGATGTGTTTTTGATTCCCTCTATCTTCAGATTATTGGAGTGTCATTAGAAAACTGATAGTAACCTTTTATTTGATGAAAACTCTGTCTATAATTAAACCTTCCTCTCCTTTATTTGCC[T/C]ACAGTTTAGGTAAATAAAAGATGCCCAAGAATTCAGTATTCAGTACAGTAAAAAGTAGCAACCATGGGGTAGGGACAAGTNCAGAAAAGGGAGGAGGTNGGGGGGTTTTCTGGGAAGA

Marker	Pos			Sequence
WI-4110	130	T	C	GAAAAATGATGTTTTGATTCCCTTCCTATCTTCAGATTATTGGAGTGTCATTAGAAAACTGATAGT AACCTTTATTTGATGAAACTCTGTCTATAATTAAACCTTCCTCCTCGTTCTTCCTGCTTATTTGCC[T/C]ACA GTTTAGGTAAATAAAAGATGCCCAAGAATTCAGTATTCAGTAAAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAAGGGAGGAGGNGGGGGGTTTCTGGGAAGA
WI-4119b	168	G	A	ACCTCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGGACAAGAACAGAGAAGAGAGGGGTT AGAGGAAGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCTTTGTTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4119	168	G	A	ACCTCTCTATGCCTGAAAGCCCTGATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGGACAAGAACAGACAGAGAAGAGGGGTT AGAGGAAGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCTTTGTTTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4123b	51	T	G	CAAAGTCAGATTTTGATTATTCAGGATAACAATTTGAAAATAGAAAAGTG[T/G]TTTAAACTATTT CAAATAAACAATAAAGAAAAAACATGATGAAATTCTTCGTTACATAATTGTATAGAATTTAGTGGGG TTCTTCCATGACATTGGCTTGTTCTTCTCTCAACAGTGGGTGGTTGGATGTTTTCCTATGCTTTCTC AGGCACACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51	T	G	CAAAGTCAGATTTTGATTATTCAGGATAACAACAATTTGAAAATAGAAAAGTG[T/G]TTTAAACTATTT CAAATAAACAATAAAGAAAAAACATGATGAAATTCTTCGTTACATAATTGTATAGAATTTAGTGGGG TTCTTCCATGACATTGGCTTGTTCTTCTCTCAACAGTGGGTGGTTGGATGTTTTCCTATGCTTTCTC AGGCACACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145	G	C	TTGTACATGTTCATTCATCCCTCCCCATTCTTTTCTGTCTTATAAAGAACCTCGCTTCTTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTCCATCAAAGCTTTCTCAGCATCTTCTATATAC[GTGCTGT[G/C]CCTTGTGAAGAAGCCAGAGCCGAGCATCTTTGCTTGAACTGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCCATGATATAAGGTAATTG
WI-4149a	137	T	C	TTGTACATGTTCATTCATCCCTCCCCATTCTTTTCTGTCTTATTCCATCAAAGCTTTCTCAGCATAC[CTTACTTCTCCACCTGAGCCACAGATCTCTTATTCCATCAAAGCTTTCTCAGCATCTTCTATATAC[T/C]GTGCTGTGCCTTGTGAAGAAGCCGAGCATCACCGAACATGATCTTTGCTTGAACTGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCCATGATATAAGGTAATTG
WI-4182	188	G	A	TAACACACTTTTCATTTGGTTCCTATTACTGCAGTTAAAGGACCATCCATTATATTACAATTCCCTC AGTTCTATGCTTTAGAGTNCTATTATAGGACTACTGTAAAATTTCAGAGGGAATTACTCCTTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAAATTGCAGGGGACTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCCTTCCCAAGTTCTTAAATTCCTAG

				Sequence
WI-4230	93	T	...	AGAGACGTTGAATGGGGACATCTTTCTATTCGATTTAGTTTAACATTTGATAAGAGAATTGATGAAAGTTTGTCACATTCCAGATTTATCTTTATAGCAGCAGAAGTCTGGCAAATAATAACAGCACACTGACTTTCCATGGTAAAAAGAAGTTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATTCTGAATACATTTAAATGGAGGAGAATGAATAGTGACCTTTGAAATTTATGG
WI-4241	118	C T	...	GAAAAATTCCATTGAAGTTTGACCTTGAACTGATCTCATTAATACTTTTNCTTGTAGTGGTTGTATTTCATTTTTGACAACAGCAACGAGACGAAAATTTCCACTTAAAATTAAATTCTC[C/T]AAGTATCTATGATTTAGCACTGTTAGCACCAGAAACTGTGAAATTATCTCCTAGATATTCTTCAGAATCTAGGATGGAAG
WI-4271b	151	A	...	CAGGGCTTTTGGGAAGATCAGTTAAAAGCAGAACTGGACCTAAAAAGACTAAGCACATTCAGCATCAACAAAAGGTGACATGTTACCCATGAGAGGTCCCTGGAGGATTAAAGATCAAATAAAGAGCCTCAGGGGACTGAATCCAACGGGGAATATTAGAGTNCTACAGGGAGGAGCCCCAACCCTCCCCCCTTTGTCTCAGGCTCTTAGAAGGTCCAGTCAGGGGCAA
WI-4271	151	A	...	CAGGGCTTTTGGGAAGATCAGTTAAAAGCAGAACTGGACCTAAAAAGACTAAGCACATTCAGCATCAACAAAAGGTGACATGTTACCCATGAGAGGTCCCTGGAGGATTAAAGATCAAATAAAGAGCCTCAGGGGACTGAATCCAACGGGGAATATTAGAGTNCTACAGGGAGGAGCCCCAACCCTCCCCCCTTTGTCTCAGGCTCTTAGAAGGTCCAGTCAGGGGC
WI-4389b	156	G A	...	AATCGAAACATTGATTTTTTGTAAAGGAACCACATTATTTGTGATATTTGTGCCCAGTTTAGCATATGAAATTTGAAAGGGATGAACCTGGAGGAAGAAGAATAGAAAAGGATATTATTGCATAACCTTTGGAAGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTAAGAGGTATTGTAGGAACTGGAAGCGGTAA
WI-4389	156	G A	...	AATCGAAACATTGATTTTTTGTAAAGGAACCACATTATTTGTGATATTTGTGCCCAGTTTAGCATATGAAATTTGAAAGGGATGAACCTGGAGGAAGAAGAGAATAGAAAAGGATATTATTGCATAACCTTTGGAAGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAGTAGAAATGGAACAGACATGATTGACTTAAGAGGTATTGTAGGAACTGGAAGCGGTAA
WI-4488	31	A G	...	GATGACAATTATTGTGTATTGGCATTTAAA[A/G]GTACCATTCCATTTCTTCTCTGGCTTTCGTGTGTTTGTTGTTGGAAGTCAGGGGTTAGTCGTATTGCTCCTTTCTAGTTCTTCTCTCAGTAGGAAGACTGATCCTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTAAAGAACATAAATCAAATTGTATTATCCTATGCTTAAAAATGCTCAG
WI-4491	145	G C	...	ACCATCAATGTATCACCTTCTAAAATTATTAGATGATTAACTGGCTCTGTTAAAAATAAAAACCTGTCTTGGACATTGAAAATAAAACATTACTATTGGTCATTTCTCGTCACTTACAAAGGTACTGCACTAAACAAGTTAAG[G/C]GTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAAATTTCTACCACTGTCATTTCTTGTCCCATAAATAAAATTTTACATGCCT

WI-4584	144	A	G	TTGGTTGGCATTTAGCCTCATAACAACTATTACAATCATAATTGTACTCTTATTTTACAAACAAG AAAAATGAGGCTTAACATCACACTTCTGCTTAGTCGCGAGAGCCAAGATTTGAACCCAGGAATCCATT CACCGGTAC[A/G]TGCTACCTGGGTAAAAATGTTAATTAAAATCTATGGCATTAGGATTTCAAAGA GTCCTAATGTGTTTGAAATAGGTGTGCTTTAATTGTTTATCAGTATGC
WI-4639	185	C	T	TTTCTGCATTTGAATGTGTATGGTCAGACTTCAGAGAGGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCGCCCTATATCAGAGAGATCTCAGTTAACTTCCAATTCCACCATTTAC TGACCATATGACTTGGGGAACATTATCTCCACCTATCTGAGTCTGTATCC[C/T]CATCTTTAAATTGTA AATTTTAAGGACACCTATCATCATATTGTGAGGATAAAATGAAATAA
WI-5327	63	A	-	AAATGAATCCGCTTTAGAGCAAATACCAGTAAGGGCTGGTGCAGGATGGTGGTGGCTGAGAGA[A/-]GATTACTCATAAAAGCATATTAATTTTATAAATATGGAAAATTTAACTAGATAATTAAAATGTGAAT TGAGTTTGAAGGTTGCATGAGAGTAGGGAGGAGGTAGTTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTCGGATGACAATGATGAACTGTTCTAAGCAGACAG
WI-5390	87	C	T	GCTTTTGAGAATGAAAAGGGGAGGAGCCTGGACCATTGCAGGGCTTCTTCATCTCTGATTATTTGTGTAT TTATTGTTCACTTATTTAT[C/T]GTCTGTCTCCCCTCTGGTATGCTTGTGTCATGAAACAATGAATTC CCCAGTGCCTGGCCCGATTCGTGGCCTCCTAGAGGGTCCAGAAGGTGTCCAGAAAAAAGTTCGGTGAATAGAATTG ACGAATGGGTTCAGAATTCGAAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	G	A	CCTTGCCTGCTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAAGCAGT GCAAAACATTATTTAATTT[G/A]AAAGAAACTTGTTTCTGAAACTTGTACTCTTGTAGTNAAATTG AATCTTTCCTTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTTAGAGTTCATAACAA
WI-5404	87	G	A	CCTTGCCTGCTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAAGCAGT GCAAAACATTATTTAATTT[G/A]AAAGAAACTTGTTTCTGAAACTTGTACTCTTGTAGTNAAATTG AATCTTTCCTTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTTAGAGTTCATAACAA
WI-5545b	77	A	C	TAGGAAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATTCTTTCACCACTCACACTGCCGCCA TATCTCCTC[A/C]CCAACACCTCTGTTTCTGACAGCCAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAAGATTTGGCTGACTTGGCTGAATTTGCTACAACTCCAAAAGANTC GAGATACACCATGAATTTTATTTCATTTCA
WI-5545	77	A	C	TAGGAAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATTCTTTCACCACTCACACTGCCGCCA TATCTCCTC[A/C]CCAACACCTCTGTTTCTGACAGCCAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAAGATTTGGCTGACTTGGCTGAATTTGCTACAACTCCAAAAGANTC GAGATACACCATGAATTTTATTTCATTTCA

ID	Pos			Sequence
WI-5860b	134	A	G	ACTCAAGTTTGGGGGGATAAAATCAGAAGTTCTATGTACAACTTAAATTTGCTAAGATTTTATTGT TTCTTTTTATATAAATTATGGATTTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACTAC[A/ G]TTATACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-5860	134	A	G	ACTCAAGTTTGGGGGGATAAAATCAGAAGTTCTATGTACAACTTAAATTTGCTAAGATTTTATTGT TTCTTTTTATATAAATTATGGATTTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACTAC[A/ G]TTATACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-6106	208	C	G	GCAAACAACCTATTATACCTGATTCCAACCCAGGTCTACTAACATTAATCAACCCTAACCACAATAC TATATATTGTCCTGTTCTGAATTATTTCATTTAGAATCTGATGAGATTTAGCATGGGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTGCTTCCAGGAGTCTCAATGTGAAGTATAATTCTTACAGAG TAATT[C/G]ATAGTAGGTCACCACAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129	T	C	AAGATAGACAAACATATGCCAGACCAACAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAAACCT[T/C] AAACCCTATATTTNCTGTCTTGTGCATACTTTAAAATGTATAATGTGGGAGGAAGGAATTTTGATGT GNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109c	147	T	C	AAGATAGACAAACATATGCCAGACCAACAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAAACCTAA ACCCTATATTTNCTGT[T/C]C]TGTGCATACTTTAAAATGTATAATGTGGGAGGAAGGAATTTTGATG TGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109b	147	T	C	AAGATAGACAAACATATGCCAGACCAACAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAAACCTAA ACCCTATATTTNCTGT[T/C]C]TGTGCATACTTTAAAATGTATAATGTGGGAGGAAGGAATTTTGATG TGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109a	129	T	C	AAGATAGACAAACATATGCCAGACCAACAACAAAAACACAGACCTGTCATATTTCTGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAGAAGGAATGTAC AAACCCTATATTTNCTGTCTTGTGCATACTTTAAAATGTATAATGTGGGAGAGAAGGAATTTTGATG GNAAAATTATCCCCTGAAAATTTTATACCA
WI-6112	96	T	C	AATGCCTATCATCCACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTTAGCACCTGTC TTCCAACACATGCTGTTTTTGTTCAATGA[T/C]CGCATATCCCAAGTGCCTTAGCACAATGCCTCCCATAC AGTGAACAGTATTTGACTAAAACATACTTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC

ID	Pos			Sequence
WI-6244	103	T	C	TAATTGCACAACTTACATATCAGGGTTCTGATTGAAAGGAAGAGAGAATATTCCTTCTTTCTTTAGTGATT GCTTAATATTAATTCATAAGAAGTGCACCATCTCT[T/C]GCTCCTTATAAATGTGTTAGAGAAGAAGG AAATTGAGTGTTGGGAATTAAGCAACCAGGAGACATTTTATATACTCCTACAGTGGGGGAGACTT CCTATTTTCTTTCCCAAGGATGGATACATTTCTAC
WI-6268	124	C	T	CTGGCCTTATAATCCAAGTTTAGGATTAATCTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTT GTCTACAAGATTTCCTCCTAGTAGGGCTTTGGGTGTTGGCACCGTTGGCTCATTC[C/T]ACTCTCCCT GGGTCTTATTGACTTTCAGGGAGCCTAGAAGAGAGCTGGACAAAACCTGCTCTTTGCAGAAAGAGTCG GGGTTCCAAAGATTTCGTTACGATTTTTTA
WI-6336b	234	C	T	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCCC ATATATTCCCCCTTTACATGTTTTCTTTATAAGACATACAGTTAATCAATTCACACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCAGTGCATTATGTCTTGGTAGAGCC[C/T]TGAGGACACTGACAGT
WI-6336	234	C	T	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCCC ATATATTCCCCCTTTACATGTTTTCTTTATAAGACATACAGTTAATCAATTAACAAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCAGTGCATTATGTCTTGGTAGAGCC[C/T]TGAGGACACTGACAGT
WI-6381	92	C	A	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAATTAGTTATGAGTATTTATACAATTA CAAAAATGGNTTCATGTTTAACAA[C/A]GTATTTTAAAAGCTCAAACATTTTAAAACAGGCACAAT ATTCTAANGGCATATGCATTCACCATGGCCTTTGAATGTCCTCCCAACTTCACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTCAG
WI-6436	198	C	G	GGTTGAGGCATTGGGAAAGGCAGAAATTGAGGCAGTAGAAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAAGTCATGACAGACAGGAAAATACAAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTTGGTGTCATAATAAGAAGTTTAGACTTTGGTGTTGGTAGTAGTAGTGGTAGTAGCGGTT[C/ G]ATTGGGTGTATTCCACAGACAAGGTGATGTTCTAAGATTGTATATTTATTGT
WI-6449	186	C	T	GAGGCCCTCTTTGCTTTTCCTCAGTCAAGGCTGTATCCAAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTTGTTCTGATTGGTTGGTGCTCACACTGCCCAGATTGTTAAATATTTTGAAAATC GTATCTGGTTCTGGTTCTATTCATCTGCATTCTGATCTTATGTCTGCCTATTC[C/T]ATCCCTATTCTCTGA TCTTATGTGTCGAAGTTCCTCTAATTTTTCTGTGGTGTATTTATA
WI-6449	186	C	T	GAGGCCCTCTTTGCTTTTCCTCAGTCAAGGCTGTATCCAAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTTGTTCTGATTGGTTGGTGCTCACACTGCCCAGATTGTTAAATATTTTGAAAATC GTATCTGGTTCTATTCATCTGCATTCTGATCTTATGTCTGCCTATTC[C/T]ATCCCTATTCTCTGA TCTTATGTGTCGAAGTTCCTCTAATTTTTCTGTGGTGTATTTATA

WI-6463	72	T	C	GCTGGAGAGAGAAAAGACCTCCAAAGAAGAAGAAACTAAATCAGAGTCTCTTGAGCAAGAGAGGAATTGAAA AGAACA[T/C]TGAAAAAAATTAAAGTAGAACTCAAAGAGCCAAAAAGTCCCCAATTGTTCCATTA TAAGAAATATTTTGAATGGAAATCTTAAGAATGATTTTATTGATCAGTTAAATGTTCTTCCTCTCCTC CAGTCCCATTTATATGACATTCCGCATGCTG
WI-6474b	76	C	T	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAAGGCACAGAGAAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGAGGAACTAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76	C	T	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAAGGCACAGAGAAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGAGGAACTAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175	T	A	GAACTCAATTAACTTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCCTGTCTATATGCTTTATTTTTGTGA CACTGTCTATTTACCCTCCCCAATAGTGGAGAATCAGAG[T/A]GCTCCTTGTCAGTGTTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACTG
WI-6478	175	T	A	GAACTCAATTAACTTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCCTGTCTATATGCTTTATTTTTGTGA CACTGTCTATTTACCCTCCCCAATAGTGGAGAATCAGAG[T/A]GCTCCTTGTCAGTGTTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACTG
WI-6559	149	G	A	CACATTTGAATGCAACTGAGAAANTGGTTTTNTAGGCCTACCTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAAACATGCAAAACATAAGGCAACAATTCTGATCATTTATAGGNTCCCAGCCCA TTAGGCAATATCTTA[G/A]TCAAATTTAAAAGAGAACAGGAAATAAGGAAGGCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54	G	A	TTCTTTATTGGTCCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGTCTGTCCTGAAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCTCATTNCTCAGAAATTGAAGGCATTTGATTATNATTTTTTGTTTGGGTCTGTGTAAAG GTTCCTTGGCAGGAGGAACATGCATATGACTTTAAAATAAAGACCAACA
WI-6564	54	G	A	TTCTTTATTGGTCCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGTCTGTCCTGAAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCTCATTNCTCAGAAATTGAAGGCATTTGATTATNATTTTTTGTTTGGGTCTGTGTAAAG GTTCCTTGGCAGGAGGAACATGCATATGACTTTAAAATAAAGACCAACA

Clone			Sequence
WI-6608b	46	C	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGCCTCAGT[C/--]AGTTCAGGCAGCTAAAGGGAGGGGGGATTCCTCCTAGTCCTCCCTAGAGCTAAATATGCATCTGGGAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAGAACTGAACTCCCAGCACTAGGTAAAACTGCAAAAAGAAAAAACACCTGTGCCCAGGCACTAGCTACAAGGCCACCAGAAAAGGAAAGC
WI-6608	46	C	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGCCTCAGT[C/--]AGTTCAGGCAGCTAAAGGGAGGGGGGATTCCTCCTAGTCCTCCCTAGAGCTAAATATGCATCTGGGAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAGAACTGAACTCCCAGCACTAGGTAAAACTGCAAAAAGAAAAAACACCTGTGCCCAGGCACTAGCTACAAGGCCACCAGAAAAGGAAAGC
WI-6666	68	C A	GTTAGACAGTATCCAGCAAAAAAGGTTATTTTATACCTCTACTTTTCCAAAACGAGGAAACCTCCCA[C/A]AAATCCCATCAACACACAGTCATGCTGCGAAGGCATTCGTGTCTTACTCTGTTGGTTTCATGTAAATGTTTGGGGTGACTCATTCCGCCTCTCTNTTCTCCAAGTTCCAGGCTTCTTGGGTAGACCAAAACTAATACACACAATGTTAGAGCACACAAGAGA
WI-6670b	120	A G	AGATTAACACATAATTATTACTGGGGCCATTGTAGGGTTNGGGAGGAGGTGTTTTTCTATCTGCAGCCAAACAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCAGCATTGCCATTCAGGGCCGGAGTCAGGGTTGTGGGCCAGGGTTTGTGGGGAATTCTGAAAAAAAAAGAAATACAGAAATCTTAGAAGGGAT
WI-6670	120	A G	AGATTAACACATAATTATTACTGGGGCCATTGTAGGGTTNGGGAGGAGGTGTTTTTCTATCTGCAGCCAAACAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCAGCATTGCCATTCAGGGCCGGAGTCAGGGTTGTGGGCCAGGGTTTGTGGGGAATTCTGAAAAAAAAAGAAATACAGAAATCTTAGAAGGGAT
WI-6704c	33	T C	TTTGAAAATAAATTCATGCACCAATGTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGAACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTCATGACACACGGNCACTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCATTGTTCTTCCCACATGGTTATTTCAATGCAAGAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33	T C	TTTGAAAATAAATTCATGCACCAATGTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGAACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTCATGACACACGGNCACTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCATTGTTCTTCCCACATGGTTATTTCAATGCAAGAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28	T C	TTTGAAAATAAATTCATGCACCAATGTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGAACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTCATGACACACGGNCACTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCATTGTTCTTCCCACATGGTTATTTCAATGCAAGAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106	G A	CCATGGACAGTTAATTAGGAAGCTTCGACTTGTTAGAATAACAGAGGAAGTCCCAGTTATCTACCT ATTCCTTAAAAACACATTTTGTCAGGCTGGAATGATCCC[G/A]TAGTAAAACTCAACATCCACACCT GCATAAACATCGCCTCCCAAGTGACTATTATTACTGAGTCGACACAGGATGTCACCAGTGAGCCTC ATCTCCAGTCCAATGGAGGAGTTGACTTAGACCTTCCTTGGACACAGGAGGGTC
WI-6766b	148	G C	AAAACAAATGGTGCATTGCATAATATTTGTGGTCACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAAN[G/C]AAAGTCAACGTTTCTCTTCTCTAGGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAAACAGTGGAGGNGAACTTACCCAAATCCCAGTCCCTTCTTC
WI-6766	148	G C	AAAACAAATGGTGCATTGCATAATATTTGTGGTCACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAAN[G/C]AAAGTCAACGTTTCTCTTCTCTAGGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAAACAGTGGAGGNGAACTTACCCAAATCCCAGTCCCTTCTTC
WI-6787b	97	A G	ACAGATAAAAGTCTTTATTCCCTGTATGTTACATAAGAAAGTTCTTACAGACTTTTTTTTATACA ATACTTGTGCAGCAATGTTCAAATTCAC[A/G]TTTTACTGCATAAGATATCTTCATGTACAACTGT ATGCTTTGTCTTCTTGGGAAGGACGCGTTAAAGACCTATGATAAACACACATCCACATGACAAAGGA GAGTGCAATAGGGCAGAGAGTAGANTACTCACAGGAAAAGAGTAAATTCAGGT
WI-6793	105	C G	GAACCCACCAGGTCCTGTTATTTATTAAGGAGCATTACATTATGATAGCAAGTTCAACACATTCA TCAACAAGGCGGTCTTCTTCAAATCAATCAGTCAACCCCC[C/G]GAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTTGGCTGTAGGAAGTAGGGTAATGCCCCTAATCCCGGAAAGGGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAGTTTCTCATCACAGGTAAAAAGGCAAC
WI-6810b	37	T C	CACAATAATAAAATCACTCCCTACCTTGAAAACTTTA[T/C]AGAAGCATTTTAATTTTACAACACA AAGCTCAAACGNACCTACAATAAGTCTAGTGTTACGNGCCAAGGGATAAGGCTGAACAATA AATTAACCCTTTAAAAATGTCTATGNACAAGTACAATTTCTTTTGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAATCCAGCGGCAATGAAGTTAAT
WI-6810	37	T C	CACAATAATAAAATCACTCCCTACCTTGAAAACTTTA[T/C]AGAAGCATTTTAATTTTACAACACA AAGCTCAAACGNACCTACAATAAGTCTAGTGTTACGNGCCAAGGGATAAGGCTGAACAATA AATTAACCCTTTAAAAATGTCTATGNACAAGTACAATTTCTTTTGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145	C A	GCATGATTAAACCAGTGCAGAAAAAATACCAAGTACATGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTTGTAATCCAGTTAAGCACCTATCAGCATATACAACTCAACAATGTAGCT GCAGGGTAAC[C/A]TGTGGATACCCTGTGTGCTCTACTNGCCTCCAAAGGCATTCAGGGGGATCATCA AAGATGTTGGACACCTTGTTGTTCAAATCTTGGTTCAGGTGCGGCCTGTGCAG

WI-6817	145	C A	GCATGATTAAAACCAGTGCAGAAAAATACCAAGTACACATTGGGTGAACGATGAGCTAGCTGTTGTTCTAGTA TTTGCTTTTGTAATCCAGTAAGACCATCAGCATATACAACATCACTAACTCACTAACATGTAGCT GCAGGGTAAC[C/A]TGTGGATACCCTGTGTGCTCTACTNGCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGGTTCAAATCTTGGTTCAGGTGCGGCCCTGTGCAG
WI-6819b	221	C	GATGGAAAGCCATTTTATTTTCTCTAAAATTTAAAATAGAAGACTTAATGGAAAACATTTAGTAC CATCATGTCACCCTGAATGCCAGCAATACCTGACTTTTACACACGCAGGAAGCCTAGTAAAAGCCC CGTCAGTAGTACACATTCTCTATGGTCCTTCAACAGTTTGCATATACAAAATTTTCTGCTATTTG CTTTAGCAAACAGCAATAACTTTGTATGTTCCTATATGACACCTAATATCCAG
WI-6819a	175	G T	GATGGAAAGCCATTTTATTTTCTCTAAATTTAAAATAGAAGACTTAATGGAAAAACATTTAGTAC CATCATGTCACCCTGAATGCCAGCAATACCTGACTTTTACACACGCAGGAAGCCTAGTAAAAGCCC CGTCAGTAGTACACATTCTCTATGGTCCTTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTATT TTGCTTTAGCAAACAGCAATAACTTTTGTGTTTCCTATATGACACCTAATAT
WI-6826b	154	A G	GCAAAAAGCTTTATTGGCTCCAACAAATTATCCCTTTAAAACTCCTCTTCTTCTGGTCTCAGTG GAACAACACACATTGAATTTCAGATTTGCAGTTTATAGCATTTTTTCCCTAAGAACCATATAAATAC ATGCAAAAACCTTGTACAT[A/G]GAGCTAAATAATATCAAAATGCAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAATTATGGCAACACACTGGACTGGGGTATACGTTG
WI-6826	154	A G	GCAAAAAGCTTTATTGGCTCCAACAAATTATCCCTTTAAAACTCCTCTTCTTCTGTGTCTCAGTG GAACAACACACATTGAATTTCAGATTTGCAGTTTATAGCATTTTTTCCCTAAGAACCATATAAATAC ATGCAAAAACCTTGTACAT[A/G]GAGCTTAAATAATATCAAAATGCAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAATTATGGCAACACACTGGACTGGGGTATACGTTG
WI-6857a	122	T C	AGTGCAAAACTATTTTGAACAAAAGTAAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAACAATATTCACTAAGTAAAATACAGCAGATGAGATGTCTCTCACATGTA[T/C]ATTTAAT TATTCATGCTTTTTCAATAGTCTCTTAGTCAACTTCAGTGTAATTCCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAATGGCAAAGTTTGGCAACTGTTTTGGGCTAATT
WI-6865	153	G A	TTATAGAATACTTATGGGGCATACGNGTAAATGAACCTTAAAATCTAAACAAACAGCTTG TTTGTGGTTCGTCCTGAAATCCTCCCTGCTCACCAAAAACCAGCTACTNGGTTTCTAAAAGACGTA ATTTTGCAGGCAAACTTC[G/A]TAGAGCCAAACTTCCACAAATATATAGCAGCTCAGTGTTTGTT TTACCTGTAGTATGAAGATATTCTTTGCGCGTGTTAGAACTGAGCTCATTAA
WI-6909	73	C T	ATTGAAAACTGGTTAGCAACAACAGATAAATTACAATAGACCTGGATATAAAAATGAGAGAAGAATGC AGACTTA[C/T]AAGCTTATAGAGAAGAAGTCAAAAAGGAGCAAGTTTTGAAATCAGATTTTATGATAC GGAAAAAATTTCCTTTTTTGCCAACAGGATTATTTCGAATAATAAATCTGCCAGTGCCAATCAG AAACACCATTTCCACAATATTTGCATGCCCCCTAGTTGCCTATTTTATACATATC

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WI-6910b	163	G T	CACTCAAAACCTTTATTCATTGATTTACAAACTGTACAATATTTACAAAGTTTAGGCATTAATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAAAATAAATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/T]TGAGATGTAATGGAGAATTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCCGGACCTTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144	A	GCTTGTTTTTTGTTTTGTTTTTAAGTGACACCTTGGCCATTCTTCACTTATCTTACCC AAAAGTGCCTTTGGGCGGGCCAGCCACTGATTTAAAACCCAGAAATGTGGTTTAAAACAATGTGGT CGTGGTGAATTCAGGTGATTTTNATTTCTATTGGTAGTATTTTCAGATTTCCCACAAAGAACATG TATTGTCTTTGTAATTTGAAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175	T C	CAATCAAAAAGTTCCAAGTTCAAAGCTGGGATGAAAAGCCAGGTCTTCTGCACTTGCACTCTGTCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCCTCCCATAAGAAGTTCACTCTTAATTTCATGTCCCATG CTTTGTCTTGGTCCCTGTGAGGAAAGGGGTCAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGTAGG TATCCTGGCCAAGATATTTCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175	T C	CAATCAAAAAGTTCCAAGTTCAAAGCTGGGATGAAAAGCCAGGTCTTCTGCACTTGCACTCTGTCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCCTCCCATAAGAAGTTCACTCTTAATTTCATGTCCCATG CTTTGTCTTGGTCCCTGTGAGGAAAGGGGTCAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGTAGG TATCCTGGCCAAGATATTTCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79	G A	TTTTTATGAAACATTTCAGATTCCCTCATATCACAGCACCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCCAATCCTAGGTAAGATATCCAAGTTACAAANTAC AAGTGCCGNTAATTAAACTATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6955	79	G A	TTTTTATGAAACATTTCAGATTCCCTCATATCACAGCACCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCCAATCCTAGGTAAGATATCCAAGTTACAAANTAC AAGTGCCGNTAATTAAACTATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6957	47	C G	AAAACTAAAAACCCTTATTGTCTCCAAGTGTGTGGCAAAATAGAAAAT[C/G]TTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATTCCACTTAAGAAGCATTCCAGTCAAATAATCACAAAA ACAAATTCAGATTGCTTGGATCTTCATTTATGGCTTGAAGAACTGGATTTGAAAACCACTTTAGG CTAAAATAAATGTATATGAATAATGCATAGACTGTGTATCTAGAAAATCATGC
WI-6996c	242	G T	ACTTCTAGTGCCTCTGTTACCCACCACTCTAATGCCTCTGGTCGCCGCACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCCGTCCCCTCCCCTGTCTTCAGCACCCAGAAGGCTCAGTGCCTCTCAGGACCCCTG CAGGAGAGAGAGGGGCGTCGTGGAGACCCCTGTCCTGACT CTCTCCTGATGTGGGGCCCTCGTGCTCTTCCTTCCIG[T/C]GTCGGATC

WI-6996b	242	G	T	ACTTCTAGTCGCCTCTGTTACCACCACCTCTAATGCCTCTGGTCGCCGGCCACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCCTCCCTGTCTTCAGCACCCAGAGAGGAGAGCGGCCAGTTCCCTG CAGGAGAGAGGAGAGCGGCTGCTGGACCCAAGGCTCAGTCCCTGCCCTCTCAGGACCCCGTCCTGACT CTCTCCTGATGGTGGCCCCTCTGTGCTGTCCG[G/T]GTCGGATC
WI-6996	228	T	G	ACTTCTAGTCGCCTCTGTTACCACCACCTCTAATGCCTCTGGTCGCCGCCACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCCTCCCTGTCTTCAGCACCCAGAGGAGAGAGCGGCCAGTTCCCTG CAGGAGAGAGGAGGGCTGCTGGACCCAAGGCTCAGTCCCTGCCCTCTCAGGACCCCGTCCTGACT CTCTCCTGATGGTGGCCCCTCTG[T/G]GCTCTCTCTCCGGTCGGATC
WI-7021b	112	G	A	TGGGGAGGACAGGGAGAGATGCTGCAGTTCCAAAAGAGAAGGTTTCTTCCAGAGTCATCTACCTGAGTC CTGAAAGCTCCCTGTCCTGAAAGCCACAGACAATATGGTCCCAAAT[G/A]CCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTTCCGTTCCACATCCACACAGCCAATCCAATTAATCAAACC ACTGTTATTAACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A	G	TGGGGAGGACAGGGAGAGATGCTGCAGTTCCAAAAGAGAAGGTTTCTTCCAGAGTCATCTACCTGAGTC CTGAAAGCTCCCTGTCCTGAAAGCCACAGACAATATGGTCCC[A/G]AATGCCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTTCCGTTCCACATCCACACAGCCAATCCAATTAATCAAACC ACTGTTATTAACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C	T	GGCAGTAGGAGACCACCAGTGTGGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCCAGGATGCGGGTGG CCCTGCAGCCTCCTCCACCTCACCTGTGTTCCAAGCGCTAAACGTTGGTGA[C/T]GGTTGGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTGTTCCAAGTTCCAAACAACAGAAAGTCATTCCTTCTTTTAAA ATGGTGCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7056b	118	C	T	GGCAGTAGGAGACCACCAGTGTGGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCCAGGATGCGGGTGG CCCTGCAGCCTCCTCCACCTCACCTGTGTTCCAAGCGCTAAACGTTGGTGA[C/T]GGTTGGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTGTTCCAAGTTCCAAACAACAGAAAGTCATTCCTTCTTTTAAA ATGGTGCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7091b	153	A	C	AATTCGCTGAAAAGGAACTACCTATCCTTACATTCACCTACTAATGTCTCTTCTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATACTGTCTATAAATAGTATTCCAATCACTGTG CTTAATTAAATAGCATT[A/C]TCTTATCATTTATCATTTATGTATTTCAAGTAAAATATTA ACATATTATTTCATTGGTCTTCTTTTTATCTGGTTCTATATGAATGCTAT
WI-7091	153	A	C	AATTCGCTGAAAAGGAACTACCTATCCTTACATTCACCTACTAATGTCTCTTCTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATACTGTCTATAAATAGTATTCCAATCACTGTG CTTAATTAAATAGCATT[A/C]TCTTATCATTTATCATTTATGTATTTCAAGTAAAATATTA ACATATTATTTCATTGGTCTTCTTTTTTATCTGGTTCTATATGAATGCTAT

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WI-7136	58	T	C	TGTGAAGCCACATTTCCAACATGAGCCTCATGAAGCCAACTAAGTGTTATTGAACTGT[T/C]AATTCTCTCAATAACTCAGTGTAGCACTTTAAAGTCTGAAGGACAGCAGCAACATGAAAGAGCATCAATGTGGTGGAGAAAGGGAAGGGGTTGGCTTTTTAATTTATTTTCTTCATCTTTATAACAAGAAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTAGCTTTCTATATATG
WI-7146c	210	A	G	GGGACGCCTGTGTTTGGCTCAATTGGGTTTGTTGGTCACATGGAGCTCTTCCATTCGTTTAGCTGAATAATGAGTTGTTCCTAGAGGAGACAGCCTGTCTCTCCTTGTTGCCCCCAAGCCCATGCCCTGCCGTGGTGGCAGCTGGGGCTGTGGGATGGGAGGGGGTCCCAACGATGTGTTGCCCCTCCTCCGCATGCCAACGC[A/G]GTTCATGTACAAGGCCCCTCTGCAACTGGAGAGAAAATTA
WI-7146b	210	A	G	GGGACGCCTGTGTTTGGCTCAATTTGGGTTTGTTGGTCACATGGAGCTCTTCCATTCGTTTAGCTGAATAATGAGTTGTTCCTAGAGGAGACAGCCTGTCTCTCCTTGTTGCCCCCAAGCCCATGCCCTGCCGTGGTGGCAGCTGGGGCTGTGGGATGGGAGGGGGTCCCAACGATGTGTTGCCCCTCCTCCGCAT[G/A]CCAACGCAGTTCATGTACAAGGCCCCTCTGCAACTGGAGAGAAAATTA
WI-7146	202	G	A	ATATTACAAACTTGCTTTTAGCTGATCTTCCATCCTCAAATGACTCTTTTTCTTTATATGTTAACATATATAAAAATGGCAACTGATAGTCAATTTGATTTTTATTCAGGAACTATCTGAAATCTGCTCAGAGCCTATGTGCATAGATGAAAACNNNNNNNNNN[A/T]AAAAAAGTTATTTAACAGTAATCTATTTACTAATTATAGTACCTATCTTAAAGTATGTAAGTACATTTACATATGTAAATGGTATGTT
WI-7153	161	A	T	TAGAATAGATGCGGTCATATTCTTCTTGGCTTCTTCCAGCCCTCATGGTTGGCATCACATATGCCTGCATGCCATTAACACCAGCTGCGCCCTACCCGTTGTCCTAAATTAATATACACCAGTGGTTCCTCCTCCTGT[T/G]TAAAGACTAATGCTCAGATGCTGTTTACGGATATTTATATTCTAGTCTCACTCTCTTGTGTCGCCACCCTTCTCTCTCTTCTCCCAACTCCAG
WI-7155	156	T	G	AGCTCCCACCAGATGCAGATTTGTGTTTGTTTCTTGTTATCACTGTCACACAGCTTATAACATGTATGCTTTTCAGAATACAGTTGTCTAGCCAAGCCATCAAGTGTCTGAAATTCAATATTGGTTTATGCAAATACAGCAAACTTTATTTATTAAGTAGAT[A/G]GGAGAATATGTTTAAAAATATTAGGAATCCTAGACCATATTTTCAAGTCATCTTAGCAGCTAGGATTCTCAAATGGAAGTGTTATATATA
WI-7169b	161	A	G	
WI-7175b	194	C	T	CTCCTAGACTAGTGCTTACCTTTATTTATTAATGAACTGTGACAGGAAGCCCAAGGCAGTGTTCCTCACCAATAACTTCAGAGAAGTCAGTTGGAGAAATGAAGAAAATGAAGAAAAGGCTGGCTGAAAATCACTATAACCATCAGTTACTGGTTTCAGTTGACAAATATATAATGGTTTACTGCTGTCTGTCCATGCCTA[C/T]AGATAATTTATTTGTATTTTTGAATAAAAACATTTGTACATTCCTGATACTGGG

WI-7175	194	C T	CTCCTAGACTAGTGCTTACCTTATTAATGAACTGTGACAGGAAGCCCAAGGCAGTGTTCCTCACCA ATAACTTCAGAGAAGTCAGTTGGAGAAAAATGAAGAAAAAGGCTGGCTGAAAATCACTATAACCATC AGTTACTGGTTCAGTTGACAAATATATAATGGTTACTGCTGTCATTGTCCATGCCTA[C/T]AGAT AATTTATTTTGTATTTTGAATAAAAACATTTGTACATTCCTGATACTGGG
WI-7178b	273	G A	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTTGCTGTCTGGCTTTTCCTCTGAGCCCAGCTGCCTGGAG AGGGGTCTCGCTGCTGGCTCCTAGGGGAACAGACCAGTGACCCCAGAAAAGCATAACCA ATCCCAGGGCTGGCTCTGCACTAAGAGAAAATTGCACTAAATGAATCTCGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGGACTGTTCCAAAGCCAGTGAAATGTGAAGGAA
WI-7178	273	G A	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCCTCTGAGCCCAGCTGCCTGGAG AGGGGTCTCGCTGCTGGCTCCTAGGGGAACAGACCAGTGACCCCAGAAAAGCATAACCA ATCCCAGGGCTGGCTCTGCACTAAGAGAAAATTGCACTAAATGAATCTCGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGGACTGTTCCAAAGCCAGTGAAATGTGAAGGAA
WI-7182b	116	A C	GCATATTTGGCAGCTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACCAGTTCCTCTGCAACCCACTCTGAGCCT[A/C]TCTCTCCTCCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCCTGAAGCCTAGTACCCCAATT
WI-7182	106	C A	GCATATTTGGCAGCTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTATTCACCAGTTCCTCTGCAACCCA[C/A]TCTGAGCCTATCTCTCCTCCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCCTGAAGCCTAGTACCCCAATT
WI-7191b	273	T A	ATAATTGCTTGTTTTCTAGCCTGGCAAGATATTTCATAAAAGAGGGATAACAATGCTGATTACTAC CTTTAAAATATTTAGATAAATGCACAGCACCACCATCTAAGCATTAGTGATGGGTAGC TGATGTCAGCTTCATGTGGGATTTTAAGCACTCTAGAAACAATGAAGCTTCTTGGCATATTTTAAGGAG CTCCCAAAATGTGTTACCTATTAAATTGTAACTCAGCAAGTAGAGAGACCATTT
WI-7199c	112	T C	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCTTCCTGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCCTTGACCTATGAGC[T/C]GGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCACTCCTTAATGTTTCTTGGTGCTCTGAATTTCTTCTTTATTAT AGTCCTATAGTTTTACTCCTCAGTTCCTCACCCATCATCTTGTCTAA
WI-7199b	112	T C	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCTTCCTGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCCTTGACCTATGAGC[T/C]GGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCACTCCTTAATGTTTCTTGGTGCTCTGAATTTCTTCTTTATTAT AGTCCTATAGTTTTACTCCTCAGTTCCTCACCCATCATCTTGTCTAA

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WI-7216c	237	T	C	TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGTCCTTTCTCCCC AAGGACAAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCCTCCAGAAAAATACGTATGT TTAAAAACCCTTCCTGCTATACATAGGAAAAGACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTTG[T/T][T/C]CTTGTAATCACTT
WI-7216b	237	T	C	TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGTCCTTTCTCCCC AAGGACAAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCCTCCAGAAAAATACGTATGT TTAAAAACCCTTCCTGCTATACATAGGAAAAGACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTTG[T/T][T/C]CTTGTAATCACTT
WI-7220b	147	A	T	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTATTTGTCTCTTTAAGCTGGCAAACCCA TCATTAAATAGCACATAAAAATAGCAATCATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAA[A/T]AATCTTGAGCACAGTGAATGACCTATCCTGCAAACATCTAATGGATCTCTA AAGGGTAACAAACCCTATAAATTCTGGCTTACTGCACATATTTAGTGTGTT
WI-7220	140	A	T	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTATTTGTCTCTTTAAGCTGGCAAACCCA TCATTAAATAGCACATAAAAATAGCAATCATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGC[A/T]CTAGAAAAAATCTTATAAAATTCTGGCTTACTGCACATATTTAGTGTGTT AAGGGTAACAAACCCTATAAATTCTGGCTTACTGCACATATTTAGTGTGTT
WI-7226	232	C		GATCGAATTTTCAGATGATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATA TACATATCACCTCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTGATCATT CCCTTTTCCATATAGGAAAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAAAATAA TTACCCACAAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT
WI-7228b	254	G	A	ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAAATGCATACCAGTAATTGGCTCCAATTCATAA TATGTTCACCAGGAGATTACAATTTTTGCTCTCTTGTAATCTATTAGTTGATTTTAATTA CTTTCTGAATAACGGAAGGGATCAGAAGATATCTTTGTGCCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTAAAATAAGAATGTTATCCAACTATTAAGATATCTCAATGT[
WI-7228a	163	G	A	ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATTGGCTCCAATTCATAA TATGTTCACCAGGAGATTACAATTTTTGCTCTCTTGTCTTTGTAATCTATTAGTTGATTTTAATTA CTTTCTGAATAACGGAAGGGATCAGAAA[G/A]ATATCTTTGTGCCTAGATTGCAAAATCTCCAATCC ACACATTGTTTTAAAATAAGAATGTTATCCAACTATTAAGATATCTCAA
WI-7233c	213	C	T	CGATCGTACTGCCAGTAGCATTGTCGTGTCTGTCCGGTCTTGTTTGTACATTCCATTTCAATTGTTACA GATGTGAACTTATTCCTTGTCACTAATTATTAAAATTATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTTCTTGCCACCTTTTGTGGCAATATTAAAGTGAACTGCTAATA GTGTAAGTA[C/T]GTGCACAAAACCACTGCCAGATAACCAGAGGGGCCTG

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WI-7233b	213 C T	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCTGCCGGTCTCTGTTGTACATTCCATTTCAATTGTTACA GATGTGAACTTTATTCCTTGTCACTAATTATATTTAAAATTATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTTCTGCCACCTTTTGTGGCAATATTAAAGTGAACTGCTAATA GTGTAAGTA[C/T]GTGCACAAAACCACTGCCAGATAACCAGAGGGGCCTG
WI-7233	211 T C	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCTGCCGGTCTCTGTTGTACATTCCATTTCAATTGTTACA GATGTGAACTTTATTCCTTGTCACTAATTATATTTAAAATTATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTTCTGCCACCTTTTGTGGCAATATTAAAGTGAACTGCTAATA GTGTAAG[T/C]ACGTGCACAAAACCACTGCCAGATAACCAGAGGGGCCTG
WI-7238	128 T C	GCGTCTACAGACAGCTCACCATTTTGTCCTGTATCTGTAAACACTTTTGTTCTTAGTCTTTTTCTTG TAAAATTGATGTTCTTTAAAATCGTTAATGTATAACAGGGCTTATGTTTCAGTTGTTT[T/C]CCGTT CTGTTTTAAACAGAAAATAAAAGGAGTGTAAGCTCCTTTCTCATTTCAAAGTTGCTACCAGTGTAT GCAGTAATTAGAACAAAGAAGAAACATTCAGTAGAACATTTTATTGCCTA
WI-7252f	520 T C	CCACCAGGATCCCAGCCCAAGCGGCCCCTTCCCCACTCGCAGCAGCGCCGGGACAGAG GCCTGCCCGGCGGCGGCCCGCAGCCCCGGCGCTGCCCCGGTCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGTGCAGGTGGAACTCAGTCATTAGACTCCTCCTCCA
WI-7252e	552 T C	CCACCAGGATCCCAGCCCAAGCGGCCCCTTCCCCACTCGCAGCAGCGCCGGGACAGAG GCCTGCCCGGCGGCGGCCCGCAGCCCCGGCGCTGCCCCGGTCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGTGCAGGTGGAACTCAGTCATTAGACTCCTCCTCCA
WI-7252d	540 T C	CCACCAGGATCCCAGCCCAAGCGGCCCCTTCCCCACTCGCAGCAGCGCCGGGACAGAG GCCTGCCCGGCGGCGGCCCGCAGCCCCGGCGCTGCCCCGGTCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCCTCCA
WI-7252c	552 T C	CCACCAGGATCCCAGCCCAAGCGGCCCCTTCCCCACTCGCAGCAGCGCCGGGACAGAG GCCTGCCCGGCGGCGGCCCGCAGCCCCGGCGCTGCCCCGGTCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCCTCCA
WI-7252b	540 T C	CCACCAGGATCCCAGCCCAAGCGGCCCCTTCCCCACTCGCAGCAGCGCCGGGACAGAG GCCTGCCCGGCGGCGGCCCGCAGCCCCGGCGCTGCCCCGGTCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCCTCCA

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WI-7252a	520	T	C	CCACCAGGAGATCCCAGCCCAGGCGGCCCTCCCGCCCTTCCCACTCGCAGCAGACGACGCCGGGGACAGAG GCCTGCGGCGGCGGCGGCCGCCGGGGCCGCCTGGCGTCGGAGCGCTGCCCGCCGCCCCTGGTCGTCTCGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCCTCCA
WI-7265m	252	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATGTAAAATATAACGATCTCTT AAAAATACCACAGTTTGTATTTTTCTT[T/]AAGGAGTAAAGATTTGCCTT[T/]
WI-7265l	231	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT GTTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTTCTT[T/A]AAGGAGTAAAGATTTGCCT
WI-7265k	121	T	G	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATTAGTGATGCATTAGTGATTTGT[T/A]TATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTTCTT[T/C]TTAAGGAGTAAAGATTTGCCT
WI-7265j	174	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTTCTT[T/A]AAGGAGTAAAGATTTGCCT
WI-7265i	227	T	C	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATGTAAAATATAACGATCTCTT AAAAATACCACAGTTTGTATTTTT[T/C]CTTAAGGAGTAAAGATTTGCCT
WI-7265h	80	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT GTTTAAGGAAACCAAGCATATAGATGCATTAGTGATGTTGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTCTTTTTCTTAAGGAGTAAAGATTTGCCT
WI-7265g	170	T	G	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATT[T/G]TGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTTCTTTTTCTTAAGGAGTAAAGATTTGCCT

WI-7265f	231	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAAACCAAGCATATAGATGCATTTGTATTTTTTCTT[T/A]AAGGGAGTAAAGATTTGCCT AAAAATACCACAGTTTGTATTTTTCTT[T/A]AAGGGAGTAAAGATTTGCCT
WI-7265e	227	T	C	AACTTGGTTATGTCAGTTCCTGTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAAACCAAGCATATAGATGCATTTGTATTTGTTATTATTATGTAAAATATAACGATCTCTT AAAAATACCACAGTTTGTATTTTT[T/C]CTTAAGGGAGTAAAGATTTGCCT
WI-7265d	174	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAAACCAAGCATATAGATGCATTAGTAGTTGTT[T/A]TATATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTCTTTAAGGGAGTAAAGATTTGCCT
WI-7265c	170	T	G	AACTTGGTTATGTCAGTTCCTGTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAAACCAAGCATATAGATGCATTAGTGATT[T/G]TGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTCTTTAAGGGAGTAAAGATTTGCCT
WI-7265b	121	T	G	AACTTGGTTATGTCAGTTCCTGTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTA GTTTAAGGAAAACCAAGCATATAGATGCATTTGTATTTGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTCTTTAAGGGAGTAAAGATTTGCCT
WI-7265a	80	T	A	AACTTGGTTATGTCAGTT[T/A]TATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTA GTTTAAGGAAAACCAAGCATATAGATGCATTAGTAGTTGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTCTTTAAGGGAGTAAAGATTTGCCT
WI-7281b	183	C		GATCACCCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGCCCCACCTTGGAGCAGAGAGCCAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAAGTCTGGCCCTGCGAGGTCTCCCATGGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTGGGGTCCTGCGCAAGAAGGCCTCCTC GTGTTGTTGAAGACCACTCGTTCTGTGGGTCCTGCGAAGAAGGCCTCTC
WI-7281	171	C	A	GATCACCCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGCCCCACCTTGGAGCAGAGAGCCAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAAGTCTGGCCCTGCGAGGTCTCCCATGGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTC[C/A]TTGGCAAAAACGGAGTCCGCAGGCCG CAGGTGTTGTTGAAGACCACTCGTTCTGTGGGTCCTGCGAAGAAGGCCT

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WI-7282b	159	G	C	:::	TGTCACCTGGCACATTCATTTTCTCAGTTGAAGAAGAGAGAAAATTGAAAAATGTCCTTATGCTTTAGA GTTGCAACTTAAGTATATTGGTAGGGTGAGTGTTCCACTCAAGATGTGTTCAACTTNNNNNNNNNT AGGCCCTTTCATAAAAACCAAACT[G/C]TAGCAAGATGCAAATGCATGGCAAATCTGTCGGTCTCCA GTTGGTTATCTGAATAGTGTCACCAAGTCCACCAAGACAGTGCTGAGATTGG
WI-7292	92	T	C	:::	CTTGATTACTTCCACTGAGGTGGGAGCATCTCCAGTGCTCCCCAATTATATCTCCCCACTCCACTAC TCTCTTCCTCCACTTCATTTTCC[T/C]TTGTCCTTTCTCTCTAATTCAGTGTTTTGGAGGCCTGACTTG GGGACAACGTATTATTGATATTATTGTCTGTGTTTTCCTTCTTCCCAATAGAAGAAAGTCATGGAGCC TGAAGGGTGCCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	A	G	:::	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGGTTACAATGAAGGAGGAAATTT[G[A/G]CGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCA ATCAAATTATGGACACATGAAAGGGGCCAGTTTTGGTGGAAGAGCTCGGGCTGA
WI-7301e	94	T	G	:::	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTG[T/G]TGGAGGATATGGTTACAATGAAGGAGGAAATT TGACGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAGAAGCTCGGGCAG TCAAATTATGGACACATGAAAGGGGGCCAGTTTTGGTGGAAGAAGCTCGGGCAG
WI-7301d	138	A	G	:::	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGTAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGT[A/G]GTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGGCCAGTTTTGGTGGAAGAAGCTCGGGCAG
WI-7301c	211	A	C	:::	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGTAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTATGGAC[A/C]CATGAAAGGGGGCCAGTTTTGGTGGAAGAAGCTCGGGCAG
WI-7301b	182	C	T	:::	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGTAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTA[C/T]AGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGGCCAGTTTTGGTGGAAGAAGCTCGGGCAG
WI-7301	88	G	T	:::	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGTAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGGCCAGTTTTGGTGGAAGAAGCTCGGGCAG

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WI-7301	205	A	C	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGGCGGGTATGGTGGTGGTGGTGGTGGACCAGGAGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGTGTTGGAGGAGGAAATTTGA CGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATT[A/C]TGGACACATGAAAGTGAAAGGGGGCAGTTTGGTGTGGAAGAAGCTCGGGCAG
WI-7314c	49	G	A	CTCTCCTTTTTTCTTCAGATCTGCTCCTGGGTTTAATTTGGGAGGTCA[G/A]TTGTTCTACCTCACTG AGAGGGAACAGAAGGATATTGCTTCCTTTGCAGCAGTGTAATAAAGTCAATTAAAAACTTCCCAGG ATTTCTTTGGACCCAGGAAACAGCGAAACAGCCCATGTGGGTCCTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAAATGTGTAGTCTACCTTTATTTTTATTAACAAAACTTGTTTTTT
WI-7314b	49	G	A	CTCTCCTTTTTTCTTCAGATCTGCTCCTGGGTTTA[A/G]TTTGGGAGGTCAGTTGTTCTACCTCACTG AGAGGGAACAGAAGGATATTGCTTCCTTTGCAGCAGTGTAATAAAGTCAATTAAAAACTTCCCAGG ATTTCTTTGGACCCAGGAAACAGCCCATGTGGGTCCTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAAATGTGTAGTCTACCTTTATTTTTATTAACAAAACTTGTTTTTT
WI-7314	36	A	G	ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGTGGGCACCATGGCCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAGTCCTGACAGTCAAGGGACTGCCTTTGGCATCCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAAATGAGACAATCAAAGNNNNNNNNNAGGGTGGCACACCCATC[C /]GTTTGCTGGGGTGTGGCAGCCACATCCAAGACTGGAGCAGCAGCAGGCTGGCCA
WI-7321b	199	C	T	ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGTGGGCACCATGGCCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAGTCCTGACAGTCAAGGGACTGCTTTGGCATCCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAAATGAGACAATCAAAGNNNNNNNNNAGGGTGGCACACCCATC[C /]GTTTGCTGGGGTGTGGCAGCCACATCCAAGACTGGAGCAGCAGCAGGCTGGCCA
WI-7321	199	C	T	AGACATTCTCGCTTCCCTGAAAGATGAGAAAGTGTAGTGCATGGACCCACGAAACTGCCCTGGC TCCAGTGAAACTTGGGCACATGCCAATGATAGGTCCAGAAGTCCTTATGTTAAGCCCTGGCAG GCAGGTGTTATTAAAATTCTGAATTTTGGGGATTTTCAAAAGATAATATTTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGCAGCAACCTATAAATCA[A/C]CA
WI-7336b	248	A	C	CTCTTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTCAAACTCTACCATGGATAATGCA AACAAAACCGAAGCTACATGCCAATGATAGGTGCAAAGAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAAAGAAACAGAATCAATATATATAAATTCAAGACTATCTGCAGCTA
WI-7338c	221	A	G	GTGTGTGTTTCTTCTTACACAC[A/G]TATACACAGACATCAGAAAATTCTGTT

WI-7338b	125	A	C	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGCAAAGAATCAATATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAAAAGAAACAGAAATCAATATATAAAATTCAAAGACTATCTGCAG CTAGTGTGTTTCTTCTTTACACACATATACACACAGACATCAGAAAATTCTGTT
WI-7338	125	A	C	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAGAATATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAAAAGAAACAGAATCAATATATAAAATTCAAAGACTATCTGCAG CTAGTGTGTTTCTTCTTTACACACATATACACACAGACATCAGAAAATTCTGTT
WI-7338	221	A	G	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAGAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAAAGAAACAGAATCAATATATAAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTTCTTTACACAC[A/G]TATACACACAGACATCAGAAAATTCTGTT
WI-7384c	146	T	A	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAAACAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAATAACTTAAAATACCATTAAAATACATTTGTATTCATTGTGAACAGGTATTCTTCA CAGATCTCATTT[T/A]AAAATTCTTAATGATTATTTTATTACTTACTGTGTTGTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAATTTAAAAAGAA
WI-7384b	146	T	A	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAAACAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAATAACTTAAAATACCATTAAAATACATTTGTATTCATTGTGAACAGGTATTCTTCA CAGATCTCATTT[T/A]AAAATTCTTAATGATTATTTTATTACTTACTGTGTTGTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAATTTAAAAAGAA
WI-7384	145	T	A	---	TGAAATCCTGGGTCTCTTGGCCTGTCCTGTAGCTGGTTTATTTTTACTTTGCCCCCTCCCCACTTTTT TGAGATCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/T]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTGTCTGTCCAAGAACTTTCCCCCAAAGATGTGTATAGTTATTGG
WI-7388c	106	A	T	---	TGAAATCCTGGGTCTCTTGGCCTGTCCTGTAGCTGGTTTATTTTTACTTTGCCCCCTCCCCACTTTTT TGAGATCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/T]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTGTCTGTCCAAGAACTTTCCCCCAAAGATGTGTATAGTTATTGG
WI-7388b	106	A	T	---	

WI-7388	94	T	A	TGAAATCTGGGCTCTGTCCTGGCCTGGCCTGGTTTATTTTTACTTTGCCCCCTCCCCACTTTTT TGAGATCCATCCTTTATCAAGAAG[T/A]CTGAAGCGACTATAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGTGTCTGTCCAAGAACTTTTCCCCCAAAGATGTGTATAGTTATTGG
WI-7438	64	A	G	TTAGATTTAATTGGCAACCAGCAACTCACTGCCACCATTCCACTGCAGATCTNCTATTCCTGG[A/G] GTTGATATGACAAGGAACCCTATTGGAACCAAGTCTTCAGATTGTNCCATGTGCAGACAGGCTCCT TGTCTGTAGGTGTAGTAGCATGTACACTGTACTGTTCACTGTAACATAGTTTGTNCTGGTATTTGTTA TTGGAAATGAATATCGCTTCCACTGACTTTACCA
WI-7454b	152	T	C	CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAAACTGAGAATGAGAGAACCCTGATAGCACTGTCTGAATTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTCT[T/C]TGTTGTTAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTTGTCTACTTCTCAAATGTTTTGACA
WI-7454	152	T	C	CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAAACTGAGAATGAGAGAACCCTGATAGCACTGTCTGAATTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTCT[T/C]TGTTGTTAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTTGTCTACTTCTCAAATGTTTTGACA
WI-7464c	177	G	C	AATTTGAAAATCTGAAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACTCAGTCCATCTTAACCATGTACAATGCCACTAAATTATAATTCCTATGTA CAACAGAGCCACAGCCACAAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACCAACAATTAT
WI-7464b	168	C	A	AATTTGAAAATCTGAAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACTCAGTCCATCTTAACCATGTACAATGCCACTAAATTATAATTTCCTATGTA CAACAGAGCCACAGCCACAAGAGGGTGGGCATAAGC[C/A]AGTTGCCAGCCAGAAGAGCTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACCAACAATTAT
WI-7464a	103	C	A	AATTTGAAAAATCTGAAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACTCAGTCCATCTTAACCATGTACAATG[C/A]ACTAAATTACTATTTATAATTTCCTAT GTACAACAGAGCCACAGCCACAAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACCAACAATTAT
WI-7499b	134	T	G	CAATTCTCAATCCAACCTAGTCTGTNTGCCTAAACCATTCCAGACAAACTTCCACTTCGAAGGTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTGAATGCTTCA[T /G]TATAGTCCTCTTCATTTAGCAATCAGTCAATCGATGAGGCAATACACTGCCATCATGATCCCTTTTTTTAGGA ACTCTGTACAAATTCCCTTGAAAATATAAATTTGGAAATGAGTGATGA

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WI-7499a	33	A	G	...	CAATTCTCAATCCAACCTAGTCTGTNTGCCTAA[A/G]CCATTCCAGACAAACTTCCACTTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTTGAATGCTTC ATTATAGTCCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTTAGGAA CTCTGTACAAAATTCCCTTTGAAAATATAAATTTGGAAATGAGTGATGA
WI-7506b	118	A	C	...	TGGGAATAGTAAGGAAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACTTNAAAAGTAGTCCTGGTGCTGCCTAGC[A/C]GGAGAGTTGAG TGCCACAGGTAAGAGTGAGTGAAGAGGAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAAATATTTAAAATATTGGACCACTCTTGTTCTACCATCCCTACCCACT
WI-7506	118	A	C	...	TGGGAATAGTAAGGAAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACTTNAAAAGTAGTCCTGGTGCTGCCTAGC[A/C]GGAGAGTTGAG TGCCACAGGTAAGAGTGAGTGAAGAGGAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAAATATTTAAAATATTGGACCACTCTTGTTCTACCATCCCTACCCACT
WI-7534b	143	C	T	...	TGTGAATTCTTAGCTCTGGAAGGTGTTTATGCCTTTGCGGGTTCTTGATGTGTTCGCAGTGTCACCCA AGAGTCAGAAACTGTACACACCATCCCAAAATTTGGTGGCCGTGGAACACATTCCCGGTGATAGAATTGCT AAATTGT[C/T]GTGAAATAGGTTAGAATTTTCTTAAATATGGTTTTCTTATTCGTGAAAATTCGG AGAGTGCTGCTAAAATTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135	T	C	...	TGTGAATTCTTAGCTCTGGAAGGTGTTTATGCCTTTGCGGGTTCTTGATGTGTTCGCAGTGTCACCCA AGAGTCAGAAACTGTACACACCATCCCAAAATTTGGTGGCCGTGGAACACATTCCCGGTGATAGAATTGC[T /C]AAATTGTCGTGAAATAGGTTAGAATTTTCTTAAATATGGTTTTCTTATTCGTGAAAATTCGG AGAGTGCTGCTAAAATTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162	G	A	...	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTAGGTGTGACTTGAAC TAGATTGCATGCTTCCTCCTTCCTT[G/A]GGAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCCTCTGGCTCCTTGGATGTGAGTCAGTTA
WI-7543	162	G	A	...	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTAGGTGTGACTTGAAC TAGATTGCATGCTTCCTCCTTCCTT[G/A]GGAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCCTCTGGCTCCTTGGATGTGAGTCAGTTA
WI-7555c	60	T	C	...	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGG[T/C]TA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCCTGCATTCCTGTTAAAGCCACTTGGGTC ATAAGAAGGGAAGTAAAAAATGAAGTCTGACTAGAAATTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTGAATTTCAG

				Sequence
WI-7555b	60	T	C	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGG[T/C]TCTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCCTGCATTCCTGTTAAAGCCACTTGGGTC ATAAGAAGGAAGTAAAAAATGAAGTCTGACTAGAAATTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTCATTTGATGTGCATTTCAG
WI-7555	60	T	C	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGG[T/C]TCTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCCTGTTAAAGCCACTTGGGTC ATAAGAAGGAAGTAAAAAATGAAGTCTGACTAGAAATTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTCATTTGATGTGCATTTCAG
WI-7567b	290	G	T	TGAGCCATCACTAGAAGAAAAGCCCATTTCAACTGCTTTGAAACTTGCCTGGGGTCTGAGCATGAT GGGAATAGGGAGACAGGGTAGGAAAAGGGCGCCTACTCTTCAGGGTCTAAAGATCAAGTGGGCCTTGG ATCGCTAAGCTGGCTCTGTTTGATGCTATTTATGCAAGTTAGGGTCTATGTATTTAGGATGCGCCTAC TCTTCAGGGTCTAAAGATCAAGTGGGCCTTGGGATCGCTAAGCTGGCTCTGTTT
WI-7569b	290	G	T	AATGTATCCCCTTTCGGTCCAACAACAGGAAACCTGACTGGGGCAGTGAAGGAAGGGATGGCA[T/C] AGCCGGTTATGTGTAAAAAACAAGTATCTGTATGACAAACCCGGATCGTTTGCAGTAACTGAATCCAT TGCGACAATTGTGAAGGCTTAAATGAGTTTAGATGGGAAATAGCCGTTGTATCGCCTTTGGGTTTAAATT ATTTGATGAGTTCCACTTGTATCATGGCCTACCCGAGGAGAAGAAGAGTTG
WI-7569b	63	T	C	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTGTTTGTTGTTGCCAAGGCCAAAC TCCCACTCTCTGCCCCCCTTAATCCCTTCTACAGTGAGTCCACTACCCTCACTGAAAATCATTTTG TACCACTTACATTTAGGCTGGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC[A/G]TCTGCTGGGCTGGGCTGACCACGTTACTCATCCCGTTA
WI-7574c	216	A	G	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTGTTTGTTGTTGCCAAGGCCAAAC TCCCACTCTCTGCCCCCCTTAATCCCTTCTACAGTGAGTCCACTACCCTCACTGAAAATCATTTTG TACCACTTACATTTAGGCTGGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC[A/G]TCTGCTGGGCTGGGCTGACCACGTTACTCATCCCGTTA
WI-7574b	216	A	G	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTGTTTGTTGTTGCCAAGGCCAAAC TCCCACTCTCTGCCCCCCTTAATCCCTTCTACAGTGAGTCCACTACCCTCACTGAAAATCATTTTG TACCACTTACATTTAGGCTGGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC[A/G]TCTGCTGGGCTGGGCTGACCACGTTACTCATCCCGTTA
WI-7574	216	A	G	AATGATGATGAATGATGACGACGACAACGATGATGCTTGTAACAAGAAAAACATAAGAGAGC CTTGGTTCATCAGTGTTAAAAATTTTGAAAAGGCGGTACTAGTTCAGACACTTTGGAAGTTTGTGT TCTGTTTGTTAAAACTGGCATCTGACACAAAAAA[A/T]GTTGAAGGCCTTATTCTACATTTCACCTAC TTTGTAAGTGAGAGAGCAAGAGAAGCAAGAAGCAAANNNNNNNNAAGAAAAAATAAAC
WI-7576c	168	A	T	

WI-7576b	168	A T	AATGATGATGATAATGATGATGACGACGACAACGATGATGCTTGTAACAAGAAAAACATAAGAAGAGAGC CTTGGTCATCAGTGTTAAAAATTTTGAAAAGGCGGTACTAGTTCAGACACTTTGGAAGTTTGTGT TCTGTTTGTTAAAACTGGCATCTGACACAAAAA[A/T]GTTGAAGGCCTTATTCTACATTCACCTAC TTTGTAAGTGAGAGAGACAAGAGAGCAAANNNNNNNNNNAAAGAAAAAAATAAAC
WI-7577q	77	T C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCA[T/C]CAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAGAGAAGTTCATTTGGTTTACACGTAGGAAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577p	50	G C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCATTTGGTTTACAC[G/A]TAGGAAGAAGAAGCATCAAAGTGGAGATGGAACTGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577o	157	G A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACAT[A/G]AGTGTTTGCTTTCCTT TAAAAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAGAGAAGTTCATTTGGTTTACACGTAGGAAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577n	48	A G	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAATC[G/A]TCTCTCATTACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAGAAGTTCATTTGGTTTACACGTAGGAAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577m	84	G A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCATT[T/C]ACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAGAAGTTCATTTGGTTTACACGTAGGAAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577l	93	T C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AAGAAGTTCATTTGGTTTACACGTAGGAAGAAGAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577k	154	C A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCATTTGGTTTA[C/A]ACGTAGGAAGAAGAGAAGCATCAAAGTGGAGATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACTCTTCTGAATTGACTGTATTC

WI-7577i	117	A	G	AACCATGTTCCCTTCTTCTTAGCACCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTA[A/G]ACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577i	77	T	C	AACCATGTTCCCTTCTTCTTAGCACCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTCCTTTAA AAATATGCA[T/C]CAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577h	50	G	C	AACCATGTTCCCTTCTTCTTAGCACCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCATTTGGTTACAC[G/A]TAGGAAAGAAGAAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577g	157	G	A	AACCATGTTCCCTTCTTCTTAGCACCACCACAAATAATCAAAACCCAACAT[A/G]AGTGTTTGCTTCCTT TAAAAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577f	48	A	G	AACCATGTTCCCTTCTTCTTAGCACCACCACAAATAATCAAAACCCAACAATAATCAAAACCCAACATAAGTGTTTGCTTCCTTTAA AAATATGCATCAAATC[G/A]TCTCTCATTACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577e	84	G	A	AACCATGTTCCCTTCTTCTTAGCACCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTCCTTTAA AAATATGCATCAAATCGTCTCTCATT[T/C]ACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577d	93	T	C	AACCATGTTCCCTTCTTCTTAGCACCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC
WI-7577c	154	C	A	AACCATGTTCCCTTCTTCTTAGCACCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCATTTGGTTTA[C/A]ACGTAGGAAAGAAGAAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTC

ID	Pos	Alleles	Sequence
WI-7577b	117	A G	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTA[A/G]ACAGTAGGAGTTAAT AAAGAAGTTCATTTTGGTTTACACGTAGGAAAGAAGAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577	107	G A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAG[G/A]GTTTTAGTAAAACAGTAGGAGTTAAT AAAGAAGTTCATTTTGGTTTACACGTAGGAAAGAAGAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7619q	106	C G	ACAAGGCGACTTGAAGAGGACGCGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAACGAGACT[C/G]TCGTGTGCTGGGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCT CTCTCGCTTTCTTTCTTACACAGAAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150	T C	ACAAGGCGACTTGAAGAGGACGCGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAACGAGACTCTCGTGTGCTGGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCCT[T/C]CTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCT TCTCGCTTTCTTTCTTACACAGAAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228	A G	ACAAGGCGACTTGAAGAGGACGCGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAACGAGACTCTCGTGTGCTGGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCT CGCTTTCTTTCTTACACAGAAAACATT[A/G]CACATACCGAGAAACCTATTTC
WI-7619n	237	G C	ACAAGGCGACTTGAAGAGGACGCGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAACGAGACTCTCGTGTGCTGGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCTCT CGCTTTCTTTCTTACACAGAAAACATACACATACC[G/C]AGAAACCTATTTC
WI-7619m	99	C T	ACAAGGCGACTTGAAGAGGACGCGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAA[C/T]GAGACTCTCGTGTGCTGGGGGGTGCTAATTACA TGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTC TCTCGCTTTCTTTCTTACACAGAAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189	T A	ACAAGGCGACTTGAAGAGGACGCGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAACGAGACTCTCGTGTGCTGGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCA[T/A]CTTTTTCCTC TCTCGCTTTCTTTCTTACACAGAAAACATACACATACCGAGAAACCTATTTC

ID	Pos			Sequence
WI-7619k	90	C	G	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCC[C/G]CTCCCTAAGCGACTCTCTGTGCTCTCTCCCTTTTTCCATCTTTTTCCT ATGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTGTCTCTCCCTTTTTCCATCTTTTTCCT CTCTCGCTTTCTTTCTTTACACAGAAACATACCGAGAAACCTATTTC
WI-7619j	206	T	G	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAAGCGACTC[C/G]TGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTGTCTCTCCCTTTTTCCATCTTTTTCCT CGC[T/G]TTCTTTCTTTACACAGAAACATACCGAGAAACCTATTTC
WI-7619i	106	C	G	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAAGCGAGACTC[C/G]TGTGCTCTCTCCCTTTTTCCT ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAAGCGAGACTCTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCT[T/C]CTAAGGGGAGTGTGGGGTCTGTGTCTCTCCCTTTTTCCATCTTTTTCCTC TCTCGCTTTCTTTCTTTACACAGAAACATACCGAGAAACCTATTTC
WI-7619h	150	T	C	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAAGCGAGACTCTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTGTCTCTCCCTTTTTCCATCTTTTTCCTCTCT CGCTTTCTTTCTTTACACAGAAACAT[A/G]CACATACCGAGAAACCTATTTC
WI-7619g	228	A	G	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAAGCGAGACTCTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTGTCTCTCCCTTTTTCCATCTTTTTCCTCTCT CGCTTTCTTTCTTTACACAGAAACATACCG[G/C]AGAAACCTATTTC
WI-7619f	237	G	C	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAAGCGAGACTCTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTGTCTCTCCCTTTTTCCATCTTTTTCCTCTCT CGCTTTCTTTCTTTACACAGAAACATACCGAGAAACCTATTTC
WI-7619e	99	C	T	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAA[C/T]GAGACTCTCTGTGCTGGGGGTGCTAATTACA TGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTGTCTCTCCCTTTTTCCATCTTTTTCCTC TCTCGCTTTCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189	T	A	ACAAGGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAAGCGAGACTCTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTGTCTCTCCCTTTTTCCA[T/A]CTTTTCCTC TCTCGCTTTCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90	C	G

ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGAGGAGAAGCACAAGAC
AGAGAAGGGCCAATGGGGTCATCC[C/G]C[G]CTCCCTAACGAGACTCTCTGTGCTGGGGGTGCTAATTAC
ATGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTCCT
CTCTCGCTTTCTTTCTTACACAGAAAACATACACACATACACGAGAAACCTATTTC

WI-7619b	206	T	G

ACAAGGCGACTTGAAGAGGACGCAGGCTTCCCCTAACGAGACTCTCTGTGCTGGGGGTGCTAATTACATGG
AGAGAAGGGCCAATGGGGTCATCCCTAACGAGAGACTCTCTGTGCTGGGGGTGCTAATTACATGG
CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTCCTCTCT
CGC[T/G][T/G]TTCTTTCTTACACAGAAAACATACACACATACACGAGAAACCTATTTC

WI-7619	189	T	A

CCTTTGTATGTGGAAGTATACCTGGCTTTTAAAATATATGTATTTAAAACAAAAAGCAACAGTAA
TCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGC[A/G]TTAAACCACCATCATGGACCAAATGTG
CCATACTAATGATGAGCATTTAGCACAATTGAGACTGAAATTAGTACACTATGTTCCTTGGACTGTCAGT
CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTCCTTGGACTGTTCA

WI-7626d	105	A	G

CCTTTGTATGTGGAAGTATACCTGGCTTTTAAAATATATGTATTTAAAACAAAAAGCAACAGTAA
TCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGCATTAAACCACCATCATGGACCAAATGTGCCA
TACTAATGATGAGCATTTAGCACAATTGAGACTGAAATTAGTACACTATGTTCTAGGTCAGT
CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTCCTTGGACTGTTCA

WI-7626c	155	C	T

CCTTTGTATGTGGAAGTATACCTGGCTT[T/A]TAAAATATGTATTTAAAACAAAAAGCAACAG
TAATCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGCATTAAACCACCATCATGGACCAAATGTG
CCATACTAATGATGAGCATTTAGCACAATTGAGACTGAAATTAGTACACTATGTTCTAGGTCAGT
CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTCCTTGGACTGTTCA

WI-7626b	28	T	A

CCTTTGTATGTGGAAGTATACCTGGCTTTTAAAATATATGTATTTAAAACAAAAAGCAACAGTAA
TCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGCATTAAACCACCATCATGGACCAAATGTG
CCATACTAATGA[T/C]GAGCATTTAGCACAATTGAGACTGAAATTAGTACACTATGTTCTAGGTCAGT
CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTCCTTGGACTGTTCA

WI-7626	144	T	C

TCCCATAACCGCTGCTTCAGGGTCTCTGCTGCCGCCCCCAGATGGGGGAAAGCACAGGTGGGC
TTCCCAGTGGCTGCTGCCCCAGGCCCACCCAGCCACCTTCTAGGACGCCACCCAGCCAAAAGGTTGTTCCTAAA[A
/G]TAAGGGCAGAGTCACACTGGGGCAGAGTCAAATAAAATGGATTTATTAGAATTTCATATGAC

WI-7689c	134	A	G

				Sequence
WI-7689b	134	A	G	TCCCATAACCGCTGATTCTCAGGGTCTCTGCTGCCGCCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCCAGTGGCTGCTGCCCAGGCCCAGACCTTCTAGGACGCCACCCAGCAAAGGTTGTTCCTAAA[A /G]TAAGGGCAGAGTCACACTGGGCGCAGCAGCTGATCACAAATTGCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGTGCCACAAATAAAAATGGATTTATTAGAATTCATATGAC
WI-7689	121	G	A	TCCCATAACCGCTGATTCTCAGGGTCTGCTGCCGCGCCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCCAGTGGCTGCTGCCCAGACCTTCTAGGACGCCACCCAGCAAAA[G/A]GTTGTTCCTAA AATAAGGGCAGAGTCACACTGGGCAGCAGCTGATCACAAATAAAAATGGATTTATTAGAATTCATATGAC GATAATATTGTGTGCCACAAATAAAAATGGATTTATTAGAATTCATATGAC
WI-7690	45	G	A	TGGAGAACATTCAATCTTGCCGTCACTATTCATCAATGAAGATTA[G/A]CACTGAGATCCAGAGAGG CTGGATGACTTGCTCAAGTTCACCAGCAGCATGGTAGTGGCAAAGAGAGAGTCCAGAGTCCTGGCCCTTGAT GCCCAGCTCAGTGCCACAAAGCTCAGTGGAGGGATGTTCCAGTGGATGAGGGCCACCAGGAAGCAC AGGTCCAAGGCTGGTCCCACACTTATCAGCAGCAACAACTGTCAGTTCATCC
WI-7703b	164	T	C	ACAGAAAAGTTGAATTTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTTGTTGAAGCAC AGTGATCAAGTTATTTTAATTTGGTTTTCACATTGGAAACAAGTCAGTCATTCAGATATGATTCAAA TGTCTATAAACCAAACTGATGT[T/C]AAGTAAATGGTCTCTCACTTGTTTATTTAACCTCTAAATTCT TTCATTTTAGGGGTAGCATTTGTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7703	156	T	C	TTAAATGAGTGTGTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAATTCTGTACCTCACTGGGGTCCTGGGGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCGCGGTCCTCCGTGTCTGCCAGCCAGCTCTCAGCC
WI-7743e	106	C	A	TTAAATGAGTGTGTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAATTCTGTACCTCACTGGGGTCCTGGGGCCTCATCCGAGGCAGGGTCAGGAG GGGCAGAACAGCGCGGTCCTCCGTGTCTGCCAGCCAGCTCTCAGCC
WI-7743d	275	C	T	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCGGAGGCCTCGGAGGCTCATCGTGTG GTGTACAGAATTCTGTACCTCACTGGGGTCCTGGGGCCTCATCCGAGCGAGCCAGCAGGGTCAGGA GAGGGGCAGAACAGCGCGGTCCTCCGTGTCTGCCAGCCAGCTCTCAGCC
WI-7743e	106	C	A	

WI-7743d	275	C	T	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAGAATTCTGCTACCTCACTGGGGTCCTGCCAGCCAGCAGCCAGCCTCTCAGCCAACG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCTCTCAGCC
WI-7743e	106	C	A	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAGAATTCTGCTACCTCACTGGGGTCCTGGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCTCTCAGCC
WI-7743d	275	C	T	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAGAATTCTGCTACCTCACTGGGGTCCTGGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCTCTCAGCC
WI-7743c	106	C	A	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAATTCTGCTACCTCACTGGGGTCCTGCCAGCCAGCAGCCAGCCTCTCAGCCAACG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCTCTCAGCC
WI-7743b	275	C	T	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCTCTCAGCC
WI-7743	106	C	A	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAGAATTCTGCTACCTCACTGGGGTCCTGGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCTCTCAGCC
WI-7743	275	C	T	TGACATTTATTCAAAGTTAAAAGCAAACACTTACAGAATTATGAAGAGGTATCTGTTTAACATTTCC TCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAAATC[A/G]TAGTTTAAACTGCATTATAAATTTTATAACAGAATTAAAGTAGATTTTAAAA GATAAAAATGTGTAATTTTGTTTATATTTCCCATTTGGACTGTAACTGACTGCC
WI-7758	144	A	G	

				Sequence
WI-7765b	126	G	C	ACAGGGGCCTTGGCAGGTGCAGCCCCCACTGCCTGCCCCTTGACCTGCCTGCCTCCCTTCATGCATGGAAATTCCCT TCATCTGGAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAGGGTCAGTATGG[G/C]TTAGG GAAAACATTCCATCCTGAGTCGAACTTGCTGAGCCTGTAAATAAAAGGTCGGA ACTCAAACCAAATCACTGAACTTTGCTGACGTTGACCTGTAAATAAAAGGTCGGA
WI-7773b	237	C	G	TTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTAAGTTTTATCCGTAGTTT GATAAAAGATTTTCCTATTCCTTGGTTCTGTCAGAGAACCTAATAAGTGCTACTTTGCCATTAAGGCA GACTAGGGTTCATGTCTTTTTACCCTTTNNNNNNNNTTGTAAAAGTCTAGTTACCTACTTTTTCTTT GATTTTCGACGTTGACTAGCCATCTCAAGCAA[C/G]TTTCGACGTTTGA
WI-7774b	170	T	C	TGCAACCTCTTTTCGTGATGGGCAGCCTGCTGGTCAGCACTCCAGTAGCGGAGAGACGGCACCCAGAAT CAGATCCCAGCTTCGGCATTGATCAGACCAAAACAGTGCTGTTCCCGGGGAGGAAAACACTTTTTTAA TTACCCTTTGCAGGCACCACCTTAATCTGTTT[T/C]ATACCTTGCTTATTAAATGAGGCGACTTAAA ATGATTGAAAATAATGCTGTCCTTAGTAGCAAGTAAAATGTGTCTTGCT
WI-7785c	165	G		GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGTCTGTAAATACTGTAAATGCATTGGAATAAAACTGTCTCCCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAAGGCTAATCCAATTATTATTCACATTTACCA TAATTTATTTGTCCATTGATGTATTTATTTGTAAATGTATCTTGGTGCTGC
WI-7785b	165	G		GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGTCTGTAAATACTGTAAATGCATTGGAATAAAACTGTCTCCCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAAGGCTAATCCAATTATTATTCACATTTACCA TAATTTATTTGTCCATTGATGTATTTATTTGTAAATGTATCTTGGTGCTGC
WI-7785	156	-	T	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGTCTGTAAATACTGTAAATGCATTGGAATAAAACTGTCTCCCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANN[- /T]NNNNNNNNGCCAAGGCTAATCCAATTATTATTCACATTTACCATAATTTATTTGTCCATTGA TGTATTTATTTGTAAATGTATCTTGGTG
WI-7789c	84	G	A	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTAGGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAAATGTGAATGAAGCTAATGTGAGTGAAGTGAAGCTCCCTCAGGCGCCGGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGGGCGTGTCTCAGACGACTAGCCCAGGACCCATCT
WI-7789b	84	G	A	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTAGGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAAATGTGAATGAAGCTAATGTGAGTGAAGCTCCCTCAGGCGCCGGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGGGCGTGTCTCAGACGACTAGCCCAGGACCCATCT

Name	No.	Allele		Sequence
WI-7789	73	G	A	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGAGACTCTCCC TGACG[G/A]TGGAATTTAAGTTTAGGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAAATGTGAAGCTAAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGGATAT GCCCTCCTGGTGACTCGGGGGGCTGTCTCAGACGGACTAGCCCAGGACCCATCT
WI-7790b	190	C	T	AATTGTCAGTCACTCTTCAAAACCTTACAGTCCTTCCTAAGGTTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTGCCTATGTGCTTATGTGTAGCTTTTTACTTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTTCTTGAACTC[C/T]TTCTATACTTT AAGATACTCTATTTTTAAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7790	190	C	T	AATTGTCAGTCACTCTTCAAAACCTTACAGTCCTTCCTAAGGTTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTGCCTATGTGCTTATGTGTAGCTTTTTACTTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTTCTTGAACTC[C/T]TTCTATACTTT AAGATACTCTATTTTTAAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81	C	A	CAGAGTGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTTGGCTCATATTTCTTTCTTCTCAT CTTGATGATGAT[C/A]GTCATCATCAAGAGAATTTAATGATTAAAATAGCATGCCTTTCTCTCTTTCTCT TAATAAGCCCACATATAAATGTACTTTTCTTCCAGAAAAATTCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7795	81	C	A	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTTGGCTCACATTTCTTTTCTTCTCAT CTTGATGATGAT[C/A]GTCATCATCAAGAGAATTTAATGATTAAAATAGCATGCCTTTCTCTCTTTCTCT TAATAAGCCCACATATAAATGTACTTTTCTTCCAGAAAAATTCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7814c	41	G	A	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCACTC TGTCTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGGATAAAATAATGGGATTTTC TTTCTTTTCTCTGGTAATATTGACTGTATATTTTAAGAAATAACAGAA
WI-7814b	41	G	A	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCACTC TGTCTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGGATAAAATAATGGGATTTTC TTTCTTTTCTCTGGTAATATTGACTGTATATTTTAAGAAATAACAGAA
WI-7814	28	G	A	TTCTCTCTCATTTTATCCCTCACCTGTA[G/A]CATGCCAGTCCCGTTCATTTAGTCATGTGACCACTC TGTCTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGGATAAAATAATGGGATTTTC TTTCTTTTCTCTGGTAATATTGACTGTATATTTTAAGAAATAACAGAA

Name	Pos			Sequence
WI-7830d	150	C	T	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAAGTCTGTCTGTCTGATGATGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACGATCCATAACTTTAGT[C/T]TAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTTCCTTTGAGGTTGATCGTTGTGTTGTTTGCTGCACTTTTTACTTTTTGCGTGTGGA
WI-7830c	54	G	A	GCAGGAAATAGTCACTCACTCCCACTCCACATAAGGGGTTTAGTAAGAAGTCT[G/A]TCTGTCTGATGATGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGACGATCCATAACTTTAGTCTTAATGCATTTGATACACATTAATTTTGTTGTTTCCTTTGAGGTTGATCGTTGTGTTGTTTGCTGCACTTTTTACTTTTTGCGTGTGGA
WI-7830b	134	G	A	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAAGTCTGTCTGTCTGATGATGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA[G/A]ATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTTCCTTTGAGGTTGATCGTTGTGTTGTTTGCTGCACTTTTTACTTTTTGCGTGTGGA
WI-7830	44	A	G	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTA[A/G]GAGAAGTCTGTCTGTCTGATGATGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTGCATTTTGATAAAATTAATTTGTTGTTTCCTTTGAGGTTGATCGTTGTGTTGTTTGCTGCACTTTTTACTTTTTGCGTGTGGA
WI-7865e	25	C	T	CCACTTCCTATCTGATTTTCCCAG[C/T]AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCGCCATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGAGGTGGTTGGGGTGGTATGCTACTCATAAGATTTCAGGGTGTCTTCCAACTGAAATCTCAGTGTTCTCAGTAAACCCAAACTGAAATCACACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865d	191	C	T	CCACTTCCTATCTGATTTTCCCAGCAAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCGCCATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGAGGTGGTTGGGGTATGCTACTCATAAGATTTCAGGGTGTCTTCCAACTGAAATCTCAGTA[C/T]GAAAAACCTGAAATCACACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865c	25	C	T	CCACTTCCTATCTGATTTTCCCAG[C/T]AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCGCCATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTCTCAATGTTCTCCAACTGTCTTCCAACTGAAATCTCAGTGTTCTCAGTAAACCCAAAATGCTACTCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865b	191	C	T	CCACTTCCTATCTGATTTTCCCAGCAAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCGCCATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTCTCAATGTTCTCCAACTGTCTTCCAACTGAAATCTCAGTA[C/T]GAAAAACATGCTACTCATAAGATTTCAGGGTGTCTTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA

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WI-7865	25	C T	CCACTTCCTATCTGATTTTCCCAG[C/T]AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTA GCCATCTAAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTACTCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865	191	C T	CCACTTCCTATCTGATTTTCCCAGCAAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCC ATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGTATTAGAGGGTGGTTGGGGT ATGCTACTCATAAGATGCCTATGTAAGGAAAGTGCTATTCAATCTCAATGTTCTCAGTA[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7867c	92	A C	TTCAAACACCTGTCTTCCACCCTCCCACCATCTGTGCAATCACTCACCCTTCAGCCTCACTAGTCCCC CTAACAATTACCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTTAATGTGGGGTTTAATATGGC CTGTTGAGTTTAATGTTAATGTTCTTAAGTAACCATTTCTGTTCTTGCTATAAATCTATGT CTATATGTCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92	A C	TTCAAACACCTGTCTTCCACCCTCCCACCATCTGTGCAATCACTCACCCTTCAGCCTCACTAGTCCCC CTAACAATTACCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTTAATGTGGGGTTTAATATGGC CTGTTGAGTTTAATGTTGATTTTCTTAAGTAACCATTTCTGTTCTTGCTATAAATCTATGT CTATATGTCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7868c	173	C T	TTGATCGATCTTTTCCACCCTGTCACTCAACGTGGTCCCTAGAACAAGAGAGGCTTAAAACCGGGCTTT CACCCAACCTGCTCCCTCTGATCCTCCATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCAA[C/T]TAGAGGCCAGAAAATGGGCAAATTAT CACTAACAGGTCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868b	173	C T	TTGATCGATCTTTTCCACCCTGTCACTCAACGTGGTCCCTAGAACAAGAGAGGCTTAAAACCGGGCTTT CACCCAACCTGCTCCCTCTGATCCTCCATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCAA[C/T]TAGAGGCCAGAAAATGGGCAAATTAT CACTAACAGGTCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868	66	T C	TTGATCGATCTTTTCCACCCTGTCACTCAACGTGGTCCCTAGAACAAGAGAGGCTTAAAACCGGGCTTT /C]TCACCCCAACCTGCTCCCTCTGATCCTCCATCTCCACGTCTCCATCTCAGTACAC AATCATTTAATATTTCCCTGTCTTACCCCTATTCAAGCAACTAGAGGCCAGAAAATGGGCAAATTAT CACTAACAGGTCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7870b	85	T C	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAAGCACTATTAATACTCTGCAGTGATTAGAAGGG GTGGGGTGGCGGGAATCC[T/C]ATTTATCAGACTCTGTAATTGAATATAAATGTTTTACTCAGAGGA GCTGCAAATTGCCTGCAAAAATGAAATCCAATGAGCAACTAGAATATTTAAAACATCATTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATCAATTTG

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WI-7870	76	C T	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAGAAAGCACTATTAATAACTCTGCAGTGATTGAGAAGGG GTGGGGTGG[C/T]GGGAATCCTATTTATCAGACTCTGTAATTGAATATAAATGTTTTACTCAGAGGAG CTGCAAATTGCCTGCAAAAATGAAATCCAATGAGCACTAGAATATTTAAAACATCATTACTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54	C	TTAGGTCTCATGCCCACTCCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCCGCTCTCCCCCTG CAGCCGGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTCGGGCGGGCCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAGGGACATGGGAATGAATTGAAATGGGGGCGCTGGACACC TACAGCAGCACGCATGTCCCTCCAAGGCTGTCTTCTCCCAGAGCACAGAAG
WI-7889b	54	C	TTAGGTCTCATGCCCACTCCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCCGCTCTCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTCGGGCGGGCCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAGGGACATGGGAATGAATTGAAATGGGGGCGCTGGACACC TACAGCAGCACGCATGTCCCTCCAAGGCTGTCTTCTCCCAGAGCACAGAAG
WI-7894c	142	A G	AGCCCACCCCCAAATATAACTGTTATCCAGAAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACACATCAATTAAACTTATGTCCTATTGTTTGTGAATTTATATTTGCGTATAC ATTATC[A/G]TATGTAAAAATTTGCATTTTTTATTGAAAATTATGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATGCTAAATCGTTAATTTTAACCGCTATAGAGTATTCCATA
WI-7894b	142	A G	AGCCCACCCCCAAATATAACTGTTATCCAGAAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACACATCAATTAAACTTATGTCCTATTGTTTGTGAATTTATATTTGCGTATAC ATTATC[A/G]TATGTAAAAATTTGCATTTTTTATTGAAAATTATGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATGCTAAATCGTTAATTTTAACCGCTATAGAGTATTCCATA
WI-7900e	84	C T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAAACTATAGAAGACATTAAAAGAAATC
WI-7900d	128	C T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATGCCCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAAACTATAGAAGACATTAAAAGAAATC
WI-7900e	84	C T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAAACTATAGAAGACATTAAAAGAAATC

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WI-7900d	128	C T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATGCCCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAACTCAACTATAGAAGACATTAAAAGAAATC TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900e	84	C T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAACTCAACTATAGAAGACATTAAAAGAAATC TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900d	128	C T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAACTCAACTATAGAAGACATTAAAAGAAATC TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900c	84	C T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAACTCAACTATAGAAGACATTAAAAGAAATC TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900b	128	C T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAACTCAACTATAGAAGACATTAAAAGAAATC TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900	84	C T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAACTCAACTATAGAAGACATTAAAAGAAATC TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7901c	33	C T	AGACTTAGGTACAATTGCTCCCCTTTTTATATA[C/T]AGACACACACAGGACACATATTAAACAG ATTGTTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTTAAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCTGGGTTATTGGGGCAGCGCCGTGGTCGT CACTCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901b	33	C T	AGACTTAGGTACAATTGCTCTCCCCTTTTTATATA[C/T]AGACACACACAGGACACATATTAAACAG ATTGTTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTTAAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCTGGGTTATTGGGGCAGCGCCGTGGTCGT CACTCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT

Marker	Position	Alleles	Sequence
WI-7901	33	C T	AGACTTAGGTACAATTGCTCCCCTTTTTATATA[C/T]AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTTAAAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCTGCATACAGACAGGTAACCTAGTTCGT CACTCAGTCGCTCTGCATGCTCTGCTCT
WI-7901	271	T G	AGACTTAGGTACAATTGCTCCCCTTTTTATATACAGACACACACAGGACACATATTAAACAGATT GTTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGACCCT TTTAAAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCTGCATACAGACAGGTAACCTAGTTCGTCAC TCAGTCGCTCTGCATGCTCTGCTCTGTCATACAGACACAGGTAACCTAGTTCTGTGT
WI-7926c	150	C A	CATTCCGCATCTGTCAACCAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAGAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATT TACAATGCAATACTTA[C/A]ATTTAATACTCTTGTAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAATATTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926b	28	A T	CATTCCGCATCTGTCAACCAGGACAGAA[A/T]GCATGGACAAGGATGAGCTTTACAAAGATGATGCACT ACTTTGGGAGATCAGAGAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTGGGAATGCCTTC ATTTACAATGCAATACTTACACATTTAATACTCTTGTAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926	150	C A	AAGAGCCAGCAGGTCAAAAAGGCCAACAACCATAAGCAGCCAGCCACCACCAGCCCACCAAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAAACACCAGCCGAGGCCACAGAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTGTCTCAATTCCATAGATTTCGAAGCCACA GA[G/T]TCTCTCCCCTGGAGCAGCAGACTATGGGCAGCCCAGTGCTGCCACCTG
WI-7947b	203	G T	AAGAGCCAGCAGGTCAAAAAGGCCAACAACCATAAGCAGCCAGCCACCACCAGCCCACCAAGGCCAGGTCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAAACACCAGCCGAGGCCACAGAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTGTCTCAATTCCATAGATTTCGAAGCCACA GA[G/T]TCTCTCCCCTGGAGCAGCAGACTATGGGCAGCCCAGTGCTGCCACCTG
WI-7947	203	G T	AAGAGCCAGCAGGTCAAAAAGGCCAACAACCATAAGCAGCCAGCCACCACCAGCCCACCAAGGCCAGGTCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAAACACCAGCCGAGGCCACAGAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTGTCTCAATTCCATAGATTTCGAAGCCACA GA[G/T]TCTCTCCCCTGGAGCAGCAGACTATGGGCAGCCCAGTGCTGCCACCTG
WI-7963b	145	T C	CATGTGCTGCATGAAGAGCTAATTAAAAAAGCAAAGTAAGACTAATTATTTAAAATAAAAATGCC ACAAATTTCATTTTCTCCTTCAAGTATTACAATGGAGTTTATTCTCTGCCTAAAAAGTGGAAGAAAT TGAGTGAATGA[T/C]AATTTGTAATTTAGGATAAGATCCAAGTTATTTCCCCAACTCTTGTTTCCC CCATAAAGTGAGCATGAGGAGGAGCACTCATTAAAGGCAGAAGACGGAAAA

Name	Pos			Sequence
WI-7972c	268	T	G	GGAGTTCTGGTTCCTACTGGGGCCAACCCTGGTGACCAGCACCATCTCTCCTCCTTTCACAGTTCTCT CCTTCTTCCCCCGCGTCTCAGCCATCCATTCTGTTCCCATGAGATGATGCCATGGTCTCAGCAGGGGAGG GTAGAGCGGGAGAAAGGAGGGCAGCAACCAAAAGAGAGGCTATGTGAGCACAAAGGTA CTTTGAGTGAAGCTGGGGAGATCCT
WI-7972b	268	T	G	GGAGTTCTGGTTCCTACTGGGGCCAACCCTGGTGACCAGCACCATCTCTCCTCCTTTCACAGTTCTCT CCTTCTTCCCCCGCGTCTCAGCCATCCATTCTGTTCCCATGAGATGATGCCATGGTCTCAGCAGGGGAGG GTAGAGCGGGAGAAAGGAGGGCAGCAACCAAAAGAGAGGCTATGTGAGCACAAAGGTA CTTTGAGTGAAGCTGGGGAGATCCT
WI-7972	268	T	G	GGAGTTCTGGTTCCTACTGGGGCCAACCCTGGTGACCAGCACCATCTCTCCTCCTTTCACAGTTCTCT CCTTCTTCCCCCGCGTCTCAGCCATCCATTCTGTTCCCATGAGATGATGCCATGGTCTCAGCAGGGGAGG GTAGAGCGGGAGAAAGGAGGGCAGCAACCAAAAGAGAGGCTATGTGAGCACAAAGGTA CTTTGAGTGAAGCTGGGGAGATCCT
WI-7981	261	T	G	AACCCCTGAAATCGGAAGGGACTTCCTCTTCTCTCCCTGTTTAAATTATAAGATGTCAT CCCCTTGTGTCGCATCTCATTGTAGAGCTTGGTGGCTGAGCTTCCATTGGTCTCTCTAAAACAT AGGATTGTTCACATGCCATCATCATAACCATTCCCATTGGTCTCTAAAACAT
WI-7992b	62	A	G	GAGCTTCCACAGTGAAGATGGAGAAGGTGAACTTGCTTGAATATNCCAGATTTGTTTGGTC[A/G]T GCGTATGGCAGTGAGCAGGTATGTGTTTCTTTCTTCACGAAAATAAATTAAATTGCTATCAAGAGCAAAC TATGAACATTATATTCAAGATGTCTCCAGAGTGAAGATGCCGAGGATGAACTTGCATTGAACATTCC AGATGTGTGAGATCATGTGTATTGCAGTGTGGGCAGGTATTGCTTTGCTTGC
WI-7992	62	A	G	GAGCTTCCACAGTGAAGATGGAGAAGGTGAGAAGGTGAACTTGCTTGAATATNCCAGATTTGTTTGGTC[A/G]T GCGTATGGCAGTGAGCAGGTATGTGTTTCTTTCTTCACGAAAATAAATTAAATTGCTATCAAGAGCAAAC TATGAACATTATATTCAAGATGTCTCCAGAGTGAAGATGCCGAGGATGAACTTGCATTGAACATTCC AGATGTGTGAGATCATGTGTATTGCAGTGTGGGCAGGTATTGCTTTGCTTGC
WI-8004b	183	C	T	ACTAAGAGAAATTATTTATTGGTGGCCTATAAAACTCTGTTCAGTCTTTACCTTGCTAATGATTTATTTT CATTAAAGTAAATGATCATCTTTGGGGAGGCATTTATAAAAACATATTTAGGAGAAATTTCTTTGA TTTATGCTATAAGGTAAATGTTGCATAATTTCTTGCCTATGTGAATTG[C/T]AGGTTCCACTTTGAG AGAATTCTCAATCTAATAATAAAGACCAAGGGCCAGAAACACTAAGATA
WI-8021c	57	C	T	ACAAATCTCAGAAGGACTGTGCAAGTCAAGTCAATGAGTCGCTTGTGAATTCTCATCTGGAAA[C/T]GATCCC ACGTCTTAGAACCTTCACCACACAGAGATTCTTTCTTGTAGTGATTCTCAAGTCTCAAGTCTTGGTAGGCATTCGA ACTGGTCCTTCCTTCACTTGAGATTCTTCTTTGCGCCCTCTATCAGTCAGCACACCTTTTCCAAG GATTTTACGTTGCGGCTTGTTAGGGGTGATTCGGTTGAATTGCCA

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WI-8021b	57	C T	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATTCTCATCTGGAAA[C/T]GATCCC ACGTCTTAGAAACCTTCACCACAGGAGTTTTCTTGTAGTGATTCTCAAAGTCTTGGTAGGCATTCGA ACTGGTCCTTCACTTTGAGATTCTTTCTTTGCGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTTACGTTGCGGCTTGTTAGGGGTGATTCGGTGAATTGCCA
WI-8021	57	C T	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATTCTCATCTGGAAA[C/T]GATCCC ACGTCTTAGAAACCTTCACCACAGGAGTTTTCTTGTAGTGATTCTCAAAGTCTTGGTAGGCATTCGA ACTGGTCCTTCACTTTGAGATTCTTTCTTTGCGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTTACGTTGCGGCTTGTTAGGGGTGATTCGGTGAATTGCCA
WI-8024c	206	A G	CTGAAAAATTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGTATTCAGGAGGACAGGGCAGAGGGGATCCCAGTGGCCACTTCCCATGGGAAGACAGAAGAGAGT GGGCCCCAGAGAGATGGAAGGACCCCAGTGTCATCACCAAACAACCATTTCAGCCGCCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAAACAGCTGGCCCTGGTCGTCAGTACACAAGGAAAGAGC
WI-8024b	206	A G	CTGAAAAATTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGTATTCAGGAGGACAGGGCAGAGGGGATCCCAGTGGCCACTTCCCATGGGAAGACAGAAGAGAGT GGGCCCCAGAGAGATGGAAGGACCCCAGTGTCATCACCAAACAACCATTTCAGCCGCCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAAACAGCTGGCCCTGGTCGTCAGTACACAAGGAAAGAGC
WI-8077	167	A G	GAATGAGCCTTCCTAGCGCCGAGGGACCTGCTGTTGTGGCCTGCCACATGCATTCTATGGAATGC TTTTTGGCCAAGCGGGGGCACTGAGGACTAAGCTCTGANNNNNNNNNATCTCGCCCAAACTCCTTTCT AAGGAGTCTGGGGTGTCATGCCCTACAAACC[A/G]TAAATTCTCATCAGATGGATTTTATTTAACGTT GTGTATTGTGACTTACTTTCCAATCTGACTCTGGCATAACAAGGGAAAAA
WI-8118f	114	G C	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAACTGGCAAATACAGAATTGCTTGTT[G/C]TTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTCCCTGCTCCTCCTATTCCTTCCT AAAAATCAGAACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAATGACCACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAAACTGGCAAATACAGAATTAGCTTGTTTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTCCCTGCTCCTCCTATTCCTTCCT AAAAATCAGAACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAACTGGCAAATACAGAATTAGCTTGTTTTT[T/G]CTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTCCCTGCTCCTCCTATTCCTTCCT AAAAATCAGAACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

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WI-8118c	44	C T	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGAATGA[C/T]CACTCCCTTGCTAAGGAAGCTATGTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCCTTGTTTGTTTCTTAGCCTTGAAGATGACCAGGTAGAGAGACAGAGTGAGACCAGTAGTCTTTCTGATTCCCTGCTCCTCCTATTCCTTCCTAAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88	T C	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGAATGACCACTCCCTTGCTAAGGAAGCTATGTACTTCATGCTGTGGAAAC[T/C]GGCAAATACAGAATGTAGCCTTGTTTGTTTCTTAGCCTTGAAGATGACCAGGTAGAGAGACAGAGTGAGACCAGTAGTCTTTCTGATTCCCTGCTCCTCCTATTCCTTCCTAAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299	C T	TTTTCTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGGAAGAGGGGTAGGAGGACCGAGCAGCATTCTGTGAGGAAGGGCAGGTGGGGAGGAGACCCTCTTGGCACACATTTATGGAGGGGTTGTCCCTGAAGAGAAAGGGCAGGTGGGGAGGAGAGGTTCCCTGTTACTTAAGAGAAGGCACCAGTGGGCAAAGAGCACAATGAAGAGGATGATGATAAAAAACAATCACGGGCA
WI-8171c	46	A G	TTTTCTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAAC[A/G]TGGCAGCAGGGCCTCGGGAAGAGGGGTAGGAGGACCGAGCAGCATTCTCTGTGAGGAAGACAGGAAGAAGGAGACCCTCTTGGCACACATTTATGGAGGGGTTGTCCCTGAAGAGAAAGGGCAGGTGGGGAGGAGAGGTTCCCTGTTACTTAAGAGAAGGCACCAGTGGGCAAAGAGCACAATGAAGAGGATGATGATAAAAAACAATCAC
WI-8171a	46	A G	TTTTCTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAAC[A/G]TGGCAGCAGGGCCTCGGGAAGAGGGGTAGGAGGACCGAGCAGCATTCTCTGTGAGGAAGACAGGAAGAAGGAGACCCTCTTGGCACACATTTATGGAGGGGTTGTCCCTGAAGAGAAAGGGCAGGTGGGGAGGAGAGGTTCCCTGTTACTTAAGAGAAGGCACCAGTGGGCAAAGAGCACAATGAAGAGGATGATGATAAAAAACAATCAC
WI-8171b	298	T C	TTTTCTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAAC[T/C]TGGCAGCAGGGCCTCGGGAAGAGGGGTAGGAGGACCGAGCAGCATTCTCTGTGAGGAAGACAGGAAGAAGGAGACCCTCTTGGCACACATTTATGGAGGGGTTGTCCCTGAAGAGAAAGGGCAGGTGGGGAGGAGAGGTTCCCTGTTACTTAAGAGAAGGCACCAGTGGGCAAAGAGCACAATGAAGAGGATGATGATAAAAAACAATCACGGGCA
WI-8314b	85	G C	GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTTGGGTGTCTGTTTCTCTATCT[C/G]TAAGGGGAGTCTCAAAACCCCAGCTCAAAATACGACACTAACATGATGAACATGCATGAGCTTTGAAAAGTGCTCTGTAGTCTTTATGATGTCTTATGATGTCTAGAAGAGCACTGTCCAATAGAACTTTCTGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT
WI-8314	78	C G	GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTTGGGTGTCTGTTTCTCTATCT[C/G]TAAGGGGAGTCTCAAAACCCCAGCTCAAAATACGACACTAACATGATGAACATGCATGAGCTTTGAAAAGTGCTCTGTAGTCTTTATGATGTCTTATGATGTCTAGAAGAGCACTGTCCAATAGAACTTTCTGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT

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WI-8321	178	G	A	TTTTAAATATGCCCGTTTAGAGCAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTTATACTGAGTCTGTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTCAGTATGGTTCAGAAT[G/A]AGTATCTTAGTATTCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACTGTTGGC
WI-8321	178	G	A	TTTTAAATATGCCCGTTTAGAGCAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTTATACTGAGTCTGTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTCAGTATGGTTCAGAAT[G/A]AGTATCTTAGTATTCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACTGTTGGC
WI-8332b	123	A	C	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAATCGCATGTTGCTCCACCTGGGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCCAGTCTTCCCTTGTGCAGCCTTAGA[A/C]ACTAAGTAG CAGTACTGTTGGTGTGTGTTGTTCTTCCCCAGCAATGCCTACTGCAGCTACTTAGTAACAACTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A	C	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAATCGCATGTTGCTCCACCTGGGGGGCGGGATATA AATTACCTCTAGATTGTCCAAAGCCCAGTCTTCCCTTCCCTGTGC[A/C]GCCTTAGAAAACTAAGTAG CAGTACTGTTGGTGTGTGTTGTTCTTCCCCAGCAATGCCTACTGCAGCTACTTAGTAACAACTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T	C	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGG GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAGGAGAAAGAGAAGGGAGAAGTCTACACACTTTT AAACAACCAGATCTCATGGAGANTTCCATGGGATGGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACCAGGCCCTCCTCCAAACACGTGGGG
WI-8378	308	T	C	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGG GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAGGAGAAAGAGAAGGGAGAAGTCTACACACTTTT AAACAACCAGATCTCATGAGANTTCCATGGGAGACACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACCAGGCCCTCCTCCAAACACGTGGGG
WI-8426	184	T	G	TTTAGGACATATTTAGCATTAAGCCTCAAACGATACAGCAATATGTTACATTCTCTTGTGAAAACAG TTGTTGTAGACTGTTAANNNNNNNNNAAATGTAACTCCGACTTGTGCCTAATAGGATTTGACCNTTAA GAGGNTTCTTTTGCTGTGGAANTTGCTTGAACTTCCATTCTGT[T/G]CCTTGTAGCTGGTG AGGCTGGGGAGTATGGGANGGNCCCGGGGCCCTTGGCNATNGNATTCAGTGAG
WI-8450h	61	C	A	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACATACACT[C/A]CA TCTTCTCTATCTTAGTTCCAAGTTTTAGTTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAAACTATGATTTAGCTTACCCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT

WI-8450g	55	T C	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACA[T/C]ACACTCCAT CTTCTCTATCTTAGTTCCCAGTTTAGTTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450f	108	T A	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCCAGTTTAGTTTTCAATCCCAATTA[T/A]ACCAATTCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450e	125	T C	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCCAGTTTAGTTTTCAATCCCAATTATACCAATTCCATTGTTA[T/C]TTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450d	125	T C	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCCAGTTTAGTTTTCAATCCCAATTATACCAATTCCATTGTTA[T/C]TTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450c	108	T A	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCCAGTTTAGTTTTCAATCCCAATTA[T/A]ACCAATTCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450b	61	C A	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACATACACT[C/A]CA TCTTCTCTATCTTAGTTCCCAGTTTAGTTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450a	55	T C	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACA[T/C]ACACTCCAT CTTCTCTATCTTAGTTCCCAGTTTAGTTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8458b	60	A G	CAAGGAAAGCTGTCAGTCTTCATAAACTTCAAAGAGTTACAAAAATACGTATTTTTAA[A/G]CTA CAATTCAAGATTAGCATCCAAACCTACAAAACATGATTCGTCACACACCATACAACCTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATACTTGTGAAAACTTATTGTGCACAGT GACATCCCATTCCGCCAGACTTAATGTTATAAAGCAGCTGAGCGAGTTCTCA

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WI-8461c	105	A T	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAAATATAAATCATTTTTT[A/T]NNNNNNNNNCCTTGTCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAAGGATTTGCAAAAAGGGGG
WI-8461b	38	T C	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAA[T/C]ATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAAATCATTTTTTNNNNNNNNNCCTTGTCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAAGGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38	T C	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAA[T/C]ATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAAATCATTTTTTNNNNNNNNNCCTTGTCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAAGGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105	A T	AATAACATGTTATGAAACAAGCTGGTTACAAGTAGTAGGTAGATGACTTAATTTTGATAAAAAAT TAAAAAGCAT[A/G]AACATGCATATAAAAAATTAGATTATGTACAAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAAATATTCTTCCCTTGTTTTTGTCTTTTAAAAAACATTATTTCTGAAAAAAAAA ATCAGAAAAACATGATCGTGGGAGAATTATTA
WI-9438	77	A G	ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTGATACAAAGTAACATTTAGTA CAGAAAATCCCAGTCTGTCAGCTCAGTACCTGT[C/T]GTGCACACTGTACCATCTCAGTCCCACTCT GCCTGTAACTTAGAAAAACAGCCCCTACCCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTACCTGTAAAACAAAG
WI-9439b	101	C T	ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTGATACAAAGTAACATTTAGTA CAGAAAAT[C/T]CCAGTCTGTCAGCTCAGTCAGTACCTCGTGTGCACACTGTACCATCTCAGTCCCACTCT GCCTGTAACTTAGAAAAACAGCCCCTACCCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTACCTGTAAAACAAAG
WI-9439a	76	C T	GCCTGTAACTTAGAAAAACAGCCCCTACCCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTACCTGTAAAACAAAG
WI-9446b	75	T C	GAAGGCTTGATTAAGGGAGGNTTATTGATGTNAACTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAA[T/C]CCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAAGCAAACCTTTTAAAT TACTCATCTTTCATAGTGTTGTNCCCTACTNTTATCACTGTGTCTTCTTGTGTCTTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT

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WI-9446	75	T	C	GAAGGCTTGATTAAGGGAGGNTTATTTGATGTNAACTTACCATTCCATAGAGACTATAAAGANCATTA TAAAAAA[T/C]CCTCTAAAGNGACACATGCGCCCAAATGACCANGNCATAAGCAAACCTTTAAAT TACTCATCTTTCATATGTGTGTTGTNCCCTACTNTATCACTGTGTGTCTTCTGTCTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185	A		ATTAAAATGTCAAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACTTTTTTTT GAGATAATTATTCTAGATTCCAGGCTTCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTNCTTAATTAATCAAAGTATGTTAATGTCACTT GGAATTCTACATGGAAAAGCCAACAAAATAACTAAAACTTGACTAATGAAG
WI-9497	185	A		ATTAAAATGTCAAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACTTTTTTTT GAGATAATTATTCTAGATTCCAGGCTTCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTNCTTAATTAATCAAAGTATGTTAATGTCACTT GGAATTCTACATGGAAAAGCCAACAAAATAACTAAAACTTGACTAATGAAG
WI-9523b	193	C	A	GTGAAAAAGTTTCTATTCATTCCATCATACAATAGATTGTGCTAAGGATCATTTTGGAAGAATGTG CAGCATTCAGAAGTTGTATCTCATCATGCAGTCAGTCACTCAGCAGCATTTATCTAAAAGTACGTGCACA GACTCAGAGACAATTACAAACTATTTCAGCCATGATCTATGGTGATTTCCACACATTGTACAGTGA AAAGCTCTTCAGCTTGGAACAACTGTCAAGGCAGCAGGCAGACTGCATGCACATAT
WI-9523a	47	G	A	GTGAAAAAGTTTCTATTCATTCCATCATACAATAGATTGTGCTAAG[G/A]ATCATTTTGGAAGAAT GTGCAGCATTCAGAAGTTGTATCTCATCATGCAGTCAGTCACTCAGCAGCATTTATCTAAAAGTACGTGCA CAGACTCAGAGACAATTACAAACTATTTCAGCCATGATCTATGGTGATTTCCACACATTGTACAGTGA AAGCTCTTCAGCTTGGAACAACTGTCAAGGCAGCAGGCAGACTGCATGCACATAT
WI-9554	202	T	C	AAAAACACAAGTTTCATACATCACAAAAAAACCTTCCATTATAACACAGAAGTGATTATTACCAGAC AAGCATCAGTGATGTATACTGCCTTNCTAGTTGTTATTGTACAATGCTGTAGATAATGCAGCCCATG CAATACACCCAAGAACAACACTAGAGTCCTACACCCAAGTACAATATGATAAAGCAGCCCTCTGCAAGTG G[T/C]CGCTGGATACCACTAAGAAGTCTACTGCAGCCATGTTGGTATGATTT
WI-9555	97	G	A	CCAAAAGCCAAACCATTCATATGTATGGATTTCATAAACATTTATTGATCCTTTTTTGAGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC[G/A]CTTGAAAAATCAATTCAAGGGACTCTTAATCA GTTAAATAATCTGCTTAGAAGGCACAAATGATCATACTTCAGATTAAAATACAGGTAAGTATTCAG GGNTAAAATGGTACAAAAAAGGCTGTAACTCTTTNCTTCACATGATCACA
WI-9625b	172	A	T	TTGAACATTTAATGAATGACAAAGAACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCNCCTTGGGAAAAAAAACTTTGGAAAAAAAACACGCACA TAAGTATCATAAACTGAGGGGTTGTGGACAAGTTACTTCTT[A/T]GTTTACCAATTTTATATTGACATAA AGTAGCACACGACTAGTTATTTCATTTAAAAAAACACACTGACAAATCTTTC

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WI-9625	172	A	T	TTGAACACATTTAATGAATGACAAAGAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTGGGAAAAAAAACTTTGGAAAAAAAAAACACGCACA TAAGTATCATAACTGAGAGGGTTGTGGACAAGTTACTTCT[A/T]GTTTACCAATTTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTAAAAAAACACACTGACAAATCTTTC
WI-9647	144	C	T	TTTTTCTGAGATTCAAAGAGCTACACATTTTGGTTAGTGTATGTCTACTATACCTTTTTCATCCTTTTCA ACATCTTTTGTCACATTTTAGGTGATGCTCTTGTGTAAACAGTGTATTGCTAGACCTAAAAATCCAAGCT TACAACT[C/T]GTCCTTTACCTGATACATTTATTCCATTTACTTCATTTGGATTTTTAAAAATGTTA ACTTAATACGTCTCTTTCAGATGTCCCTGCTTTTTAGTTAATTGTGTTT
WI-9676n	114	A	G	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAATTGGCAATCTTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCA[A/G]GATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676m	184	G	T	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC ATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGC[G/T]CATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676l	84	A	C	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTTA GGGGTACCAAGGNTCTG[A/C]GTTTGTACGGTCTTTATAAATGCAGAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676k	202	C	T	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGAGCAAGATGTGGCTTTCCTGCC ATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGGG[C/T]GAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676j	92	C	T	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTTA GGGGTACCAAGGNTCTGAGTTTGTA[C/T]GGTCTTTATAAATGCAGAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676i	173	T	C	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGAGCAAGATGTGGCTTTCCTGCCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT

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WI-9676h	134	C A	GGCCACTGTCTGCCAAAGTCTGTCACAGTCCTCCATATGGCAAATGAAGAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC[C/A]ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTCTTCAGCTTTGTT
WI-9676g	202	C T	GGCCACTGTCTGCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG[C/T]CAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676f	184	G T	GGCCACTGTCTGCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACCATGGCT[T/C]CCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676e	173	T C	GGCCACTGTCTGCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC[C/A]ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676d	134	C A	GGCCACTGTCTGCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCA[A/G]GATGTGGCTTTCCTGCC CCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676c	114	A G	GGCCACTGTCTGCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676b	92	C T	GGCCACTGTCTGCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTA[C/T]GGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT
WI-9676a	84	A C	GGCCACTGTCTGCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGA[A/C]GTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTTT

				Sequence
WI-9738b	40	C	A	TGGACCAAAACACAGACAGAGATGTATTCCTGGTGCCTGTGTA[C/A]ATTACAACTCATTGATTCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAAACAGTAAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACCTTGGGGGCACATGTCTGTATTGCTGTCC TCTTTTTATTTCTGTCCCTTATGTTGGTGGGCACATGTCTGTATTGCTGTCC
WI-9738	40	C	A	TGGACCAAAACACAGACAGAGATGTATTCCTGGTGCCTGTGTA[C/A]ATTACAACTCATTGATCACATGC AGCAACACATCAACATCTCAAGGAGTCCATTTGTTCAAAAACAGTAAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACCTTGCCTGGGGGCACATGTCTGTATTGCTGTCC TCTTTTATTTCTGTCCCTTATGTTGGGGGCACATGTCTGTATTGCTGTCC
WI-9756	47	A		ACTGAAATGTAAATGGCCAAGGCACCCAGGACCTTAAAAAATCATAAGAAGTTAATCTGTGGGAAAA GAGTAACTACAAAAGCATCTAAACAAGAGCAGGATGGTAATGTGTCCCCTTATCACTTAGTC AGTAAAGATAAGAAAGCCCCTGGTGAGTATCCACTTCCACAAAACACAGAATATACACTTTTGGAAG ATTTCCACTTAACCACTTGATTCTTCACTTTTTATGATTTAAAAACTCTCCGTGG
WI-9758	135	A	G	GATGGTCCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATGAATAAT TAGGAAACTGGGAGAATTCAATTCAAAGAAGAGAATTCTGTTCGCAAGGTCAATTTTTATACTATTTA A[A/G]TAAAATAAACTCTGGTAGGTTCTATAGCAAATGCTAAGTAAAGTAACCGCTGGTTCTCAAATT ATTACG
WI-9778	127	G	A	ATTTAAATCCAGGCAGGCGGGGGGAAAATGGATACTTTCATATGTCTCTGTACCCAACTATAAACTTTG GTTCTCATGCCACCATTTCATTTGCCTTCTCCACTCCAAGTACCACTGATTTTACCAATT[G/A]CTCTC ATAATTGACTTGCTACTGGAAGAAACTCTTAGAATGTTGGAATTCTCTATTACACACTTGCCTCA AAGAATGTGTCAGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGCAGCC
WI-9832	116	C	A	TCTCCCCTTTGCCTCCTCATGCCCCACTCCCTCCCAGCCTGCACAGAGCGTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGCTGACAATGCAGTTTC[C/A]TGGATCCCCACCCAGGA CTCAAAAAAAACTAGGAATTGGGAGAAGAGGGGACCTGGAATCGGTTGTTGCTGCTAGCAAGCCCCCAGGTGG TTTGTAAGTGGACTAAAGTTTGAGGGACCCAGACATGGAAGGTTGGCTTGGC
WI-9841	101	A	G	TGGAAAAATAGCTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATTCCATTTTGAATGAATAAAATATAC[A/G]TGTGTATGTATATATACTTATTAACACTT AGGATTATATACACACAATAAAACGTCTGTAAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGGATGTGTTACTTGATATGCTGTTG
WI-9880c	222	G	A	GAACTAACACCTTTCTTGCATGGATTTTCTTGATTATTGGCAGTTAACAATAAAAATGTTATTAGATC ACTGGTGCTTCTGTGTGTGGGGTTGAGTTTTTATGGATATCTCCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGACTATATATAAGATCCTCTTTTAAAATTATATTTTATATAAGCACATGAA AATGGGAATAAATAAATGA[G/A][A/T]TGACATAGGAATTACCTACACATATTTG

WI-9880b	157	C	A	GAACTAACACCTTTCTTGCATGGATTTTCTTGATTATTGGCAGTAACAATAAAAATGTTATTAGATC ACTGGTGCTTCTGTGTGGGGTTGAGTTTTTATGATATCTCCTGTTAGACCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGA[C/A]TATATAAGATCCTCTTTTAAAATTATATTTATATAAGCACAT GAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTG
WI-9880a	108	C	T	GAACTAACACCTTTCTTGCATGGATTTTCTTGATTATTGGCAGTAACAATAAAAATGTTATTAGATC ACTGGTGCTTCTGTGTGGGGTTGAGTTTTTATGATATCT[C/T]CTGTTAGACCCATAAGGGAGGCTG TGAGTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTAAAATTATATTTATATAAGCACAT GAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTG
WI-10183	127	C	T	ACACTGCAGGCACTCCAAATCCTNACAGACATATGCACTTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTCTGCTGGAGTTTATTTAAAAAAACACGCCCCCAGTTATCACAGTTTCTNTTTTGT[C/T]CACC ATTTTCCATAACAAAAGAAGCTACACAAAATTNGGGGGAGAACTCTCTTGGAGACTGACACATT TGCAGAGGGGTCATGAAATAATGATTCCAAA
FB25G10b	109	A	G	TCCCTCAATGACAGATGAACTAAATTTCTCTGGGTAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGAA[A/G]TGATTTTAGATCCTCCCCCAG TGACAAGTAAACTGAACTGACCATATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
FB25G10	109	A	G	TCCCTCAATGACAGATGAACTAAATTTCTCTGGGTAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGAA[A/G]TGATTTTAGATCCTCCCCCAG TGACAAGTAAACTGAACTGACCATATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
IB3071	102	C	A	ACAACGCTGAACTTCCATAACAGTCAATGGTACAGTCAAACATCACATGTACAGAACACACAATTA GATGAACTGAAATTATAAGNTAAATAAAATAAAAAT[C/A]CAATTTCAGNAAACAAAAATCAAAAC ATTAAGGNTCCCTGNNATATTCTTAAACCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAAATGACCCTATTAACCCAGTCTAGGGATTCTG
NIB551	161	C	T	CGTCCTTTCCTTTTGAGATTGCAATTAAGTAGAATAATATGAGAGAGAACTGACAATGGGTTGTCC TACTGAGCTTGGGGCCAGGTGTGTACTTAGGAACCATCCCAACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGTC[C/T]TGACCACATACGGGCCATTGGTTGATTTCAGCTTT GCAAGCAGGCTAGTGAGTCAGAAAAACCAAAAGCTTGTCC
S72904	51	G	T	AGCATAGAAAGTGATTTATATTTTTAATGGTTTCAAGTGGAAGTTCCTTT[G/T]AATTTGTCAGTTC ATTCCTGGAAAATCTTTTGAGTTAAAAATAAGGATCCTAGGACAGCACCTGAACTACAGGCCCTAAA GAGAAATTGCCTCAAACCACACAAGTGCTAAACTTCCTCCCCCTTTCTGTCAATTGGTTGTCTTTAAATA TTGCAAAAGTCCTGATGCTAAACAGTATTTGGAGTGTTTTCAGTGTCTGTA

UTR-00481	115	C T	TATTCTTTTTATCTCGGGGCCCACAGTTCTTGATTATTCCTCTTGTGTGGTTAAAGACTGAATTTGTAAACCCATTCAGATAAATGGCAGTACTTTAGGACACACACACAAACACACACAGA[C/T]ACACCTTTTGATATGTAAGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTCAGATTGAGC
ESTC1	33		CCCTGTAGCAGTCTTCAGCCTCCTCTACCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37		GCTACTACCACGGCTGCTTCGTTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21		GCCATCAAAAATTTCCTTCACANTCAATACTGTTGAACAACAGATAACACATCTTCTTGCTCATCCCACTTGAA
ESTC107	20		TGCTGGCTCACTTCCTCACANGCTGTATTACCTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35		AAAACCAGGAAGCCCTGCCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23		AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37		AAGGGACACAGTGTTGCTGACAAGGTGACACTGAACANAACAGTTTTCCTTTAATTGTAAAAGCGGGCATCG
ESTC117	24		AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCTATCACAATTTACAAAAAGCCTCCA
ESTC119	24		TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTT
ESTC122	34		GACAATAAACAGCTAAGCTACTGACATAAAATATNCAATAAAATTATGAGATATAAGGTACAGATGAGAAAAATCTGAAA
ESTC123	21		GAAGCCAGTATGTTGTGGCAAANATTCGAGAAAACACACTGAAAA
ESTC128	42		GCAGAGGCATCAGATAAGGCCTCAGAAAGCCCAGGCCATCATNTTCCATGGGACCAGGCTGGCTCAATGTGGAACTGG
ESTC129	20		AGTCACCATGCCCAGCCTAGNATGAGTTAGTAAGATTTGGTTATGCTGGGGAG
ESTC13	46		GTGTATCTGGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGGTCTGGATCAGAAAA
ESTC130	49		GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAATGAAACANGAGAAGCTGAAACAATCTACACCTGAATG

ESTC132	30	---	GGTAAGTCTAAATTACTGCCTTAGCAAACNCTATGTGTGTCAGGTTTTTCTGCTGCA
ESTC137	21	---	CCAGTTTGGCTTCTGTCCTCANAGTCTCTCTCCATGTGGCAAACA
ESTC139	45	---	AGGAGCACAGCCTAAGGACATGAAGGTCAGAGAGTTTCTCAGAGAGAGNGGGGCTGGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	CCCATTGTGGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTTCCCTTGCATGGTTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTATTCATTTTAAATC AAAGANACCATTCCATTTCCTAACAAACA
ESTC143	29	---	GTTTACGAAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCCTTTTG
ESTC144	26	---	AAATCCATATTTTCTTGACATGAGGTNGCTTTTAGCAGCATTTCGG
ESTC146	20	---	CATGTCCAGGATAAGGAGCANACACCAGGATTTATACGGTGGCAGCG
ESTC148	42	---	TCTTTGGTTGTCTACACAGACACTTAAGTACTGTATCGCTGTNATGCAGCGGCCTGTGGAGGCCCCTG GGGGTGGCTGGGCCTGTGTCCTGAG
ESTC149	28	---	TCAGTTCATTTATTTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTTCTTCAGTGATCTT
ESTC150	20	---	CCAGGAAAACAAAGCACACANACTTATAGAATACTTTGGTTTAAAAATTATTCATAATATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	GAAGCTAAGGCCCCATTTTTTTCTTTAATACAAAATCTACTGGTGCTNAAAACTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	TTTTAATTGACAACTCAATCTCTACATACATACAGTNTTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAAACTCATGAGCATTTACA
ESTC156	32	---	GCAGCATTTGTGACAGGAGAGCGCAAAACAAANCCTGGCTGCCTCGGGGATGGAGCGGGGGGCCTCA CCACCACTGCAT
ESTC158	35	---	ACCAAGCCCTGGGATTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	AGCTGGCAAGAGAGACTTCCTGAGGCACACATCAGNTACGTTGGTCAATTTAGGGCACGGTTCTGGTTCTGCA GCTTTGAAAGG

ESTC16	23	⋮	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCACCCACAAGGACAGGTT
ESTC160	38	⋮	TTCTAGCATTGCTGGTGCAGTGGGGGGGCCTGAGCTGGGGNGCAGTGGCAGTGTCACTGGGCCCGTTTG GGACTGGGTTGA
ESTC162	36	⋮	CTCTTCGTCCGTTTGCAAGTTGCTGTTGTTTCCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	⋮	TCATTCTCCATAGAATATATTGGTTTTGTAACANCGAATACAATCCAATATATAAACATTAAAACAATCC GATACATACCA
ESTC169	22	⋮	GTCTCTGGTGTGTGCAGGGAATCANTTTGCTGGATTAGAGGAAAGGTGCCGCCGTCTGTTTCCATGACTT
ESTC176	23	⋮	CACCTCCTCCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	⋮	TGGGTGGCTCTTTAAATACCTTCCATTATATTTCAAATTTTNCTTTATTCTATTAAAATACCTTTAT TCTCTTTATTCCCATAAAAAGGCAACCAA
ESTC18	29	⋮	TCAGACACTGCCGACATCAGCATTGTCTCNTGTACAGCTCCCTTCCCTGCAGGGCGCCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	⋮	TAGGGATTCCAAGTTGCCTGGNTTTAATATAATACATATTCACAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	⋮	GCTTGACTAGCGGAGGCTACATCACAATTTATAAAGTGCCAGATNAGTGCTAATTGTCATTCAGCTTG ATTTTTCACCTCA
ESTC187	24	⋮	ACCATGATTGCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG
ESTC188	25	⋮	TCTATTAACAGGGTTATGTCACACCNTGTCAACCTCAAAACAGATGATGACTACTCATCACTTGTCTTCCAT CTTGC
ESTC189	27	⋮	AAAGTACAAATCCAGTATATGCAGAAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	⋮	TCCTCAAATACCACTTTCCCCTAACTTATCCAGTCTAGTAAGCNTTTCAAAGGAGGAAAATGGGTTAC CTTTCAGGGG
ESTC197	26	⋮	ATCTCCAGTGTCTGCTGCCTCCTCCCNGCAAAGTCTCCCACAAGCACA
ESTC20	33	⋮	AAGATTAGGACAGACCGCCGGTATAGTAAGTAAGCTCTGNGGAACTCCAAGAATCTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	⋮	TTTGGTGAAAATCCCAATATATGAGTTTAAAAAAAAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGCCTGCAACAG

ESTC201	35	---	TCTTACTTGGGTAGTTTAGCAAACACATTTTTAAAANNCCACATCCAACAGATTGGTT
ESTC202	22	---	CTGCTGGGAGGAGGAGACAGACGGNCAGGCGGCCTGGGTGGCGGCCCCAGAAAGGCTGGCGTGGCGTGGATGTT CGAGATGAGCC
ESTC203	27	---	ACACTTAACAGGTTAAAATATCCAAATNAAATTTACTGCAACTTTTGTAGAATTTTATTTGTGCTAC AAGACACGTTGCA
ESTC208	43	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAAANAGCAATAACTATTGTTTAAAAGC CTAAGAGTGAAAA
ESTC210	29	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAAGTGAGTGACGGTGACCTGTG
ESTC212	27	---	GGGTAACCTGATGAGGAAGCTCTAGTGNGAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGT TCAAGTC
ESTC214	21	---	CTCCAGAGTCCCTCCTCCTCANACCAGGGCAGGAGGGAGTTAGGGAAT
ESTC216	49	---	TGGCAAGAAATTTATTTACACTAACAAATTAAATTAATCACAGGTATTNTTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	---	TTTTGTCAGTAAATGAGCAATACACTGANTCGCATGATTAAATAACATTAACAAGTTCAT AAACACACCCA
ESTC219	32	---	GTACACATCCTGGGGGTGAGCACACAGCAAAANGGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAAGGAAGC
ESTC22	41	---	TCATTGAAGAAAATTATGGGTTTATTCTTATTTCTAATTGNGAGAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC223	27	---	CTTCTGAAGCCCAAGAGAGGGGGCAGAANGTAGTTCTTGATTTAAAAAAACAGAAAGGGGAGGAGGA
ESTC224	37	---	CGAAGGTAGATTTCCCTCACATATTACAAAATACACANAAACACACACACACACA
ESTC225	20	---	TGCACTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGCTTCAGAAGGA ATGTGTAGGATCG
ESTC23	27	---	TTCTACTTTATTTCATATTCCCACCACNATAACGACTCCTTTAATTTAAACTAAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	---	GCTTCCTCCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAATTAAGA
ESTC231	24	---	CAAAAGGGGTTAGTTCATATTCCCANCAACAGCATGATAAAATAATTCAAC

ESTC28	23	GAAGAGCTGGGCACGCATCTGACNTTTCTTCCTCTATTCCTATAAAAATAAAAGGAAGCAGAAATCTGC
ESTC3	20	CAGACATGACCTACCGTCCCNGGCCCTCAATTCATATTTATTCTTGAGCCGCTTGGTCAGGTTTGATTCGCACACTCC
ESTC31	32	ACAGCCCCACAGAACTATTGTAAAACAATATTNTCAGTCGGTCATCATTGTAATATACAATACAAAGCAATTCCTCAGA
ESTC33	25	AGCACTTCCAGCTCCTTGACGTTGTNGGACCAGGGAACTTCCGGAA
ESTC39	26	AAGGAAAGGGAACCCACCTGGGCTTTNGGTCACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	CCACTGAATCACACAACATGGACNAATCTCAAATCATTATGCTGATGGAAAGAAACCATT
ESTC40	22	GGCATGCTAGACAGAGAGGCATTANTTTTGAAGATCTTTAAAAATATTTGACTTGTTCCCCCTTCAC
ESTC45	37	TTTGGAGGTTTGTGTCTGGAGTTTTGTTCTTTGTAACNCTCTCATCATCGAGGCTATATATTAA
ESTC50	56	CTGTCCGTGGTGAGCCCTGCCGCTGTCCCATGGGCCCAGGGAGCCCACTGGTGCGGANCCGGGCAGATGTTTACCCTGT
ESTC56	45	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTGGCAGGAAGNAGTGGAGGGAAAGGACACCAAGT
ESTC57	20	AAGTGGGCCCTCCCAGTCCCNTCTCTGGGCACAGATCCCACCAGTCTGCTC
ESTC59	38	GAAACACAAAGTGTTGAGAAAAAACTTCTCAAAATTNGTTCCAGACTTCAGGAAAATGATTTCCACATGGTAAGGCC
ESTC6	27	TCTGCAGCACTTCACTACCAAATGAGCNTTAGCTACTTTTCAGAATTGAAGGAGAAAATGCATTATGTGGACTGAACCG
ESTC61	57	AGTGATTTTGGCTAGGCGTGGTTCTCATCTGTGAAATTCCACAGCGCAATGACAGCANCCTCTCTCCCACCCACTCAAG
ESTC63	20	ACAGACACAGCATCACCACCANAGGGCCCACGGGAGGGTCGGGGAGACGACACTTTTTCCCTGGGAAAGGCAGCTCTAATC
ESTC69	20	GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTTAAATCCCCACACTTACTTACTGCTCATCCGTCACTTTCGGCTAA
ESTC7	45	AGTTTCCCTAGAGCTGTGCGGGCCAGATAGCTGTTCCTGAGTTGCANGCACGATTGGAGATTTGGACACTG

Clone	Position			Sequence
ESTC72	37		---	GGGCTTCCAAAATGGGTATTGGGGGCCCAGGAGGAGGCTGGGCNTTTGGCGGTGAGCGCCTAAAAAGTGTGACC AACAATTCACAGCTACAGGAGAAATCTAGAACAAAATCAAATATTCATCACNTTGGGTTGAAAAGTTG
ESTC74	49		---	GAAGA
ESTC77	40		---	ATGACTTTCCTGTCCCATCGGAAACCAGAGTTTCCCCAGGNGAGCCCTTCCTATCTGCGGTTA
ESTC81	20		---	GGCTCAGCACAGGGATAAGANCCCCACTCCGCATGTCCCCAGAGGGCAGCACTCCAG
ESTC82	25		---	TTTCAGATGATGGGGTCTGAGATGTNTCCTCAGGCTGCATCAGCTGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC83	53		---	CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTTAGAC TTTCACAAACCT
ESTC85	28		---	TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGCTGGTTGGGGAGGCTACAGCCTGACCACATTC TTTGC
ESTC89	22		---	ATTGCAAAGGAAGTGGAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC90	33		---	CTGGTTCTTCGTCTTGGCATTCGTCCTCCTCNGGCCACCAAGTGTCCTTCCCGATGAT
ESTC93	29		---	CTCCCCTCCTCAGTTCACAGTGGAGACTANGGAGATTCAGGGCAGGATCC
ESTC95	32		---	GCACGTTCTTGTTCTCTCTCCAGAAGTTGNAGACGTCTATTTAGTTTGATTATCTGTCG
DWU-100	127	C T	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATTCA GTGGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCCTTGACTGTTCTCCA[C/T]GCCAG ATTCTTATCAATGATCTTTCACCTAAGAAACAGCAAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGCGATTTTTCACAAAATCAAAGAAGAAGAAAGAAGAGGCTTAGCTG
DWU-177	77	A G	---	TTCCATCCTAGATATCTACTCAAAATAATTGAGACAAGTGTTCAAACAGAAAGAGACGCTTGTGCTGAA TGTTCATGGC[A/G]GCCCTATTCACAGTAGCCAAACGATGAAAACAACCCCAAGCTATATATTACCA GATGAAAGGATAAACAAAATGTGGTCCATCCATACACAATGGAGTATTACACAGCCATAAAAAGGAAT GAAGCAGTGATCCCTACTACACTGTGGAT
DWU-286	213	A C	---	CAAATACCTGGACTATCAACCTTGTTGCTTAATCCCTGCAGCATTCAAGGTTAATCCATCTAAGTGAC ATTTTGAAATTCCAGCGCGGTGCCACCCAATCATGCCCAGCTTCGTCATATGAATGAGATATACATTT ATGTCTGACCTTCCCTCAAGACTGATTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGGA[A/C]TGGGAAACCAGCCCTATCTGAGTCTTCGGCTCCCTCC

Clone	Pos.				Sequence
DWU-252	94	A	G	---	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGTGCTGACAAGGCACTTCATGTAAAGTGT CAGAAGGAGCTACAAAACCTACCCTCA[A/G]TGAGCAGCATGGTACTTGGCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTAAGCTTTCCTGTTGAATGACAAAGTATGTGGTTTTGTA AT
DWU-330	85	C	T	---	GAACATTCCTCTGCGAGCCACTTCACTACCAAATGAGCATTAGCTACTTTCAGAATTGAAGGAGAAAA TGCATTATGTGGACTGAA[C/T]CGACTTTTCTAAAGCTCTGAACACAAAGCTTTCTTCCTTTTGCAA CAAGACAAAGCAAAGCCACATTTTGCATTAGACAGATGACGGGCTGCTCGAAGAACAATGTCAGAAA CTCGATGAATGTGTTGTTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231	A	G	---	GAAAATGTTAATTGGGCAGGTGAAAAGGGTACAGATGTGCTGTAGCAGACCTTTGGTTTTAAAAGAG AAGCATCATTTCCCCAACAGGGCAACTGTGAGAAGGCCAGCTGAAGAGTAAAGGAAAAGGTCTGAGG ACTGAGCCTGTGGCTGCTGGAAAAAGGTGAATGTTGAGGGCCCTTCACTTCCATCACAAGAAAGTC ATTAGACGGTACCAATTCAGTGTCTGTTCCT[A/G][GCATCTATTTCCTCTGTGC.
DWU-1537b	89	A	G	---	CTCTTAACTTCAGTTCCCTCATCTATAAGAATAAGGGATTCAGTTGTGATCATGATCACATAGCTCAGGTAATC CAGGAGCCAGAAACCCAGGGAGC[A/G]TGGGGACCTGATCCACAGCTAGAGGATGGGGGACTCTGTAGCT ACAGCATTTCCTGAACACACAAGAAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52	C	T	---	CTCTTAACTTCAGTTCCCTCATCTATAAGAATAAAGGGATTCAGTTGTGATCA[C/T]ATAGCTCAGGTA ATCCAGGACCAGAAACCCAGGAGCATGGGGACCTGATCCACAGCTAGAGGATGGGGGACTCTGTAGCT ACAGCATTTCCTGAACACACAAGAAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196	C	G	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGAGCCCTCTCTCCCTGGGATTGAGTGGGGTC CCCAGCTCCACCCAGAGCCCCTGGGAATTCCAGGGTCACTGTTCCTTCCTGTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAGTGGGACTGTGAGGACATGGAGGCCCTCG[C/G]ACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCTCTGAGTCTTCCTC
ESTD-ADAa	184	G	A	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGAGCCCTCTCTCCCTGGGATTGAGTGGGGTC CCCAGCTCCACCCAGAGCCCCTGGGAATTCCAGGGTCACTGTTCCTTCCTGTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAGTGGGACTGTGAGGACATGGAGGCCCTC[G/A]GCACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCTCTGAGTCTTCCTC
ESTD-ANT1	160	T	C	---	TCTCCTGTCATTCCTACTCCATTAGTTCAAGGTCAGTGAAGAACTGGGCAATTAACCAAGTAATTCA TGGACTGCCCAACTGGCAAACAAGAAAGGGCCCAGTGGAGCCAGGAGTATTATGCTACGCGGTTACCTT TTTTTATGGAGGACCGAACTGAGGC[T/C]GAGCTCAGATGATCCTGT
EST10398 2b	168	A	G	---	TGCCTGGGGTGGCCACCTCTTATCTGCAAACAAGAGGAGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTGATGATGTTCACATTGGGGCTGACTTTCCAACACGGAGGAAG CATTGTTTTTCTTCGGGGCCAAGAAGGTATCTACC[A/G][A]TAGTGTCTATTAGGCATTTG

Name	Pos				Sequence
EST10398 2a	147	C	T	---	TGCCTGGGGTGGCAAGGCTGCAAACAAGAGGAGCAACCCAGGAGGCTTTTATGAAGGGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTCACATTGGGGCTTGACTTCCAACACGGAGAAG CATTGTTTTCTT[C/T]GGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTTG
ESTD-C7	14	G	C	---	ATATCGTGGCCTTA[G/C]TTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-D4S95	90	T	C	---	CTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAATTTTGAGAAGAGCAAAACAACTTTCAAGG ATAATGGGCAATCACTTTCTT[T/C]CTTCTTTAGAGTCTACCGG
ESTD-GPPK2L	38	G	A	---	AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTCACC[G/A]CCGAGAACTGCTCGATATC
ESTD-HRASb	82	A	G	---	CTGGGCTCGCCCCGCCAGCAGCTGCTGGCCACCTGGACGGCGCGCCCAGGCTCCACCTCTATAGTGGGGTCG TATTCGTCCACAAA[A/G]TGCATCTGGATCAGCT
ESTD-HRASa	37	C	T	---	CTGGGCTCGCCCCGCCAGCAGCTGCTGGCCACCTGGACGG[C/T]GGGCCGCCCAGGCTCCACCTCTATAGTGGGG TCGTATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD-NRAMP	81	A	G	---	GGAGGCAGGAGGTGGGGAGGGGGTCTGTCTGCTCCAGGTCCCACAGACCAGAGAAGCGGCCTCAGTG TATCCCCACCCCCA[A/G]TGTGGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18	A	G	---	GTGACCTTCTCACTTTAA[A/G]AAACTTTACCGGAGAAGAAATTAAATATATGCTATCAGC AGATCTGAAAATTTAGGATAAAACAGAAAGGAGAGGTATGTAACA
EST36751 7	36	C	T	---	CCAAGTCGTTCAATTTTAGCTTTGCAGGTTTAACT[C/T]GATTACTTTTCTATTCAAATCTCTGTA AAATTGAAATATGAACTTAGTTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	109	A	G	---	CACGTGGAAAGGAGCTATTTTTGGAGGGCTTTAAGAGTAAAGAATCTGTCCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTTCACTGGATGCATTAATAACAAAAT[A/G]TTTACCTTTTGAAAAAATAA ATGAAAGGATTTGACCTGCTGCTCTGGAAAGAGTATCCGTACCGTCCTGAGCGTTTTGAAACAATACA GATGCCTTCCCTTGTAGCAGTTTCAGCCTCCTCCTA
EST18288 3	121	C	T	---	GCTCTCTATACCCCTGTGGTCCTCCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTCATGCAGCTGTGACAGGATGGAAGACTGGCTGCTCCTGA[C/T]GGGAGCCAGT GTGGAGCAGCACCCTGCCTTCAACACCTACGTCCACTTCCAAGGTAAGGCAAACCTCTCTGCTGGCTC TGGCCCCTAGGACTTAGTATCC
ESTD-AK-168	31	C	T	---	GGGAGTGACAGCTAGAGCACCAAGGGGGGCT[C/T]TACAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATTCTGG
ESTD-ALB	180	A	G	---	AATCCCAGCACTTTAGGAGGCTGAGGCAGGCAGGCATATCACCAGAGGTCAGGAGTTTGAGACCAGTCTGA CCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGGTGCATGCCTGT AATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCG[A/G]AGGTTGTGGTGAGCCGA GATGGCGCCATTGCACTCCAGCCTGGGCAACAAGAGTAAAACTCTGTCTTC

ID	Pos	Allele	Sequence
EST70523 3	182	G T	TTCCCGCCAGCGCCCCATCCTTGGCACCCTGGTCCCCTCAGGGGGCCACCCGCGGCACTCACGCGCTCT CGCTCTCGGTAACATCCGGCCGGGGGCCGGCGGTCCTTGAGCACACATAGCCTGGACCGTTCCGTATAGGAGG ACCGTGTAGGCCTTCCTGTCCCGGCCCTTGCCAGGGCCAGCCCT[G/T]CAGAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCCACGTG
ESTD-APOA2	101	C T	CCAGGTGTTGTTGGCACGTGCCTGTAATCCCAGCTACTCGGGAGACTACTGAGGCATGAGAATCTTTTGAAC CGGGGAGGCCGGAGGTTGCAGTGAGCTGAGATCATCG[C/T]GCCACTGCACTCCAGCCTGGGTGACAGAGC AAGACTCC
EST58707 7	112	C T	CAGTGTATCTGGAAAGCCTACAGGACACCAAAATAAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTCAGCACATCTTTGGCTCACATGAAGGCCAAATTCCGAGAGAC[C/T]CTAGAAGATACACGAGAC CGAATGTATCAAATGGACATTCAGCAGGAACTTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATA GCACACTTGTCACCTACACATTTCTGATTGGTGGACTCTTGCTCTGCTAAGAACCTT
EST74167 6	137	C	AGACCATGAAGGAGTTGAAGGCCTACAAATCGGAAACTGGAGGAACAACTGACCCCGGTGGCGGAGG AGACGCGGCCACGGCGTGTCCAAGGAGCTGCAGGGGCGCAGGGGGCGGGACATGGAGGA CGTGCGCGGCGGCCGCTGGTGCAGTACCGGCGGGAGGTGCAGGTGCTCGGCCGCAGGCACCGAGGAGC TGCGGGGTGCGCCTCGCCCTCCCACCTGCGCAAGCTGCGTAAGCGGCTCTC
EST43211 8	132	C	CGCCTGGTCGCAGTACCGCGGCGGGGCGGAGGTGCAGGCCATGCTCGGCCAGGAGCACCGAGGACTGCGCGGGGTGCG CCTCGCCTCCCACCTGCGCAAGCTGCGTAAGCGGCTCTCCCGGGATGCCGATGACCTGCGAAGCGGCC TGGCAGTGTACCAGGCGGCGGGGCGGGGCGGGCCTCAGCGCGCCTCCAGCCGCCCATCCCGCGGAGCGCCCTG GGGCCCCTGGTGGAACAGGGCCCGCGCGTGCGGGGGCTC
ESTD-ARSB	126	A	GGAAGAAAATGGAGCCTGTGGGAAGGAGGCGTCCGAGGGGTGGGCTTTGTGGCAAGCCCCTTGCTGA AGCAGAAGGGCGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAAACCATCAGTGAA GGAAGCCCCATCCCCCAGAATTGAGCTGCTGCATAATAATTGACCCAAAC
EST36770 4	144	C	TGTAGCCAAAGTCACCTGCATCATCATTTGGCTGCTGCCAGTTTGCCAGCTATAATCC ATCGAAATGTATTTTCATTGAGAAACACCAATAATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCCTCCCGATAGGGCTGGGCCTGACCAAAAAATATACTGGGTTTCCTGTTTCCTTTTCTGATCAT TCTTACAAGTTATATCTTATTGGAAGGCCCTAAAGAAGAGGCTTATG
EST26021 1	137	A	TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTGAGGTTGAGTGACATGTTCGAAACCTGT CCATAAAGTAATTTGTGAAGAAGAAGGAGCAAGAGAACATTCCTCTGCAGCACTTCACTACCAAATGA GCATTAGCTACTTTTCAGAATTGAAAGGAGGAAAATGCATTATGTGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTTCCTTTTGCAACAAGACAAAGCAAAGCC
ESTD-BA511	29	A G	GGGCAACATAGTGAAACCCCATCTCTACA[A/G]AAAATACAAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTGTAGTCCCAGCTACTTGGGAGGCTGAGGCTGAGGTGGGAGGATCCCTTGAAGTGGGAGGCTGGGGAGGTGGAGGCTG CAGTGAGCCGAGATGGTGCCACTGCA

ID	Pos				Sequence
ESTD-BCL2	116	A	G	---	AGCTGGATTATAACTCCTCTCTTCTTCTCTCGGGGGCCGTGGGGGTGGGGAGCTGGGGGTGGGGAGGAGGGTGCCGTTGGCCCCCGGTTGCTTTCCTGCTGGGAAGGATGGCGCACGCTGGGAGAAC[A/G]GGGTACGACAACCGGGAGATAGTGATGAAGTACATCCATTATAAGCTGTCGCAGAGAGGGCTACGAGTGGGATGCGGGGAGATGTGGGGCGGCCCGCGCACCCGGGGGCGCCCCCGCACCGGGGCATCTTCTCCCCA
ESTD-BCR	69	C	T	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGACCCGGAGACTCATCATCTGCGCAAGAGA[C/T]CAAAGAGGTCAGCTTCTGTTCCCGGGAAAGGGAGGCAGGTGACAAGCTAACTCTGCTTCAAAATCAACCATCCGGTGGACACTGTTGGTGGCTGCCATCTGCCTGCGCACA
ESTD-BRCA1aa	119	C	T	---	AAGAGAGAGAAACTAGAAACAGTTAAAGTTGTCTAATAATGCTGAAGACCCCAAAGATCTCATGTTAAGTGGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCA[C/T]GGTACCTGGTACTGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAAATAAAT
ESTD-BRCA1bb	139	A	G	---	ACTAAATGTAAGAAAAATCTGCTAGAGAGGAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAATGTTTTTAAAG[A/G]AGCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTACTACTAATGAAGTGGGCTCCAGTATTAATGAAA
ESTD-BRCA1cc	126	A	G	---	ATGCATCTCAGGTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAAAATAAAGGAAGATACTAGTTTTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTTAGCAAAAGCGTCCAGA[A/G]AGGAGAGCTTAGCAGGAGTCCTAGCGCCCTTTCACCCATACACATTGGCTCAGGGTTACCGAAGAGGGGCCAGAAATTAGAGTCCTCAGAAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
EST512120	122	A	C	---	ATCCTGAGCTCGCCAATAAGCTTCTTGGTTCTACTTCTCTTCTCCACAAGCCCCCAATTTCACTTTCTCAGAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTGTGCTCCCCACTCAATACA[A/C]AAAGGCCCCTCTCTACATCT
ESTD-C1R	40	A	G	---	ACACAGGTGCTGGCCACTGGGGCTGGGGATCCTCCTCTCCCCT[A/G]ATTTGCTCCGGGAAGCACATTCATCAA
ESTD-C1R	40	A	G	---	ACACAGGTGCTGGCCACTGGGGCTGGGGATCCTCCTCTCCCCT[A/G]ATTTGCTCCGGGAAGCACATTCATCAA
ESTD-C6	31	A	C	---	CCCAGTCAGTTGGGGGACAGCCATGCACTG[A/C]GCCTCTGGTAGCCTTTCAACCATGCATTCCATCTAAGCTCTGCAAAAT
EST201182	119	C		---	GTTCCGAATCCTCCTCCTGAAAGTGGCGCGGGTTTAATCTGCTCATGACGCTGCGGGCTGTGGTGTCAGCTGAGGTGAGGGGCCTTGAAGCTGGGGAGTGGGGGTTTAGGGAGTGGGGGTTAGGGACGCGCGGGGTCTCTGCGTGCATCCTAAGCTCTGAGAGCAAACCTCCCCTTGAAGCTGGGGGTTGGGGGGTTAGGGACGCGGGGGTCTCTGCGTGCATCCTGTGCATCCTAAGCTCTGAGA
EST530186	67	A	G	---	ACAATCCAGGTCACACATTCCAGAAGAGGAGGGGGTGGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA[A/G]GGGATTCAGGAAGGACCACGAGGATCGAAGTTAGTGAAGTC

				Sequence
ESTD-CB22	119	C	T	GGCAAGTTTTATTGATAGAGAGGAAATCAAATAATGGCAATGAGGAGGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGGATGGACAGACAATGGCAGTGCCAACCCATAGGG[C/T]GGATACAAAAG ACAGGCAAGGAAGGGGTAGAAACCATCAAAGAGGAATAGGCTGGTGACCCCAAAGCAAGGAGGACCT AGTAACATAATTGTGCTTCATTACATATGGTCCTTTCTCTCTCACACAC
ESTD-CB23	136	C		TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCCTTTCTCTCTCACACATACAGAGAGCCCCTCACCAGGACCCAGACAGCT CTCAGAGCAACCCTAGCCCATTACCTCTTCCCTTTCCAGAGGACCTGAAAAACGTGTTCCCACCCGA GGTCGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCCACACCCAAAA
ESTD-CB24	145	A		ACCAGGACCAGACAGCTCTCAGAGCAACCCTAGCCCATTACCTCTTCCCTTTCCAGAGGACCTGAA AAACGTGTTCCCACCCGAGGTCGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCCACACCCAAAAG GCCACACTGGTATGCCTGGCCACAGGCTTCTACCCCGACCACGCCCGCACCCCTCAAGGAG GAAGGAGGTGCACAGTGGGGTCAGCACAGACCCCGCAGCCCCTCAAGGAG
ESTD-CB25	146	A	G	GTTTCTTTCAGACTGTGGCTTCACCTCCGGTAAGTGAGTCTCTCCTTTTCTCTCTATCTTTCGCCGTC TCTGCTCTCGAACCAGGGCATGAGAATCCACGGACACAGGGCGTGAGGAGGCCAGAGCCACCTG TGCACAGGT[A/G]CCTACACTGCTCTGTTCTTGTCAACAGAGTCTTACCAGCAGAAGGGGGTCCTGTCTGCC ACCATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGTATGCCGTG
ESTD-CB27	125	C	T	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGGCCTGGTTGCATTTCAGGAGGTGTCTGTGGAGTTCTGCTCATCACTGAC[C/T]TATCTTC TGATTTAGGGAAAGCAGCATTCCCTTGGACATCTGAAGTGACAGCCCTCTTTCTCTCCACCCAATGCT GCTTTCTCCGTTCATCCTGATGGAAGTCCTCAAAACACCATTTCCATACC
ESTD-D4S338	59	A	T	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGA[A/T]ATGTA TTCTTAAACAATAAACTTGAAAGTCCAAAATTACTCCTTGATCCATGGACTGCAGAATAAATGTTA TTTTAGCTGTCAGAAAAACAATACTAATATTTTGCATATGTTCATCAGAGCCCTTGGGTGACCAGGTGTA TTGCCAATAAGCAGTAATATTTTGAGAGGAATCTTGTTTCAATGCAGTAG
ESTD-CYP2D6	61	A	G	CAGGCCAGCGTGGTCGAGGTGGTCACCATCCCGGCAGAGAACAGGTCAGCCACCACTATGC[A/G]CA GGTTCTCATCATTGAAGCTGCTCTCAGGGTTCCCCTTGGCCTGAGCAGGGGCCGAGAGCATACTCGG
ESTD-D11S1873	40	A	C	AAAAAAACATTTAACACCTTTCAATCATATACACCATA[A/C]ATTTCCATTTTCACATAAGTCA GTTGAGCTGAGTTTTCCAATTACTTGCAATCTAAAATGTCATAAACTGATTAATGCAAGTTCAACAG ACAACTTTCCCAAGCATCTACGATCCAGAAAGGTCAAAATTATTACATATCTGGATTAAATTATGCCCA TATCTGCATGTC
ESTD-D17S33b	169	C	T	CATCCCCAAGCCCATCCTCTTAGCCACCTGGCATTTTTTGGCCGCCTCTGACAGATCACTCAGGGCGT CATGCTGCACACATCCAGGGGGGCGCCCTACCCTTTGTAGTCCATGGAAAGGCTCCTCTGGGGCGGGTG GGGTTGTGTGGGCTATGTGGTCTTGTGTAGA[C/T]GGGGGCTTTGGTTTCAGTTGCACTATTGCGTT ATTGCAGATTGCTTTGTCTTTGTCTTTCCACCTGAGCGAGCCTC

ESTD-D17S33a	75	C T	CATCCCCAAGCCCATCCTCTTAGCCACTGGCATTTTTGCCGCCTCTGACACAGATACACTCAGGGCCGT CATGCTG[C/T]ACACATCCAGGGGCGCCCTACCCTTGTAGTCCATGGAAGGCTCCTCTGGGGCG GTGGGGTTGTGTGGCTATGGTGGTCTGTGTGTAGACGGGGCTTTGGTTCAGTTGCACTATTGCGTT ATTGCAGATTGCTTTGTCTTTGTCTTCCACCTGAGCGAGCCTC
ESTD-D18S8	133	A G	TTTGAGACCACCCTGGCCAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGGTACATGCCTATCGTAATCCCAGCTACATCGGGAGGCTGAGGCAGGAGAATTGCTTGAACCC[A /G]GGGAGGCAGAGCTTGCAGTGAGCCAAGATCACACCACTGCACTTACAGCCTGGGTGACACAGTGGA GACTCTGTCTCAA
ESTD-D3S11	44	G A	AACTGATTAGAACCTGAAAAATACATATTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTTGCATCATTAAAAAATCCAATAAAGTACACTGTAATAAAGAAATTAACAGAATATCATTGT TTATTCAAACTACTATTTATCACTTATTTATTGGTAAGCCATACTAAATTCTAAAGCATGTTTCTGAAAG TTTA
ESTD-D3S12	37	A G	AGGTTCCACATTATTGCTGATGTTTGCTGATGTTTCC[A/G]GGAGCCTTGATGTCATTCTGTATCTCCT CAGGTATCCCACCTTGAGACGTACTTTCAAAAACTCTCTACAGCCGGTGTGTTGTTATTAATTCAAGGT TGAACATAAAGTA
ESTD-D3S2b	247	C T	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTCCTGC TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAGTGAAACATACTGCTCCTAGAAGCCAGAGTCATACTGGATGTTCGTTCGGTCTTCACGATGG CAGGTATGAAATAAATAATATCGTCCTTTATTTGGAAGGATGC[C/T]GGT
ESTD-D3S2a	248	G	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTCCTGC TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAGTGAAACATACTGCTCCTAGAAGCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCGTCCTTTATTTGGAAGGATGCCGGTATGT
ESTD-D7S399	83	A G	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTAGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCC[A/G]GTCTCCTACATCCTTTCACAAACATTTCATCCATGGACTCCATAC TAGAATATTTTGAAGAAACAAAACATGACAAACATTTTC
ESTD-DMb	146	A C	GTGGGGGACACCGAGGGCTCCAGGCTGGCGCTTGCACGTGCTGGCTCAAGCAGCTGCTCGGCCTCCACT TCCATGGGTGTGGGGCCTGGGACCTCACTGTCCCTGGGGAGGAGGGGAGTGGGGAGGGGAGGAGACA GAATGCTGATT[A/C]TCTGGTGGAGAACCAGAACTTCTGGCCTGTTCTGGCCTGTGCTTCCAAG ACCTCCTGATTTGAGGAGAGGGGAGCAGCAGCGAAGAGAACAGAGT
ESTD-DMa	66	C G	GTGGGGGACACCGAGGGCTCCAGGCTGGGCGCTTGCACGTGCTGCTCAAGCAGCTGCTCGGCCTCCA[C/ G]TTCCATGGGTGTGGGGCCTGGGACCTCACTGTCCCTGGGGAGGAGGGGAGTGGGGAGGGGAGGAGGAGA CAGAATGCTGATTATCTGGTGGAGAACCAGAACTTCTGGCCTGTTCTGGCCTGTGGGTAGGGGCAGCTGCTTCCAAGA CCTCCTGATTTGAGGATTTGAGGAGGGGGAGCAGCAGCGAAGAGAACAGAGT

Gene	Pos	A1	A2	Sequence
ESTD-DRD1	154	C	T	TCCCAGCCTATCGGTCATCATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACCATCAC ACAAAACGGTCAGCACCCAACCTGAACCTGCCACACATGCCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGG[C/T]TCGCTATTAAGAAACTAAGGTAC
ESTD-DRD2	144	C		TCTGCCTTTGGTGCGCAGGAGGCTGGGCGGGAGCCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCCACCCGAGAGGACCCGGTACAGCCCCATCCACCCAGCCACCACCAGCTGCTCTCCCCGACCCG TCCCACCACGGTCTCCACAGCACTCCCGACAGCCCGCCAAACCAGAGAAGAAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD-DRD3	109	C	T	AAGAGGATGGCCAGGATGAGCGCGCAGTAGGAGGGCATAGTAGGCATGTGGGCGGCGGCCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTCAGGTGGC[C/T]ACTCAGCTGGCTCAGAGATGCC ATAGCCCAGAGGGAGGTGCGTGATGCCAAGGGGCTTCCTGTGAGGAGA
ESTD-ERBB2	93	C	T	TCTTTCAGGATCCGCATCTGCGCCTGGTTGGGCATCGCTCCGCTAGGTGTCAGCGGCTCCACCAGCTGG GGTGAGGGGTGGTGGGTGCAGTGC[C/T]GGGGCGCCGGTGCGACCCCACGCGGGCGGGGGCGGGACTTCA CCCCGCCCTCACCTCCGTTTCCTGCAGCAGTCTCCGCATCGTGTACT
ESTD-ETS2	43	A	G	ACTCACAGTGCTCTTTAAGTGAAAATGGTCGAGAAAGAGGCACC[A/G]GGAAGCCGTCCTGGCGCCTG GCAGTCCGTGGGACGGGATGGTTCTGGCGTGTTTGCCTTTTGAGATTCTCAAAGGAGCAGCAGCATGTCGTGGACACA CACAGACTATTTTAGATTTTCTTTGCAACCAGAACAGCAAATGCAAAAACTCTTTGAG AGGGTAGGAGGGGTGGGAAGGAAACAACCATGTCATTTCAGAAGAAGTTAGTTTG
ESTD-F9	111	A	G	AGATCCTGATGATTTTTTTTCCTATTTTTTCTAAATGTTTACAGTTTGAAGTTTAGATTATGCCCA TGCTCCATTTGAGTAATATTTGTGTAAAGTATGATGTTTA[A/G]GTCAAACTTCATTTTTTTCC ATAGGTATGTCCAATTTATCCAGCACAATTGTTAAAACAAAAAC
EST687875	144	A		CTTCCTATGGGATTTGACTTTATTTTCTCCATTGTCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGCAGCTCATGACAATTTGAAGCTGACAATTACACAGAAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTGAAACATTGAAGTTGTTTTGAAACTTGGTGTCACCTTTAATTACAACCTAG CAGACGGAACTGAACTCAGGGTAAGAAT
ESTD-GCDH	200	C	G	CGCAGACCGGTCAGTGTGGGGTCGGGGAGTGTGGAGGGAAGGAGGGAGGAGGAACTGGGGGTTTAGGGACT TTCCGGGGGTGACTTTCCCGTTCTGCTGCGAGAGAAAAGGCGGGAGAAGACCACAGAGCCAACTGGCTAA GTGTAAGGGACCTCTGGTCGCACCGTGTGTTCTGCGCCCTGTTCAGCTGTCGTGCCGCAGT[C/G]
ESTD-GCK	88	A	G	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGCCCCTCTCAGGA[A/G]CACAGTAAGCCCTGGCAGGAGAATCCCCACCCACCTGGC TGGAGCAGGAAATGCGAGCGCGCGCCTAAGTGCGCGGTCCCAGGAAGCAGCGGCTAGGGATGTGAGAGACACAGTC ACCTGCCAGCCTAATTACTCAAAAGCTGTCCCCGAGGTCACAG

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EST34088 2	62 A T ---	GTGGGGGCAACAGTGGGAGAGAAGGGGCCCAGGGTATAAAAGGGGCCCACAAGAGAGACCGGCTC[A/T] AGGATCCCAAGGAGCCCAACTCCCGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAG
ESTD-GNAT2	56 A G ---	GACCCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCAC[A/G]GGCATCA TTGAAACCAAGTTTCCGTCAAAGACTTGAATTTCAGGTAAGTGCATGGTTCCCTAGG GGGCTAAAATTTCCGAGCAACTTGCATAGACTGTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGGAGAAGATGTGTTACAGTTTGTCAGAGAGAATAAAAAGGGATAACCTGGGGTTTTCTGTGC TTTGCTTCTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTTCAAAGAACGGTATACAGGGACAGCA
ESTD-HT2	154 G ---	AAGCGCCAGTCGTGAAGTTTTCAAACAAGACACACCTT AACACACAAGCCCCAGGCGAGAATTGAACTCGCGACCCCTGGTTACAGACCCAGTGCTCTAACCCCT GAGCTATGGAGCCCCTCGTCTGCTGGTTTTTCTTCGGTTTTTCATCTTATAGATTGATGTTTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTTAGCTTGAGTGAAATTCCAGGATATTCTCCTACAAAATGAAA ACATTTTCGTGCTCTGTAAATCCCTCGAAAAGGTTCT
ESTD-HT5	149 C ---	CTGAGAAACAATTGGCAAAATAAAGGAAATTTGGCACTCCCCACCCCCCTCTTCTTCTTCCCCTTGGA CTTTGAGTCAAATTGGCCTGGACTTGAGTCCCTGAACCAGCAAAGAGAAAAGAAGG[A/G]CCCCAGA AATCACAGGTGGGCACGTGCGCTCTACCGCCATCTCCCTTCACGGGAATTTTCAGGGTAAACT
EST37382 5	124 A G ---	ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGGTGC[C/T]CTGGGAGAAGAAGGAAGATG TTCCAGGGCACACATAGCTTAGTGGGAGACTC
ESTD-IGFBP1	43 C T ---	TTTACTATTTCAAATGGATACAGACAGAATTGTGGGAGTCACTACTATATTCCTATGAACAAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCTACATTGTGTGAGTGACGGGGCCAGTGGATCCGGAGAGTGTGGTGGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAAATACTTCACAAAATACTAATAAACGGAGTTGAATATAAAACCCA
ESTD-IGHV4-6	120 C ---	CAAAGTAAGCACCCAATAAATGTTAGCTATTACTATCATTATTATTATTATTTTTATTTTTTTTG AGATGGAGTCGGCTCTGTCGTCCCAGGCTGGAGTGC[A/G]CAATCTCGGCTCACTGCAAGCT CTGCCTCCTCGGGTTCATGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGAATACAGGCACCCGCC ACTGTTCCCGGCTAATTTTTGTATTTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1A	110 A G ---	CCACTTACAGATGGATAAAATGGGTACAATGAAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT
ESTD-IL1B	99 A G ---	GGGTCTCTACCTTGGGTGCTGTTCTCTGCCTC[A/G]GGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T ---	TCCAGGGTGGCTGGACCCCAGGCCCCAGGCTCTGCAGCAGGGAGGACGTGGCTCGGTCGTGAAGCATG TGGGGGTGAGCCAGGCGGCCCCAAGGCAGGGCCACCTGCCTTCAGCCGCCTTCAGCCGCCTTGGCC T[CCCAGATCACTGTCCTTCTGCCATGGCCTGTGGATGCGCCCTGCCGCCTGCTGGCC CTCTGGGGACCTGACCCAGCCCGCAGCCTTGTGAACCAACACCTGTGCG

ID	Pos	Allele 1	Allele 2		Sequence
EST45311 0	151	C	T	---	GCCCTCCTCTCTTCCAATTCTGTCCCTATAGTTTTCCTCTATTAAGTGAACTACACATGCATTCTTTTAGT GGATAGATGCACACAAACACACAGACCATTATGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAAAT[C/T]ACCTCTTTCATTTCATTTGTTGAAT GTACATACACATCTGTGTCATTGTTCATT
EST65258 8	80	A	G	---	TGCCCCATCACGCGGCCGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTTCC[A/G]CCCTCAAAATGACAGCCATGCCCGCCGGGTGCTTCTGGGGCGTCGTGCGGG GGGACAGCTCCACTCTGACTGGCACAGTCTTTGCATGGAAGACTTGAGGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTGCGTGTTTCCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	26	A	T	---	ATGCAGGATGAAGGTGGACAGGGAGG[A/T]GAGGGCCAACCTGTCATCCCAGGGCCTGCAGATGTCG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	149	G	T	---	ATACTAGTACAAGTGGTAATTTTTGTACATTACACTAAATTATTAGCATTGTTTTAGCATTACCTAA TTTTTTCCTGCTCCATGCAGACTGTTAGCTTTACCTTAAATGCTTATTTTAAAATGACAGTGGAAG TTTTTTTTTTCCTC[G/T]AAGTGCCAGTATTCCCAGAGTTTTGGTTTTTGAACTAGCAATGCCTGTGAA AAAGAAACTGAATACCTAAGATTTCTGTCTGTGGGGTTTTGGTGCATGCA
ESTD- KRT10b	183	C	T	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTGTTCAGTGTTACCTTTTGGCAATATT AAAGGAAGAAGAAAATGCATTTTAAAGTAAACTGCTAAGGTTTTTCCATTAAACCACTATTCTCTAAG AGAACTGTACATGACAAATATTGCCATTACACTATATAAGTTATAACCAGTATTGATA CTCTGCCCAGATACACATCTCCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133	A	G	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTGTTCAGTGTTACCTTTTGGCAATATT AAAGGAAGAAGAAAATGCATTTTAAAGTAAACTGCTAAGGTTTTTCCATTAAACCACTATTCTCTA[A/ G]GAGAACTGTACATGACAAATATTGCCATTCAACTATGTAGCTGCTTTTTAAATAGTC TCTGCCCAGATACACATCTCCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231	C	T	---	ACCCTCACCCCTCCCTTAGCCCCGTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGGCCTGACATGAGAACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAATGTTAAGTACAAAAGTGAGGCCCCATAG GCTGCCTATCTCTCCCGTCTCAGGTTTACCA[C/T]GTCAACATTGACACA
ESTD- KRT8a	21	C	T	---	ACCCTCACCCCTCCCTTAGCC[C/T]GTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGGCCTGACATGAGAACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAATGTTAAGTACAAAAGTGAGGCCCCATA GGCTGCCTATCTCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
EST75099 6	82	C	T	---	CACTTGTGTGTCTAGATCGTCTCTCAGTGCGCCTCTACTGGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAA[C/T]GGGGGCAACCGGAAGACCATCTTGGAGGATGAAAGAGAGGCTGGCCCACC CCTTCTCCTTGGCCGTCTTGAGGTGTGG

Name	Pos			Sequence
ESTD-LF79	142	A	G	GGGTGATTTGAGGCTCAGTTAATATTTCAAAAATTGTAACCGTAGCAAAACTGCATTGGTATTAGA AAAATAAAAAATTTCCAATATGTAGTGCTGTGTTATACCTGCCTCCTGCCATGCAGCATCATAGCCTGT GGGAACC[A/G]GGAGGGCTTCCCTTACCACCCAGA
EST35879 9	142	A	C	GAGATCGGTGTGTGAGTTATTAGGCATGGTACCTGTGATTCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGGCTGTACCCAATTAGGTGAACATGGCTTCGAG AGAGTTG[A/C]ACAGATTCCTGGAAGACAGCAGCGGGATGGGGGCAGGAGGAGAAGAGCTGCCTGGATGA A
ESTD-LMP2	35	C	G	TACACACTTTCCTTACCCATTCACTGAAAACGACT[C/G]GCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCCAAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	113	C	T	TGTCAGTGTCCCCTAGGGGCACCTCACCACTCCCAGCTTCTTCAGCTCTGGCCTGTCCTGCTGCCTGCA AGGGTTTGCTTAATTCTCAATTCAATGTCTCTTCATCTTTAG[C/T]AGCTGTGGGGTTTTGTTGTTG TTCTTCTGTTTTTGCTTAGTATCTGACTACTTTTAATTATAAAAAGAGATGTATCTAAACAAAATAG AGATTGTTATCAGAAGTTCACAACATTTATTAAAAATTTTTCACCTG
ESTD-MCC	45	C	T	TTGTCAGGAGTGTGCTGATGCTGCCTCCCCAGCTCTGTCCCCAGC[C/T]GAACTTCAGGACAACGTGC AG
ESTD-METH	118	C	T	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGTCTTCCAAGGGTTTGGTCTAAGTTGCTGAATTACC[C/T]TGGATTTTCTGACG ATCTTTCAACTGCTAGAGCATCTGGTTCCTGTTTAGCATGG
ESTD-NF1	25	A	G	ATTATCCAGATGAATTTACAAAACT[A/G]TACCAGATCCCACACTGATATGGCTGGT
ESTD-NFKB1	107	A	G	AACAATGGACTTGTATATTTGTACAAAAAAAAGTTTATTTTTCTAAAAAAAGAAAGAAGAAA AAATTTAAAGGGTACTTATATCCACACTGCCACTGCCT[A/G]GCCCAAAACGTCTTATTGTGGT AGGATCAGCCCCTCATTTGCTTTTGTGAACTTTTGTAGGGGACGAGAAGAATCATTGAAATTCT GAGAAAACTTCTTTAAACCTCACCTTTGTGGGGTTTTGGAGAAGGTATCA
ESTD-NPPA	45	A	G	TGTCCCTAGGCCCAGCCCTGCTTGTCCCCCTGGCTTATCTTC[A/G]GTACTGCAAAGAGAACACA GACAT
ESTD-NRAS	202	C	T	GTGTTTTCTTAATCTTTCTCCAGGAACACAGTGACCATATTCTTTCTGCGAGGCATATAGAATTTGGT GGGTTTTCTTTTTATGTGATGGGTGATATTGGATACTTTGTTGTGATTATATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTTAGATGCTTATTTAACCTTGGCAATAGCATTG[C/T]ATTCCCTGTGTGTTTTTTAATAAAAT
ESTD-PAI1	100	A	G	GCCACCACCACCCCACCCCAGCACACCTCCAACCTCAGCCAGACAAGGTTGTTGACACAAGAGAGCCC TCAGGGCCACAGAGAGTCTGGACACGTGGGG[A/G]GTCAGCCGTGTATCATCGGAGGCGGCGGGG CACATGGCAGGGATGAGGGAAAGACCAAGAGTCCCTGCTGTGGGCCCAAGTCCTGTAGACAGACAAAACC TAGACAATCACGTGGCTGGCT

ESTD-PAR	120	A	--	CTCTTCAGGAACCACCAGTCTTCTTACCAAACACGACTTATTGCTGTCGTCCGAGAGAGGTACAACCGTGAGA ACTTCTTCCTAACTGTAATTAGTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTCATTAGCTCTGTGAGTGTTTCTTCACTTCTGTGTTCTAGAACGTTTTCTAG GACTGGCAGTTAAGCTTCACTTAGCCTTTCTGTGTATACCCATGCCC
ESTD-Per/RDS	74	A G	--	ACCTACAGACGTCGCTGGATGGTGTGTCCAACCCGAGGAATCTGAGAGCGAGAGGCAGGGGCTGGCTG CTGGAGA[A/G]GAGCGTGCCGGAGACCTGGAAGGCCT
EST68308 5	29	C T	--	GGAAAGAGAGATTTAAGAGAGCTTGAAATTTGGA[C/T]AATTCTGGTTCTTTGAGTGTGGAAGAGTTCATGTC TCTGCCTGAGTTACAACACAGAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT GGAGAAGTAGACTTTAAAGGTAAGAAAGTAGTTATTTTTA
EST54045 6	39	A G	--	GGAATATTAAAAATATTTTAAAATACCTCCATTTGCTT[A/G]TCCTTTAGTGAAGATGAATACCTGC AAAGACATGGCTAAAGTTATGATTGTGGCAATTTGTTTTCTACAAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTGTTTGCCTTGGAATTGGATTTTTAATGTTGACTTTATCAT
ESTD-PXMP1	88	A G	--	ATGAAACATGGTTCTTTAATTTATGATATGTTGTTATAGCTATCTTAAAAGGGGCTTCTTTTTTA ATGCAGAAAGAGAGGGGAAAAA[A/G]GAGCGAGCTGTGGTGGAAGAGGTGTTTTTCTCAAGGCTCATAC AGATTCTGAAAATCATGGTCCCTAGAACATTTGTAAAGAGGTAAGTCTTATGAAATTATAATCTT
ESTD-RDS	127	A	--	CCCGAGGAATCTGAGAGCGAGAGGCGTGCTGGCTGGGGCTGGCAAGAAAGAGCGTGCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAAGCTGGCAAGGGCAACCAGGTGGAAGGCGCGCAACGCGCAGG CCAGGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCCTCCCCGAACACTGAGAAATAGTGCACT CCAAGAAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD-s14544	94	G T	--	TTGGGAAGTTAGAGCCTATATTAAAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTC[G/T]TCTGTGTGGGTTAGATGCAGGATTTATATGATCCGTTA ACCTCT
EST52908 0	45	A C	--	ATCACAGGTCTCTGGTCTCTGGCCATCATTCCTGGGAGAGATGG[A/C]TGGTGGTCTGCAAGCCCTT TGGCAATGTGAGATTTGATG
EST19590	55	C T	--	AGGAGAAGCTGAGGAGGGGGAAGAGAGAGACAAGAGAATGACATTGATGAGTGAAGATGT[C/T]GGCTCAG GATGCCGGAAAATGAC
EST76136	39	C T	--	TGAAGCTTCTGCCCAGCTTGCATTGTTTCTAGGAGAACC[C/T]GCGTCATACCTTTATCTATAGCCTT CCCCTAGGTCTT
ESTD-SPTB	176	C T	--	TGAAACACCCTGTGGTCCGGAGCCAGGTTGTGTTTCTCCTGGGAGCCTGAGGAGTTTGTTGTCGTGTGTG CAGTCCCCCGCGCCACCTGCTGGTTGAGCCTGGACATACACCTTCACCTCCTTGGCCCGGAGAAGAC ATTTACCCACCTGGCCATGTCCCTGGCCGTGTTGTGCACA[C/T]CCTCTGTGAAGACCCCAACCCCTGC CTCCCCCCACCCAGCCAAGCCAGTTTCCTAGCAAGGGCAGGAC

Name	Pos.			Sequence
ESTD-TAT	224	C		AAATGGTCAGGACCCTGATCCACAAGAAGTGGTACCATTTCATCAGGGCCCATCAGTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATCATCTTAAAATGACTTGTGGGACAGGATCA ATTTCCTCTCACCTAGAAACGTTTGTTTACAACTTTCTTCCCAGTATGGATGGGATTATGATGGGGGG GAGAAGCAAATTTAAATAGGACCCATGAGACACATCA
ESTD-THRB	125	A	C	TGCGGCCTTTCCTCCGGCAGGGTAGACTTCTTACTTGGCTGTTGATTTCCAAGAGAGAAAGAGTCCAAG CACACGAAAAACAGAAGTTGCAGATCCCATGAGATCTCAAATCACACAGGATC[A/C]CTTCAT CCCACACTGGATTGGCCCAAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCCCTGTAGATGGG
ESTD-TYR	122	G	T	TAGTGAAGTTTTCATCTCCTGTCAGCTTCTGGGATTTCTTGTTCCCACCGCAACAAGAAGAGAGTCTATGC CAAGGCAGAAAAGCTGGTGCTCATGGGCAAAATCAATGTCTCTCCAGATTTCA[G/T]ATCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCATAAATATTGATGTCGTTAAA CATGGGTGTTGATCCATTTTCATTTGGCCATAGGTCCCTATGGGGATGACA
ESTD-TYRP1	222	A	C	AGTAGTGGATGAAGCTAACCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTATTAACTGTATTTCTTCACTTATTATTACCTTCTTTCT AATACAAGCACATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD-TYRP1	222	A	C	AGTAGTGGATGAAGCTAACCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTATTAACTGTATTTCTTCACTTATTATTACCTTCTTTCT AATACAAGCACATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD-VB12	148	C	T	TTCCCAAGGCCTCAATACAAGTCTTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD-VB12b	148	C	T	TTCCCAAGGCCTCAATACAAGTCTTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD-VB12a	74	A	G	TTCCCAAGGCCTCAATACAAGTCTTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACAC[A/G]TGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTCACAGAGACAGGAACACCA GTGACTCTGAGATGTCACCAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT

Name	Pos.	Allele	Allele		Sequence
EST58607 0	105	A	G	---	CTCTGGATGGGTTCACAGGTGGCAGGCACAAGCCAGTCCATCCTCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCCTCCACTGGAGAACAAGGACAGCCAC[A/G]TGGGCGCGGGATGGCCGGCGGGGAGTTC TGGTTGCGGCCACGGCTGTGGCCTCGTTGTGAACGGTAGCCTTGCGGTTGCGATGCCTAAACCTTTGT TTCTTGGCCAAGGAGGGGCGGGGTGCCATGCCTGAGATGTGAGATGCGGCC
ESTD-VWF	36	G		---	AGGTAGGAAAGCAAAGAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCCTTTGG TCCCCTAGAGTCTG
EST71770 6	189	C	G	---	AGCACCACCTCTCAGCCTCAAGCCTCAGCCACCAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGAGTTATTTTATTCCTGAAGTCCGGATCTCATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAAGAGAAAACCACTGCAGAGTACCAG[C/G]TGTTGGTGGGA AGGAGTGCCCAGTCCCAGGGTGACACTGGACAGAGAAGAGGCCATCCAAGG
ESTD-TNFAb	152	A	G	---	TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGGTTCAGCCTCCAGGGTCCTCACACAAATCAGTCAGTG GCCCAGAAGACCCCCTC[A/G]GAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTGATG CTTGTGTGTCCCCAACTTTCCAAATCCCCGCCCCGCGATGG
ESTD-TNFAa	88	A		---	TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGGTTCAGCCTCCAGGGTCCTCACACAAATCAGTCAGTG GCCCAGAAGACCCCCTCAGAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCCCAACTTTCCAAATCCCCGCCCCGCGATGG
EST52418 6	113	A	G	---	CAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCAGTCACCCTTTGGCTACAAGATGTCG GGGAGTGGCCGGGAGTTGGGCGGAGTACGGGCTGCAGGCATACACT[A/G]AAGTGAAAACTGTGAGTG TGG
EST13586 3	89	A	G	---	CCCACTCTATTGCCCAGCCCAGGGACAGAGCTGATCCTTGAACTCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC[A/G]GGGCTGGCTTATCAGCCTCCCAGACCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCCTGCGCCTGCC CCGGTCACTC
EST51976 7	123	A	T	---	AGGCAGAAACTGGGCCCCCATGCGGGGGACGTGGAAGGCCACTTGAGCTTCCTGGAGAAGGACCTGA GGGACAAGGTCAACTCCTTCTTCAGGCACCTTCAAGGAGGAAAGAGAGCCAGGACAAG[A/T]CTCTCTC CCTCCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGGTGCAGATGCTG GCCCCTTTGGGAGAGCTGAGCTGCCCCTGGTGC
EST11458 6	140	A	G	---	CCACTTTGGTAGTGCCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCTGCTCATCTTGTTCTGCAGTTTT CTCTGCCATGTTGCTATTGCCAGGACGGACCTGTCCCAAGCCAGTGATTACCATTTTCCACAGTGGT CCC[A/G]TTAAAAACATTCTATGAGCCAGGAGAGAGATTACGTATTCCTGCAAGCCGGCCTATGTG TCCGGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

Name	Pos	A1	A2		Sequence
ESTD-AT3aa	60	C	T	---	AGACCTCAGTTCCTCTTCTGTGTAAAAGGGAAGTTTGTTGTTCTTGGATCTCCATGGGCCCAGC[C/T]AGCA CTGGTGCCCTGTGAGTCTGTATCAGGTAGAGGAGGATGGGACCAGGTGGAGGAATTTGAAAGGGCA TTGGAATTCAGAGAGACAGACAGATATTAAGAGCTGGGGAAATGTGG
EST398528	106	C	G	---	CGGTCTTCCTTCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCCACTCTCTTA[C/G]GGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAAAGGCCTGTTCCAGTGTTAAGGCATGCAAAAGGCCTCCACAGGCTGCTAT AATACAGCCCT
EST624480	112	A	G	---	ACCTGGTGTGCTGGTGGTGGGTGAACCTGGTCCTCTTGGCATTGCCGGCCCTCCTGGGGCCCGTGG TCCTCCTGGTGCTGTGGGTAGTCCTGGAGTCAACGGTGCTCCT[A/G]GTGAAGCTGGTCGTGATGGCA ACCCTGGGAACGATGGTCCCCAGGTGCGCGATGGTCAACCCGGACACAGGGAGAGGCGCGGTTACCC TGGCAATAT
EST360272	120	A	C	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGGCCGCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACACAGCATTGCATACATGATGAGGAGACTGG[A/C]AACCTGAAAA AGGCTGTCATTCTACAGGGCTCTAATGATGTTGAACTTGTTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTTGTAGATGGCTGCTCTAAAAAGACAAAATGAATGGGGAAAGACAA
ESTD-COL2A1cc	112	A	G	---	AGAATGTATATAGTCCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTCGTGCTATTTATGCTCTCTTTCTGTCCACTTTC[A/G]GGGTGTTCAAGGTGGAAAA GGTGAACAGGGTCCCGCTGGTCCTCCAGGTGTAAATCACCATACCGTACCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD-COL2A1dd	97	C	T	---	TGAGAGAACACCTAGTCCTCCATCCTCCTCTCTCTCAATGGCAAGAAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGCTGGGACCTGGAACA[C/T]TTGGACTTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAATGGCAAAGATATACAATCAATTTTATTTGACCAAACACTATCATGGAACA GCATT
ESTD-CPT2	150	A	G	---	GCCGCAATGCCCGGGGAGTTTCTCCAATGTGTGGAGAAGGCCTTAGAGAGACATGTTTGATGCCTTAGAA GGCAAATCCATCAAAAGTTAACTTCTGGGCAGCAGAATGAAAAGCTACCATCACTTCCTCATCATGAAAAC TGGGAGGCCGGCGGCCAT[A/G]GTGCTCATGCCTGTAATCCAGCCATTTTGAGAGGCTGAGGGGTGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACAT
EST122740	135	A	G	---	CCCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGTAT TACATAAAGTAAGTCAAGTGGTTTACTCCTCATGACCAAATATTCTTCCCTCCTTAGGATGAGGTG[A/G]TAGTAAATGACCGATGGGGTCAGAACTGTTCCTGTCACCATGGAGGATACTATAACTGTGAAGA TAAATTCAAGCCACAGAGCTTGCCAGATC
EST76807	91	G	...	---	ATGCTAAGGGGATCGGACATGAAAGGACCCTGTGAGCCGATTGTCTCATCTCCGAGGCGCCCTGTCATC CAGCTCACTCATCAATGGGCCAGTCAGGCCCAGCGACTCAGGGCTCCGGAGGACTCACCACTGCCCCCT GCTGCCCATGTGGACTCGGTGTGCAAGGTTGAGGACTTCTTG

Clone	Pos	A1	A2	Sequence
ESTD-SSA1	111	C	T	TTCACTTTGTGGATTGTTCTTTGCTGTGTGCAGCACCTTTCAACATGATGTGATCCCATTGTCCAAG TTTGCTTTGGCCGCCTGCTGTGTGGGGATATTTGAAAGAGAT[C/T]TTTGCCAGTCCAATGTCCTAGA GAGTTTTCCCAAGTGTTTTCTTGTAATAGTTTGAGGCCTTAGATTTAAGTCTTTAATCCATT TTGATTTGATTTCTGTA
ESTD-RYR1	109	A	G	CTTCGTGACGGGAGGTCACGTCCTCCCGCCTCTTTCATGGACATATGGATGAGTGTCTGACCATTCCC CTGCTGACAGTGATGACGCAGACTTGTCTACTATGAG[A/G]GGGGAGCTGTGTGCACTCATGCC CGCTCCCCTCTGGAGGCTGGAGCCACTGGAGTGGGGAGCCACCTGCGCTGGGGGCCAGCC ACTCCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70	A	G	AAGACCTACGTGAATGTTCACATGTCTTAAAGCCTCCCTTCCTCTCTTACTCTCTGCCTGCAGGATGTG CG[A/G]CGTGTGCCTGGAGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCAGTGAGAAACGCCC CTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST444387	100	C		GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACCAAATGGCCCTCCAAGGCCCGTAGGGGGATCTAGGGGAACTGGGGATGGGTGAGGAATGGCCC AGCCCAGTCCCGGCCCCGGGTCCTGGGTCCCAACAGAGGAGGCCGTGGAGGAGGAGACAGGAGATGGGC TGGATGAG
	62	C	T	GCAGCCAGGAGGCCGCTGCACCATGCCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGA[C/T]G TCCTGTTCCGACCTAAGCGGAGCAGCCTCAAGAGACCCGAGCCGAGGTGGG
ESTD-PBDA	103	A	G	CCTTCTCATGCCCAGATGGAAATTCCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGGCAGGAGTAATCCAA[A/G]TCTCTACCCGCCAGCTTGCTCGCATACAG ACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACC
EST128393	122	A	G	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCCTCTTTGCT CCTAACACTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAG[A/G]TCAAGTCCA AGGCCATTGGCTATCTCAACACTGGTGAGTGAGTGATTACTTGAGTAAGGAAACTTGAATGTTATTCAAC TGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
ESTD-CTLA-4	48	A	G	ATGGCTTGCCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCT[A/G]CCAGGACCTGGCCCTG CACTCTCCTGTTTTTCTCTCTTCATCCCGTGTCTTCTGCAAAGCAATGCACGTGGCCCAGCCTGCTGT GGTACTGGCCAGCAGCCGAGGCATCCGCCAGCTTTGTGTGAGTGATGCATCTCCAGGCAAAGCCAC
ESTD-ACE	96	C	T	GATCAAGCAGTGCACACGGGTCACGATGACCAGCTCTCCACAGTCTCCCAGTAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCC[C/T]TGTCCCCTGCGGGGGGCCAACCCGGCTTCCA TGAGGCCATTGGGGACGTGCTGGCCGGCTCTCGGTCTCCTCCACTCCTGAACATCTCGAACATGTCGACAAAATCGGCCTGC
EST544198	88	A	G	CTTCTGCCTAATTTGAATGATATTGTTGCTGTGTGGGGACCAGAGCACTTTATTGGCACAAATGATCACTA TTTTCTTGACCCCTACTTAC[A/G]ATCCTGGGAGATGTATTTGGGTTTAGCCGTGGTCGTATGTGTCTA CTATAGTCCAAGTGAA

Name	Pos			...	Sequence
ESTD-PS-1	99	A	G	...	GGGGAGTAAAACTTGGATTGGGAGATTCATTTCTACAGTGTTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACAACCATAGCCT[A/G]TTTCGTAGCCATATTAATTGGTTTGTGCCTTAC ATTATTACTCCTTGCCATTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD-B3AR	104	C	T	...	GGCTGCCAGGGGTTCCGTGGGAGGCGGCGCCCTGCCGGGCCCTGCTGCGGGCGCTGGCCACC GTGGGGAGGCAACCTGCTGGTCATCGTGGCCATCGCC[C/T]GGACTCCGAGACTCCAGACCATGACCAA CGTGTGTCGTGACTTCGCTGGCGGCGACCGTGGTCGCCTGGTGGTCGTGCCGCGCCGGGCCA CCTTGGCGC
WI-567b	48	A	G	...	TCTCACACTGCACCCCTTACCTTCATCCTCACCTCTGCTGCCTTGGTTC[A/G]AGCCCTCATCTCTTTA CAGGGGATCCGCGCCACAGCATCCCAACTGATCTGGCCTTAGGTCTCTTCTCCAATCCATTCTTCAAAAG GCTGCCACTGTGATCTTCCCAAAGGTCATTCTGATGCTACCATCTTGCTTCAAGCC
WI-801c	58	G	T	...	ATGGAACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCACACATCCCCTTTCT[G/T]AGATGG TATTGGAGAAGTAGACAGAGAAATTAAGTAGGCAATGCATGTTGCAGGGGGTGGGGGCTGTGC ATCTGTGTATGTTAGTTACACATGGGCACATATACGCTCATGTTTGTCCTCAGCCCACCAGAGAGTTAA CATTTCTGCCACCCTC
WI-801b	58	G	T	...	ATGGAACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCACACATCCCCTTTCT[G/T]AGATGG TATTGGAGAAGTAGACAGAGAAATTAAGTAGGCAATGCATGTTGCAGGGGGTGGGGGCTGTGC ATCTGTGTATGTTAGTTACACATGGGCACATATACGCTCATGTTTGTCCTCAGCCCACCAGAGAGTTAA CATTTCTGCCACCCTC
WI-1099b	76	A	G	...	GAAATTCACCTATACAAGAACTATTTCTCTAATTATTACATTAGTCTCATTATTCTGAAATATTAT TTTTTACA[A/G]TACCCTTTGATTATTTTGATTCATTGTAACGAGAGATTACAATATCAGTAACGC TGTTCATTGATAGTGCTATCACAAATGTCTAAAATACTTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTTATTTGCTTTATGGTTTA
WI-2529	71	C	T	...	AGGAAATGGCTGATACTCCTGGTGGCTTCATTATAGTAAAAGGAGATGTAATTGCTTGATGAGCCTCT CAA[C/T]TTCTTAACTGCTGCTGCCTCAGTGAACATTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAAATGCTAAAGCTTGAAATAAAGTGAAAGAGGTAAAGAAGAGGAGCAACTGTGCTTT TTAAGAAATAGAAGAGTCACTTCATTAGAAATGGCTTGGGGATGACAAGTA
WI-10088	205	C	G	...	TAAGGGCCTGCTGTCTTCCCCCAGAGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACACATATACATAAGAGAAGGACCTGTACCCTATGAGGTAACCTGAGGATGAAGGA GTGAGTCATATTGGGGTGGCAATTAAATGACCCAGCCTCCTCTCCAAGAGACTTTTACATTTTAGAC AGGG[C/G]AGCAGAAGCAGCAAAGAGGAGAAAGGAAGT

Marker	No.	A1	A2	Primer 1	Primer 2	Sequence
WI-2625	98	G	A	---		GGGCAGTCCTGCTGCTGTAGTGGTAGACAGCACTGAAGGATGGAGGAAGAGAAGAAAACAGGCAGAAGCACTGTGGTAGTTAACAAGGCTTATTTAGGA[G/A]CAAATTGATGATACTCCCTGAGGACTCGCAGAAATTACCAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATTCCACTTGCAGGAGGAAAGCCAGCCAGCAAAG
WI-2924	54	G	A	TGACCTTCCTAGTCTTCTTTATAGG	GCCCTAAGTGTAATCACAGGG	TCTGTTGTCATATTCCCTCTTTGACTCTGACCTTCCTAGTCTTCTCTTATAGG[G/A]ACCCTGTGATTACACTTAGGGCCTACCTGGATTATTTAGAACAATC
WI-2939	72	G	T	GGCTTGTCTCAGTGCCTTT	CTTGTTGAGGGAAGGTCTTG	CCATTGTTGAGGTTGGGTGGGGTGGGGTCCACTTGTCATTCCCTCGCACTCAACAAAGTGGCTTGTCTCAGTGCCTTTT[G/T]CAAGACCTTCCCTCAACAAGAATGTCTTCCATGCTCCCGTGTTCTTTGAAAATTCGACT
WI-3203	99	G	A	GGTTATGCCGCAGACGAG	TCAAGTATTGCCTTGTGTGG	CTTGCTACCATGCATTTCACAGCATACAACCCTCAGTGAAATGCCGTAAACCCCCATTATAAAACATCTTGCCCATCGAAGGGGTTATGCCGCAGACGAG[G/A]CCACACAAGGCAATACTTGAAGTGACTTGGAGAATAAAGATTTTGGATGGATGAAAGCAGAGAAGGAGAGATGCTAAAAGTGA
WI-3473	101	A	G	AAGCATTTTAGCCCTAGGGA	CCTGATGTCACCAACATTTTCT	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTGGGAGATAGTTGGTGATAGGCCCTGTTGGAGATTGCAGAAGAAGGAAGCATTTTAGCCCTAGGGA[A/G]TAGAAAAATGTTGGTGACATCAGGGCT
WI-1796b	29	A	G	---		ACACACTTTTCTGTATGCTCTTCATCAAA[A/G]TGCAGGCCGTCATTTCTGCACATGGTGATATTTAAGCAGGAGAGCCATTGTTCTTGGCTCCCC
WI-1796	29	A	G	---		ACACACTTTTCTGTATGCTCTTCATCAAA[A/G]TGCAGGCCGTCATTTCTGCACATGGTGATATTTAAGCAGGAGAGCCATTGTTCTTGGCTCCCC
WI-4360	93	C	T	GTAGTCACATTAGGTATTTTCCAAATAA	GAGAGATATTTTCAGAGGCATTTT	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCCTGCAGAGTAGGAAAGAAAGATGGGGTGAGTAGTCACATTAGGTATTTTCCAAATAA[C/T]AAAATGCCTCTGAAAATATCTCTCCCATGTCCCTGTCTAAATATAACATTTTCCC
WI-1959b	87	C	T	---		GCTGAGCTTTGTGGCAGAGCCAGGGACCAATTCAGCTGCCGGATTTTAATAGATTCTGCAGCACTGCAACAGGAACCAAAAATCAGTC[C/T]TGGGTAACTGAGAGTGGTTTTCACACCCAAA
WI-1973b	28	A	G	---		GTTGTGCCTGTAGCAGACACAGAAGGGCA[A/G]AGAGGAAAAAGCCTTTTGGTCAGGGGCTTACACTGAATCCCTCAAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACAAAGGTATAGGGTTTG
WI-1980b	140	C	T	---		CTTGAGTATGCGTGGATTTTGGTATACACAGAAATGGGAAGCTGGAACTAATCCCCCATATACCAAGGGAAACCAAAATGTATCTGTTTCTACAATTATACAGTAGGAGACATTATGTTCCATGACAATGGTAATTTTTAA[C/T]GACAGTTTTAATTGAGTGAAATTACCATAAAAATAATAATAGTAGCAGCTAATATTTACTGAGCTGTTACTAGGTGCCTATAAATAGC

Name				Sequence
WI-2015b	190	A G	---	TGTCAGATAGTCCGTCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAATTATGCTATATATTATACAATATACAATTACTTGCGAGATAGCATGAGCATGCTAGTGAACCCCACAAGACTATGTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACATGGTGCTTTTCCAACT[A/G]CATATACTTCTAATACCATAGAG
WI-754b	49	C T	---	GAAGGCACAGGGAGAAGATGGCTGTGTCATCTACCAGCCAGGGAGGAGAGAGC[C/T]ACATTTATTGGTAATCCTATAAAGTGCATTCTTAAAATTGTATTTACTTTAGA
WI-754	22	T C	---	GAAGGCACAGGGAGAAGATGGC[T/C]GTCATCTACCAGCCAGGGAGGAGAAGCCACATTTATTGGTAATCCTATAAAGTGCATTCTTAAAATTGTATTTACTTTAGA
WIR-1b	56	A G	---	AGGCAATCAGACCTACAGAGAAGGAAACCCCAATAAAAAACTCTGATGATCGTACATCC[A/G]TGCCGCTGGAGGGTGATGCCTCCTGAGGACATGGGAGCTTCATGTTTGGAGCCCTCCTG
WIR-1	56	A G	---	AGGCAATCAGACCTACAGAGAAGGAAACCCCAATAAAAAACTCTGATGATCGTACATCC[A/G]TGCCGCTGGAGGGTGATGCCTCCTGAGGACATGGGAGCTTCATGTTTGGAGCCCTCCTG
WIR-3b	72	A G	---	TAATTTAAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAAGAAGT[A/G]TCTAAAAGTTATTAGCTCAGATAAGAAGCTGGGTGCTGAGATAAGA
WIR-3a	69	A T	---	TAATTTAAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAAGA[A/T]GTATCTAAAAGTTATTAGCTCAGATAAGAAGCTGGGTGCTGAGATAAGA
WIR-4	47	T	---	GAGCCCTTCTAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCCTGCTCCACACATGTGCAAGGCAGCAGCAAATTTGCCCAGCTGCC
WIR-5g	209	C	---	CGGGACAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAGAGAGGGTTATTAGGACTCAGTTCTGCTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGAGCCTGTGGTCCCACTGTTAGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGGTTTTACGTCCAG
WIR-5f	196	C	---	CGGGACAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAGAGAGGGTTATTAGGACTCAGTTCTGCTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGAGCCTGTGGTCCCACTGTTAGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGGTTTTACGTCCAG
WIR-5e	194	C	---	CGGGACAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAGAGAGGGTTATTAGGACTCAGTTCTGCTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGAGCCTGTGGTCCCACTGTTAGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGGTTTTACGTCCAG

Label	No.			Seq (short)	Sequence
WIR-5d	191	A	---		CGGGACAGAGAGACAGAGAGAGAGAGAGTTCTGCGCAGCATTCACAAGAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5c	177	C	---		CGGGACAGAGAGACAGAGAGAGAGAGAGTTCTGCGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5b	159	A	---		CGGGACAGAGAGACAGAGAGAGAGAGAGTTCTGCGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGAGCCTGTGGTCCCACTGTT AGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACAC AGGTTTTACGTCCAG
WIR-5a	37	A	G	---	TAACCCTGAAACTTTGTCTTCCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGCAGTCTTGGGGTTGGGGCAG
WIR-6	63	A	C	---	TTCGTTGACTATT[C/T]AAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-7	12	C	T	---	GGGGTCCTATGACTATCCTGGTCATTGATT[C/T]GACTAATGATTCCTG[C/T]GCCCTTG
WIR-8	46	C	T	---	AAACAGAAAAATAGAGGTTATAAGGATGAACTAAAGTTGTCAGAAGAGGTATGA[C/G]CTGAAG AAAGAATTACTCTCTTTGACCAATAAATACAATTGGGAAAACCATGGCTTGATTACT GACAAC
WIR-2	56	C	G	---	TGTCCTTGCTTATGCCTGCCTCTTCGCTTGGCCAGGATGATGCTGTCATTAGTATTTCACAGAGAAGTA GCTTCAGAGGGTAACTTAACAGAGT[G/A]TCAGATCTATCTTGTCAATCCCAACGTTTTACATAAAA TAAGAGATCCTTAGTGCACCCAGTGACATTAGCAGCATCTTAACACAGCCGGTGTGTTCAAAT GTACAGTGGTCCTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCACTC
WI-7069	93	G	A	---	GGTCATTTCCTTTTATCTGTCAGGCAGCCAGCTCTGACTT[A/T]CTCTCGTGTTCTGTCATCTCTCCC CCACATACCAACTTCTTCCACCATGATGATTATACCAATAAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41	A	T	---	
WI-18612	37	A	G	TGC	CCTATATTTCA AGTTTGGAAA TTGTATTGCTG CTTGCAAAT CACACTGTTCACACCTATATTTCAAGTTTGGAAATGC[A/G]TATTTGCAAGCAGCAATACAAAAGTA TTCATGAAGAATGCATAATCTCTGAAAATTATGAAAACATCCCT

ID	Pos	A1	A2			Sequence
WI-18517	87	C	T	CAGGAATCAG CAGCCTGA	TGTTTGGACAA GTGCAACA	TTAAAAAATCAACTAGGGCTCACCCTCAACACCCCCCTCCATTGTCAACCTCTCACAGCCTGCATGCC ACAGGAATCAGCAGCAGCCTGA[C/T]TGTTGCACTTGTCCAAACACAACAACTGACTGC
WI-18668	76	C	T	GGCGAAAAAC TAGGCAAAAA	GCTAAATTAAA CTGCACTTTTT GC	CGATTGACAACCTTTATTTTCAACTTAGGTAACAGTCCAAAATCAGTGTAGATTGGCGAAAAACT AGGCAAAAA[C/T]AGCAAAAAGTGCAGTTTAATTTAGCAAAGGCTCAAGACAGTGTGGAAGGAA GGTGAGATTTCCCTCCTACT
WI-18680	75	T	C	A	CCTCCTGAATA TACAACGGAGC	TAAAACATACGAGTACTGTACACGCAAGCATGCATCCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT[T/C]CGCTCCGTTGTATATTCAGGAGGGGA
WI-18704	99	A	C	GGGTTCTCCGA GGGGTAC CTGG	TGAAGGCCCTG	CACCCAGCTGTACCCAGGCTTCTTGTGCGAGCACCACCAAGGGGCAGGTTGGGCTTGAAGGAGCC CTTGAGGAAACACGGGTTCTCCGAGGGGTAC[A/C]CCAGCAGGGCCTTCAGCTAAAGTCG
WI-18673	29	A	G	---	---	TGTGGGCAAACCTTGTTTAATTGCAAAC[A/G]ACTTAATTTACAGCACACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAACATATGAATATATATAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T	C	GTCGTGGGGTG GGGG	GCAAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTATTTGGAGGTTAATTCCTATTAGGATAATGAAAGGATTCAGCAACGATTGAGATT GTGTTCCTCACGGAGGGGCTCGGGCCCAAGGTCGTGGGGGGTGGGGGGGGTGCAGAG[T/C]GTGTCCTCTTC AGTGGTATTTGCGGACC
WI-18533b	91	T	C	---	---	GGGGAGGAGGAGGTAGAATTGCCAAATGAGGCATTTTTTTAAACTCCCGAGATTTTTCTTCTTTATTT TATATTTTCATTTTTCATCCTAA[T/C]TTACTGAAGCCATTTTCTTTGGTTAACTTTAGA
WI-18533a	59	T	G	---	---	GGGGAGGAGGAGGTAGAATTGCCAAATTGAGGCATTTTTTTAAACTCCCGAGATTTTTCTTAATTACTCCTAATTTACTGAAGCCATTTTCTTTGGTTAACTTTAGA TTTTATATTTTCATTTTTCATCCTAATTTACTGAAGCCATTTTCTTTGGTTAACTTTAGA
D11734	83	A	C	TCATCTGATAC AACCAGGATA CTTGTTCAGAT AGGCTACAACT ATTT	GAGCCATATGCTGCATGAGGACCTTTCTCATCTTACATTATGGCTGGGAATCTTACTCTTTCATCTGATA CCTTGTTCAGATTTC[A/C]AAATAGTTGTAGCCTTATCCTGGTTTACAGATGTGAAACTTT
D49493	159	A	T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGGC	CAGGACTTGTGGTGCAGCTGCAGACGCGAGACAGAGCACAGCTCATGGGCAACATCACTGGGCCCAGAGAG AGCTGTCCGGCCAGTGCATCATTAGGGGGTCTTTCATTGCTAGTGACTACTAGCCCCTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATT[A/T]GCCCTGGCCCTGAAAGTGGCCCATCATTCATCACCACCACTGTT CT
EST100307	98	T	C	CATTTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TATTTCATAGAGAGACCTAGGAGGAGGAGGTTGACACAGCACACTGCTCAGCAGATGACTTAAAATTTT CCCTTAGCCATTTTGTTCTCTCAAGTCCC[T/C]CATCCATACCACCACTGCTGATTTG
EST100522	24	G	A	GCTCACTTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG[G/A]GAAGTCTAAGATTGAGGTTCCACATCTTGTGTGAGGGCCTTC CTGTTGAGTCATAACCTGGTGGAAGTCATCATGTGGAAGCTACAGAGAGCAAGAGGAA A

ID	Pos						Sequence
EST10605 2	118	C	G	---			CTTGCGTAAATCACAGTTCTGTATTCATACAAAAACTTGTTTTCTCTGACAAACTGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTTAAATTTGTGGAGATGCGCCCATGTC[C/G]TGTGTGAGACTTAA AAAAAAGAAAAAGATCCC
EST11048 0	61	T	G	CTCTCAAGTAG ATAAGAGGCA TAATCT	GCTAAATTTC AGAAAGAATT TTGTTT		CATGTGTCAATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCT[T/G]AA ACAAAATTCTTTCTGAAAATTTAGCTTATGAACTCATTACACTGCAAACCAGAGAAGGAGCAC
EST11260 8	101	G	T	---			TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTGCTGAAAGAAATGAAGTGTCAACACAAA TTCTATATCCAGCTAAATATCATTCATTAAGAATGAAG[G/T]GGAAAATGAAGCAATATCAGATAAA
EST11349 9	109	C	T	---			TTTGATGGAGAAATCCGAGGCCTGCCAGCATCCCCACCAGTAGATTCTTGGACGAAGAAAATCCT TCTGTGGGATTCAGCTTTACCGCCTTCCTCATCTGCTGGTGT[C/T]TCCTCAGAGCTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI-16632a	71	A	G	CCAACCTACTT TGGAGCCCT T	TCCAGCTTTCT CTAAAAACTCC		GAATTCTGGGTATTAAATAGCGGGTGCCACAGGAGCACATAGGAGGAGCATCCAACCTACTTTGGAG CCCT[A/G]AGGAGTTTTAGAGAAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGGAGGAGGAGTGGGAA
EST11772 6	74	A	G	---			CCAGGAATAAAAAGAAAAAGAGAGTCAGAGGAGAAACAGTCTTGATGTTATGAGGCTGAGACACTACTC TTCCTTCA[A/G]GACTATTTCATTCTGACTATAAGTGAATAAATACATTGAAGACTTCAGGAGCTCA
EST11795 3	82	G	A	---			CTTGTCCATTTATTTGTGCATGTGTTCTTAAAAGGCTTGTGAAAGATAACTTGGAATGTGGGAAAC ACATAGATCCCAGA[G/A]TATTAAAGGGGCTGGAAAAGTAGCCTTAAGAC
WI-16644	42	G	A	CAATAAGCAG CTCATTTTGAT TATAC	ACTTCATGAAT TTTACTTCATG TATACC		AGAGCAATGGTGCGATCTCAATAAGCAGCTCATTTGATTAC[G/A]GGTATACATGAAGTAAAATTC ATGAAGTAAAATTCATTACCAAAAAGCCTCCCACAGAACTTCATGCACCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST12005 9	56	A	G	TTGTATAATA ACACTCAGTA CAAAGTCTGT	GGCTGGTCACT CCTGGAT		GCCTAGTAATTCCAAAAGGAACATGTTGTATAATAACACTCAGTACAAAGTCTGT[A/G]ATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCATTCCATAGTTTTGAAATC
EST12055 9	32	T	C	---			GTGGAAAATTTTTTATCTGTTACGTCTTTCC[T/C]ATTATATTTATCTTGTCCTTGATTTCAGCACCC CACCCGATTTGCAGGCAGTGCTTTCTAAACTGTGCCGTGTTAAAAGTCTTCT
EST12492 1b	95	A	G	---			CCCCTAGCAAATGACTTGGAGTTGTGTCCAATTACCAAGTTACATACTGTTGCCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT[A/G]GGAAACGCACAGCAAAATTGACGATGCAGCTTTTTA CCTTTTA
EST12492 4	25	A	G	---			ATCTTGAGGTTTCTGGGCCTGTCAG[A/G]AAGTGACATCTTTTACTTACCACAGGTCAGGAACCCTAT AAAGAAACTGTGTAGAAAAGATATCAGGTCAGACTTTTTATAAAGGGGCTTCTTATCAGCTCAATAAA

EST125022	52	C	G	---		ATAACTAGGGAGGAGAAAACCAAACTGGAGGCAAGTCCACAGGTCACACTTGTCA[C/G]CAGCAAGTAT AACCAAAGTGGGGTTCGATGAAGAGAAAATGCTCACGGGGGAAAATGACCATTTTAAGGGCCATGTG GTCGTCGAGGCAGTTAGAGG
EST126198	105	T	C	---		CCAGAGAAAAATTAGAATGTATCGGTAAAAGAAATAGGAATGCATATTCAACTCACTGTCACAAA CAGGTGTTTTATTATCCCAAATGACAGTGTTGCCTGAGA[T/C]GATGCATGTGGCAGACGAG
EST126200	67	A	G	---		TTTCTTCTCTCCTTCATTTATTCATTTGTTCAAAACACTGTCTAGTACCAACATTGTCCACGGGGC[A /G]TTGAGAATACAATATTGAAGAAGAGTCACTGCCTGCCCTGGAAAAATCAGAGTATTTGA
EST128179a	22	C	A	---		TTGGGGTTCTCCAGGATTCCAG[C/A]CTCGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGG GTTCTTGGGAGTGACCGGGGATGGGGAATCCATGTTGCTTTGCGTACTCCATCAGGTCATTGCG
EST129418	23	T	A	---		TCTCAGCTTCCACCTGACCTGCA[T/A]CAAACAGCCCAGTTATTCACCAGAATTTTGTTTGCGTTTCA ATGTAGTGTTTAGCTTTAATACACTGCACTGTTTTG
EST129492a	52	A	G	GGCTTTAATCA TAACCTAATA GATACTGTT	TGTGTCCCTGT GGGTCTC	AGGATTTCATGAGGCTTTAATCATAACCTAATAATACTGTTAAAAACAACAC[A/G]TTCTGTCACTTG CAGAGACCCACAGGACACACATTCTCTTCCCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST130674	104	C	T	---		ATTTTTGTTTTCTTAAATGAAGCATAATAAAATCTCAGAAAAATCATCTATAGTTGA GTGTAAAACTCCCCTAAATCAGTCTTCTAGGGCCACA[C/T]TGGAGCAGAAGCAGCTTCCCACCCAAG CACCTCTGAACT
EST131176	66	A	G	---		TGCTGTCTGCATCAGTCCTTTAAAAATTTAATCGCTTTATACAATTGACACCAAATAAAATGCAC[A /G]TATTTAAAGTTTACAATTGAGAAGCTGACACGTGTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST131216	44	C	T	---		TCTGCTTTAAAGATTCTTCATAGCTGCTTAGGTTTTGTTCTTCC[C/T]AGCATATTCAGCTATAATCA CCTACATTCCCTCCACAAATATTCCTGTGTGCCAGCCAGTCTCCTCACTGTCCCATGAATAGCC AGTCTTATTTCCACTCT
EST132266	74	T	G	---		AACTGTTTACTAACAACAAGGTGCTTTAAATTTGAAAAGCATTTGAGGAAATAAATTAATGAAATAGTCT GGGCCATT[T/G]GACTAACCAGTTCTACAAATTTCACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAAACAAAACATG
EST132306	72	G	A	GCTCAGATGTG AGAGACGC	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACTTACAACCAACTTGCCGCCTCAATATGCAGCTCAGATGTGTGAGAG ACGC[G/A]TCTCTGTACAGGAGCGCGGTACTGTCTTCAATCCTTGCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST132369a	70	T	C	AACCAGATTT TCTCAGGCCT	ACAAGAGGGTT TGACAAAGA G	AAAGATATAAAAAACAACTCCCCATCCAGTAGCAATACAAGGTTATACATTTTAACCAGATTTTCTCAGG CCT[T/C]TTTTGGATACCCTTAGTAGTTAACTCTCTTTTGTCAAACCCTCTTGTATATAACCA

EST	Pos	Allele	Flanking	Sequence
EST13278 2a	51	A G	CTTTCACCGAA CAATATTTTAG CATATTCTTGG GTGGTGAGAA	TTCGCAGAACGTTTACAAGCTCCAAACCTTTCACCGAACAATATTTTAGG[A/G]ATTTGAAATTAT TTCTGTAGTTCTCACCACCCAAGAATATGACAGCTTG
EST13282 0	99	A T	CCACACATTTC GATGGAAAATT AGTCCAAGA TGAGGAAGGTT GG	GCTCACTAGATGAGCATTGACCAAATATTAGATAATACCTGTTGGGAAAGTGCTGAATTACTAGCC TGCCTGAGAATCCCACACATTTCCTCAAGA[A/T]AACCTTCCATCTCCCATCAGA GG
EST13290 9	39	A G	CAATTTTAGA AGTTTGGGTTT CTT AAATCACTTCA TGGAAATTTCA G	AGCTCATCTGCAAGCAATTTTAGAAGTTTGGGTTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTTT TTTCTGTGCTTAACTTCAGTTACTTAAAGACCTAAAAGACAAAGTGGTATCACATCACATATTTTGT ATGTGTGGGCTTTTTG
EST13518 2	45	C G	---	GAAACATCCTCCAGTAGTATTGAGGTTAAAAATGATTCAGCATTTA[C/G]ACTTTAAAAATTACCTCA ATGTTCCTCGGAGTCGTCCATAGTTTAAAAATGACTTCTGCACCTTCCTATAACCTTGATTG
EST13522 8a	66	A G	---	CAGGTTGGTGATTCTCAACTAGGAGCTATTTTGCCCCCCATCCCCACCCGGCAGTGTCTGGAGAC[A/ G]GTTTTGATTGTTCACAACTGCGAGAGGTGGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69	T C	---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AA[T/C]GCACACAAGGAATAAGGGAGAAGGAGGTTCGGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101	C G	---	AAGATTACGGACCACCATAGAAGAACTGCCCCCCGACCCCATACACACACAATTTATAGCAGGTAAAACCAA CTGAAAGGAACAAAGTAATGACTTTCTTGAACAAA[C/G]TGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25	A G	---	CCTCAACCATCTGTAACCCGAGCCC[A/G]CAGTGACCGGGACTTGCTGCTTCCCCATCCCAGCCCTCT CCTATCAGCCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23	A G	GGAACAAGTC ---	CAATGGTGTCCATGTGAACATAT[A/G]ACCTATTCATAAAGTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAAAGTCATCTGCTAAAATGACCGAACAGGAGGGTAGGAGG
EST14221 5	42	T C	GCATGCTAGA CAGAGGCATT AAAATATTTTT AAAAGA	AATATCAATGCATTCTTGTTGGCATGCTAGACAGACAGAGGCATTA[T/C]TTTTGAAGATCTTTTAAAAAT ATTTGACTTGTTCCCCCTTCACACTCATTTTTAAATTGT
EST14812 2	50	A G	CAAGTCAGCTT CTACATTCTGA TAAAGATTTAC TTAAATCCCAT ATA TATGTACT	TTCACTTAGTACCAAGGATGCCTTTCAAGTCAGCTTCTACATTCTGAATA[A/G]AGTACATAATGGG ATTTAAGTAAATCTTTAGAAGTCCCGGAGTTGCCTTTTCTAACATTTCATATCAGGTGAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	128	A T	CATCACCCACC ATACTGGTT CGGGAAAACA GTACCGGAA	TTTGCTTCGGCAATACATAGTGCGCAATGCAGCGTGAGTTCGCGCCGTCTCCCCACTGAACCAGTAAT TCACCAGACAATGGCGCACCACTTAAATAAACTTGCCCGTCATCACCCACCTATACTGGTT[A/T]TTCC GGTACTGTTTCCGTA

ID	Pos			Fragment		Sequence
EST154206	109	C	A		...	TTTTAACCCCAAGACTTGTAGAGTGTCAGGACTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTGTCATCATAATCATATAGCCAAGGGACT[C/A]GGAATTTGGCTGCTTCAAGTCA TTCCAAAACCTCTCAGG
EST157006	48	G	C	GGA	GAAAAGACAA AGACAACAGA GGAATAGCTGA AACAGAGATA TTATTCTC	GTCACCAGCACTTTATTAAGACGTGAAAAGACAAAGACAACAGAGGA[G/C]AGCAGAGAATAATA TCTCTGTTTCAGCTATTCCAGGATGTTATGCCAATTATCCAGAGTCCTTGATCTGATGTAGTA
WI-16739	57	G	A	CACAAGC	GGTTTTGCCAT TTCATTATTCC CTATAA GATAGTTGATG	AAGGATTGAAAACATACCTAGATCATATAAATTTGTGAAGGTTTTGCCATCACAAGC[G/A]TTATAG GGAATAATGAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAAATTGCCTCCAAGGT
WI-16782	96	C	T	CACTGTAAGG	GGTGGGAGTCT CTGTTCCTCCA CTTCTATCTTT	CTTCTTCCTTCCTGAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAGGA[C/T]GATGGAGGAACAGAAAGATAGAAGAAGTTTGGGGT GCTGATGAAATTGTGGGG
WI-16783	64	A	G	G	TCCTGAGATGT CTGCTTGGTTC CTTTTACCTGA AATCCTTATTA	AAAAATGTAAAACTTAGAGAGGTTGCCTCTTTTGTGTCACTTTCCTGAGATGTCTTTTACCTGAG[A/G] CTAATAAGGATTGAACCAAGCAGTATTTTTAATGGCAAAGTCCAGATGTAACTCGAGT
EST159482	58	T	C		...	CAGGACTTAAGGTCATTTGCCTGGAGACTTAACTAAAGGTCAGGGCAACATAGGA[T/C]TGTGA CAGCACCACTCGGACCAGGAAGTGCTGAAAATCGTCACACTAGCGGTGCCCAGCCCCTTTTTCCTGGC TGCTCTGCCTCCCCAGAGC
EST160888	89	G	C		...	GGTTTTGAAGACGCAGCTTATCTCCACCTGCCACTGGGATTCTCATTTGAGAGCGTGTTTGTCAGCC TTTTCCAGAAAAGGCCGCGCTC[G/C]GGGGTTTCTGAACCCTCTATGGGCATTTTAGAAT
EST160899	96	C	T		...	CGTCTGAAGTTTTCTTTATCACAAGTCAAGTCCATCAATCCCTCGGGCCCGCTCAAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC[C/T]AAAGAGCCACATCCCTGCCCCCTTTCTTTGCT
EST161001	24	C	G		...	ATCCCAGCTGTGAAGGGACGCAGAGGAG[C/G]GTAAAACACAGTCCATTTATTATAAGGGGTGTGCACATTCCCA GGGGCTCCAAATAATGCAACATTGTTCACTCGTCCATGCCGTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACACAGGTTGGCTC
EST161049a	83	A	G		...	TTCTTTTAAATAACCCACCAGACACACCCATGACACTTCCAAATTTACAGAGCAAAAAAGTGATTTGCAG CTGGTTCCTCCAGGGA[A/G]TTGGCCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST161180b	119	T	C		...	ATGGTATAACAAATCAGTTCCAGGTTTTTTT[C/G]TGAACAAATGATCCTTTGGTCTTTCCCGTGGC CTCCTAAAACAACTAAAACACCCTCTACGTGTCTAATCAGTCACCTAAGATAATCGAGTGGCAAGT CTTTCACA
EST161180a	32	C	G		...	ATGGTATAACAAAATCAGTTCCAGTTTTTTT[C/G]TGAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCCTAAAACAACTAAAACAACCCTCTACGTGTCTAATCAGTCACCTAAGATAATCGAGTGGCAAGT CTTTCACA

Clone	Pos	Allele	Extra	Sequence
EST16151 2	53	C/T	---	AGCCAATTCAAACGAACTCTATCAAAAACACACAAAGGCCTAGAGGAGGAGATTA[C/T]AATGAACGT AAATAATTCAAGGCAATTTTGATCTAAAGCATTTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTTGTATAGGA
EST16182 6	54	G/A	---	CATTGGTTGGGTAGGGAAAGATAGTAGTGTGCAAATAAAATGGTAAAACAGCAG[G/A]AAATGGAA TTATAGCTTTCTTTCATATAGGGAATTGAAATTTATTACTGAGGGTGATAGGCAGAAGTAGTA
EST16183 2b	59	A/G	---	GCGAGGTAAACTGTGGTTCACAACGTATTGTTCTTTCATAAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACTGTGTCTCCTGGCCCTTCTCGTTCATATTTTATGTCACTGTCCTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28	G/A	---	AATCTTAGGCTCTTGGCTTTCAAAATCA[G/A]TACAGACAGATAAGAGCTTTAAGTATTTCGCATTT CCCCAGAGGAGGAAAAAGTCAGCATCATAAACCACATGGGTCACATGCTCACGCACATGGTGTC
EST16229 2c	52	T/C	---	TGTGAACTCGAATTCGCTTGTCCAAGTCCTGAGTCACAGTTTCATTGGGAG[T/C]CCCTGTGCAGCC CTTGCCAGTTCCACGAGGCAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
EST16229 2b	45	T/C	---	TGTGAACTCGAATTCGCTTGTCCAAGTCCTGAGTCACAGTTTCATT[T/C]TGGGAGTCCCTGTGCAGCC CTTGCCAGTTCCACGAGGCAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
WI-16816	124	A/G	GGAGCCATTGT TGGGGTTA GTTCAGGACAG	CAGACTTTCCTCACACCTCATTGGCTGGAACTGGGTCACATGCCACATCCTTGAACTATCATTGGCAA AGGGAAATGGGTCATCAAAATTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGGTTA[A/G]ACTGTCC TGAACAAAATCTAGGCTC
EST16269 5b	49	G/A	---	GCCACTCTCCTGTGGCTTGCTCCTGTCCAGCTGCTGTCCCAGTGCCACA[G/A]TGGTCTAGCCTCATGG CAGAAGCATTTTAGCCAACTCCTGGTCTGCTCCCACTCTCTCCTCTTCCCGCCGCTGGGGCCTCACCACC TCTTCCTCCTCAATC
WI-16824b	83	G/A	---	GTCACCCCAGCCAATGCTTCAGGAATAAATGATGGTGCTGCAGCTGT[G/A]CTTACACCTTTAGCACGGA AGCTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTCCTGGTCCCAAGTGGGGTGTGGAGC GCCTTCCATTATGGGAATA
WI-16824a	47	T/C	CAGCTTCTGAC TTCTTCATAAG AA	GTCACCCCAGCCAATGCTTCAGGAATAAATGATGGTGCTGCAGCTGT[T/C]GTTCTTATGAAGAAGTC AGAAGCTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTCCTGGTCCCAAGTGGGGTGTGGAGC CTTCCATTATGGGAATA
EST16445 3	96	T/C	---	TTGCTTTATTAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTATTCATTACAAA AATGGCTTCCAAACCATTAAAAATGAACT[T/C]GGAATAAAAACGGAACAGTAACATCA
WI-16857	47	G/A, A	CAAATAAGCA GCTAATGGCA AGACCACT TGTGAATTGGG	TATAATCCATCCTCCAACACACACACACAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTCACAAGACCTGTGCTTCAAATTGTTTCCTGATAATGTGGGAGAAATCTGCTCTTTATGTA

Marker	Pos	A1	A2	Sequence 1	Sequence 2	Sequence 3
WI-16879	79	C	T	GATACAGGCC ATATTTCCCA	CAAGGCTTTCT AGAACTAGAGT CC	AGACAGGTCAAACAAACTCCTAGGGATAAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCA[C/T]ATAGGACTCTAGTTCTAGAAAGCCTTGGGGAGAACAGGCACCCAG
WI-16882	99	A	G	GAAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGGTGGGAGAAGACAATTCTCCCCCTTTCACCCAAAGGTTACTCTGAC AAGGCTATGAATGAAAATGCCACGTCTCTGAC[A/G]GCGATTTACCTGACATGTGTCATCTCCCT
WI-16888	70	G	A	GCTAACTTTGG GCAGGTTC	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAAATGTTCATCACTACCCGGGGAGAGCAAAGAACCATGAACGGTAGCTAACTTTGGGCAGG TTC[G/A]TTAAATTGGTCAATTCAGAACATTCCAAAT
WI-16905	75	C	T	ACTTGGCCTGT GTTGTTCA	GTCTATACTCT TCTAGGCAGTG GG	TTTGTTGTTGTTATTGCCTCCCAACATCAGAACATAAGTTCCATGAAAACAGGAACTTGGCCTGTG TTGTTCA[C/T]CCCACTGCCTAGAGAGTATAGACA
WI-16910	74	G	A	AAGAGTAAAG ATGGCGCTAG AA	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTCATCTCAGAAGAGTAAAGATGGCG CTAGAA[G/A]GTATCTGTTATAGAAACGATACTTCATTTGGGCCTGAACCAGTGAAGGT
WI-16918	93	C	T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAAATAAACTACCACCATTCTCTCTGCTACCACAGAGCACTAAAATCTAGGAATTTGAC TTTACTGCAGCCATTAACACCAGCAC[C/T]GATGCCACTTCTGTATCAGGAACTTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127	A	C	GGAAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGG[A/C]CCA CGGGCAATCACATGAGATG
WI-16947a	58	C	G	CATGGAAATA GGCCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAG[C/G]ACAGG ATTTGGCTGAGGCTTCAACTGACATCATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGGACCA CGGGCAATCACATGAGATG
WI-16966	43	T	C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTTACTTAAAATGCACACTACATAACAACCTAATA[T/C]CTTAACTTGGTCCAACTATTT AGTATAACTAATATGAGTTTTTATACTGATAACTTGCAATGCCATTAAA
WI-16995	55	T	C	GAGCAGTAGA GACTGAGGTA AATAGTATT	CATGTTGATTT CCAGCCGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAAATAGTATT[T/C]ACGGCTGG AAATCAACATGCCTCTTCTTCTGTGAAGTTGTCAGCATGGAGCTGAGAAGGCTGAGTCAATCT
WI-16992b	60	T	G	---	CACATTCCCTT	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAGTACACTGTGCCCCTCATCTGAGA[T/G]GTG TAGGACTGTAAGGGAATGTGTTTGGGGGTTTAGGAA
WI-16992a	46	G	A	AAGCACCCAG AAGTACACTG TC	ACAGTCCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAGTACACTGTC[G/A]CCCTCATCTGAGATGTG TAGGACTGTAAGGGAATGTGTTTGGGGGTTTAGGAA

ID	#					
WI-17010	23	T	C	TTCAACAGGA AAAGCCATG	AATAATACGGT GTTTGAATGT CA	ATGTTTCAACAGGAGAAAGCCATG[T/C]ATGACATTCAAAACACCGTATTATTAGAAGCTCATTTAAT TGTTTAATGCAGACAAAAATCAAGGCTAACTAAAACAGCAGATCCAATAACCAGTGATCAACCTAGA GGTTCCCACG
EST171279b	74	C	T	CACTCGGCAC AGACAGAGT	GGGAGGGCCAGG GGTG	ATTCCGTCTCCAAACAGCATCCCAGGCCGGCCATCTCCCCCAGATTTTATAATACACTCGGCACAGA CAGAGT[C/T]TGGGGAGCACAGCCATGGGGCCATGGCACCCCTGCCCTCCCCAGGCTTCCTAAGTAACAACT
WI-17040	94	T	C	AATTCTCTTAT CATCTCAAGCC A	GGACTATGGCT TATTCAGTGAT G	CACGCGTTCATTAAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC GAGAATTCTCTTATCATCTCAAGCCAGT[T/C]CATCACTGAATAAGCCATAGTCCCAGTCTCGTTTTCC AAATCTTTCTCATATTGT
WI-17044	47	G	T	GCCAAGGGAT TAACGTATAG G	GGGGATCCCCT TGTTTAAGA	TTGTTTTTGTTTTCTCTCCTGCCAAGGGATTAACGTATAGG[G/T]TCTTAAACAAGGGGATC CCCACTTATAGCTGACAGCAGCAGCTCCTGCGAATGGCAGGAATCGAAT CAAAAGAAAAGCAAGTG
WI-17021	62	T	A	TGGACTTGTCA GCCTATAACT ACTC	TGTAGAGTTAG TGGCAGCTGC	GCATGTGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTCAGCCTATAACTACTC[T/A]G CAGCTGCCACTAACTCACAGGCACAGTAACTACACTTTATACAGGAGCACATGCCAAAGTGCCTGG GAGGTGCCAATAAAATCAA
WI-17065	90	T	C	CCAGAAAGGA AAAGCATAAA CTT	CCCAAGAGAC AATGAAATCCT	TGTAAAAAATGTAGACACATGGGGAGGAAAAACATTCGTAATCAACATGTGCTGTTTCTACTTCCGGTA CCAGAAAGGAAAAGCATAAACTT[T/C]AGGATTTCATTGTCTCTTGGGT
WI-17066	32	A	C	TGTACAGCCA ACATCACTGTT T	GAGATGTTGAA AATGTTCTGGA A	TTCATAAGGTTGTACAGCCAACATCACTGTT[A/C]ATTCCAGAACATTTCAACATCTCAAAAGA AACTCTGCACCCATTAGCAGTCATTCCCTGAGCTTCCCTGTAGCTCCCATAGGCAATGGCAACTGCTGATC
WI-17074	86	T	G	...	...	TGCTGACTGTCATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAAGCAT AACCTCCTACACAGGCCT[T/G]CTACACATAGGAGTATATTGGCCAAGACTCACCACTAGAAGTGATT
WI-17104b	108	T	C	...	...	CAGATGAGAACTCATGCTGCTCATCTGCAAGCTTCCTGATGCTTTGCGAGCTTCCCATTCCATTCCA AATCAGAAGCAGTCAGTGGCCCGTGGTTCCAGACGGC[T/C]TCTCTTTGTTAAGAAATTA
WI-17114a	37	T	C	TTTCCATCAAG GACTTGTTT	TTGTATTATAA ATAGCAGAGTG AAGAGAC	AGCGTCCAACAGATGTTTCCATCAAGGACTTTGTTT[T/C]GTCTCTCTTCACTCTGCTATTTATAATAC AAGCTACCTCCCAAGGCCAGATGCTCTAAAGTGCTAAAAGAAGACTGCAGCCAACAATCAGAGTTACAT GGGA
WI-17150	76	T	G	GATGAAATTC AGATAGTCTTC GCTCTT	TTCTCAGAATC CTGGAAGATAT G	CGTGGCTGGACTAAGTGCTCTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC TTCCTCTT[T/G]CATATCTTCCAGGATTCTGAGAAGTGCTCTTGTGTGCTCTAATTT
WI-17163	43	A	G	CATTTCTTTGT AAAATAACAA TAACGTT	CAGAATCTTGC TTTTTGCCTT	GAAATCGAAATACGTCCATTTCTTTGTAAAATAACAATAACGTT[A/G]AAGGCAAAAAGCAAGATTCTG TAAACCAACATTGGAAAAGGGGACACAGGGAAAGGGAAAGGGCCAGATTTTCAACGGTTT CCTCCACATCTGCAGACAAA

WI-17178	127	T	C	GGACTCCCTCA TGAGGAGC	CCCTCAATTTT CAACTGCTTC	AGCAAATGTCCCCTCCAATTCATTAGCTATGATGAGGAGTTATCAGTTCATTCAGAGAGCGAATTACTGG GGCGAGGGGGTTTAATATCCTGATGGGTTTAATTCAGTGAGGACTCCCTCATGAGGAGC[T/C]AGAA GCAGTTGAAAATTGAGGG
WI-17180b	81	C	G	---	---	TCATGGACATCCTGAAGCAGCAGACACAAAAATATAGAGAATCCTGCACTTCCCAAGTCTCGTCGCCACAG GCTTCAACAATTAC[C/G]AACATCTTGTTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
WI-17180a	47	T	C	CACAAAAATA TAGAGAATCC TGCA	TGCGACGAGAC TTGCG	TCATGGACATCCTGAAGCAGCAGACACAAAAATATAGAGAATCCTGCACTTCTC[T/C]CCCAAGTCTCGTCGCA CAGGCTTCAACAATTACCACCAACATCTTGTTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
WI-17156	54	G	C	TGTTCTCTAAA CTTTAGATATC TCCCA	CAAGAAATAT ATATTTGATTC TGTGGAA	TGAGGTAGCAGGGCATTCTTAAGAAATGTTCTCTAAACTTTAGATATCTCCCAT[G/C]TTCCACAGA ATCAAAATATATTTCTTGGTTGGAAATTTAAATGTTCTTAACTATCTGCCTACCACCTCAAT TAATATTCTTG
WI-17149b	79	T	C	---	---	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATCTCATGCACGTGCGTGGAA ACCCAATTGTCAT[T/C]GTGTATGAACTACAAAGGATGGGAAAAGAACACATTTCCTCACA
WI-17149a	48	C	G	CAAGGTTTGA AGGAGGAACA CATGA	CCACGCACGTG CATGA	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACAT[C/G]TCATGCACGTGCGTG GAAACCCAATTGTCATGTGTATGTGTATGAACTACAAAAGGATGGGGAAAAGAACACATTTCCTCACA
WI-17197	67	G	A	GCAGAAGTAG CTGGGGCTAC	GGTGAGGTGGT GCATACC	ATTTTGCTATGTTGCCTGGGCTGGACTCCAGCAATCCTCCTGCCTCAGCAGAGTAGCTGGGGCTAC[G /A]GGTATGCACCACCTCACCCTGCCTATCAGTTCGTTTAATAGAATATTTGACTTTAGATGCGCA
WI-17198	38	A	C	TCCCCCCTTGTC CCTAGTTT	TCCATTTGTCC ACTGAGAAATT	TGTATTTCAGTACTTTCCTCCCCCCTGTCCCTAGTTT[A/C]TAATTTCTCAGTGGACAAATGGACAA ACCATCTCTGTTTGAATTTGAATACACAGATACATCAAGATATCTTACAAGAAACAATGCACATCC TTC
EST18753	27	C	T	CTACCCAGGCT GGTCTCAT	GGATCGCATGA GCCTGA	TCGCTATGCTACCCAGGCTGGTCTCTCAT[C/T]TCAGGCTCATGCGATCCTCCTGCCTCTGCAGTGGCTGG GATAAGACACAACTGCCCACCAGGCCTAGGAGTAGTCTTAATGCCTGATGGTGGG
WI-17108b	74	C	T	GCCATTCAGTC TCAAAGTAAA TGTACTTAATG	AACTACGATTT ATCATATGCTC CC	TTATTTAAAACATAACCAGATGCACCTTGGTTTTTACATTCTCTGGTTGCCATTCAGTCTCAAAGT AAACAC[C/T]GGGAGCATATGATAAATCGTAGTTTAAGGAAGCCATAGCACTTACAGAGT
EST19067 2b	41	A	G	---	---	ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTCA[A/G]GTGGCATTAAGTACATTCAACT TTTTGAGCAACCCGCCATCCACCATTCATCCATCCGTT
EST19067 2a	40	A	C	CGTGACCATTT AAGGGTATAG TTC	---	ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTC[A/C]AGTGGCATTAAGTACATTCAACT TTTTGAGCAACCCGCCATCCACCATTCATCCATCCGTT
EST19125 8	28	A	G	---	---	CTGTTTCTCAGAGATGACACTGCCAACA[A/G]TCACAGATTTGCATCAATACAGTTATGTATTGGC TATTCACAATTTACAGTAGTGTTTTTTCCTCTGAAAAA

EST20824 8	115	T	G GCTGATTG	AGTCGGGAGT	AAGATTTTATC TTGGACCCGA	GTGTGGAAGCCGGAGTTTATTATTATTCAAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTA AGGATAAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTG[T/G]TCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50	A	G CTTCTCAGCCT	ATCCTCAGAA	TCAAGCATCCA	TTGGTTAAATGATGCCCAGATGGGGTCACATCCTCCTCAGAACTTCTCAGCCT[A/G]TAGCACAAGTGG ATGCTTGAAGAAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGGATGTGAGTGGGACCA
EST21904 b	128	G	A GTG	TTCATATGGCC ATTTTAATAA	GGCAGGTGTTC AGAAAGCAT	TGATTGTGGGTCTGGGAGCAGGTGGGCAGTTCAGTGGAGGAGAAGTAGAGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAATGTACTAGGCTTTCATATGGCCATTTTAATAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82	T	C T	GAAGATCTGT CTGGCATTCTT	TGGAAAAACA GCCCCAC	CAAACAATGTAGACATAAGGGAACAAATTCAGAGAGAGCTCAAGTCACCATGTTTGCTAAGAGAAGAT CTGTCTGGCATTCTTT[T/C]GTGGGGCTGTTTTCCAAGGCACA
EST22197 2	78	T	C TATTCCTGCCA	AATTATTCTGC ATGCGGT	ACCATGAAGG	GTTAATGATCACTCACCAAAATCCACAGGAGAATCTTAAATGTTACAAGCACCAATTATTCTGCT ATTCCTGCCATT[T/C]ACCGGCATCCTTCATGGTAGAGTATCACAAGTAAAAGTTTCTGGTTGTTTCATC TACTTAAAACCA
EST22311 9c	92	T	C	…	…	TTTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAATCCACCACTGTAAAACAG TAGCATTCAATGGTTTTACTCTA[T/C]TGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATTCCAG
EST22311 9b	54	A	G	---	---	TTTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAATCCACCACTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATTCCAG
EST22311 9a	41	T	C GAGTTATAA	GGATTAGATC ATCTTTTTATT	TTGAATGCTAC TGTTTACAGTG G	TTTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATA[T/C]ACATAAAAATCCACCACTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATTCCAG
EST22319 9	19	A	C	---	---	TCGAGGAGCTCTGAGGAGC[A/C]CACCAAGGGACGTGTGTCCCAGGGCCACCGTGCGAGGCAAGTGTG GTCCAACTCCTCCTCCCTTTACAAAACTCCAGCCTCACCCACACAACACTGGCTGACAGGCCTTCT TAAGCCTTTTTTAACTGT
EST22433 c	103	A	G AA	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAACTGACAGA	GATGTTAATGACTTTCCTTTGAGATATGATGGAAAAATATTCCAGTACACATGGAAAAGACATGTT CACCAAGTGAAAACCAATCTAACCAGAAAGCTTTACC[A/G]TCTGTCAGTTAAGCTGAAGCTGAAATT CTGGGGAGCTTGACATGCTG
EST22657 9	71	A	G TTATCTGCACA T	AAATGGATCC GCATGAATTT AGTTTCAGTTT		TATCCATTTCAAGAAAAAAAAAAAATGACTTAAAAAATACAATTCTATCCCAGAAATGGATCCTTATCTG CACA[A/G]CCATTGAAGAAGAAAAAAAAATTCATGCAAACTGAAACTATGCTTT

ID	Pos					Sequence
EST22993 5b	71	T	C	ATCCTTTGTT TCTACCCCC	TTGCCTGTTAA TTGACTGTAA TG	GCCTTTTATTGTCTCCTTTAACATCAAATGTTTATAACACACTTGATCCTTTGTTCTACCCCA ATT[T/C]CATTACAGTCAAATTAACAGGCAATATAATAGGTCTAACAGAATGCTTGCATT
EST23021 0	108	T	A	...	...	TTATTTCTCAGCTTACCATTGTGTACTTATATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAATTTATTAATCTTTGCCTT[T/A]ATGGTTTGACAGTTTGTGTCTTTCT T
WI-17387	55	C	G	CCTTTGCAGAT GTGAAGAAAAA	GCTTTTGCCTA AGATTAATAGT AACTACT	ACAGAATTTTAACATGCAAGTTCATTACATTACCTTTGCAGATTGAAGAAAAA[C/G]AATATTAG TAGTTACTATTAATCTTAGGCAAAAGCCATTTCTTTG
EST23669 1	101	A	C	AATGTAAGCT CCAGAGGCAG	CCTTCCCCTCC TGTAAGC	TTTTTGGCTTGTCTGCAGAATAGATGAAAAGAGAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGCACACTAGGCAATGTAAGCTCCAGAGGCAG[A/C]GCTTACAGGAGGGGAAGGGACGGCTGAGGC CAAGAGTGCTGGCTCACTG
EST23733 9	31	T	G	GGCTGTTAGTT TTGTTTTTGTTT TT	TGCACTTTAAA TCCCATCAAT	AAAGGCTGTTAGTTTGTTTGTTTTTTCCT[T/G]TATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCCTAGAGAAAGATATGAGGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA
WI-17470	83	A	G	GTCCCGTCCCG CCAG	CCAGTGACGAG GCCGA	CTGACACGTCCCGTGTGTGCGGGGGTGTCCATGTGGCGGTGTGTGAGTGAGACTTTTTACTGCGTCCC GTCCCGGCCAGCCCT[A/G]TCGGCCGCCTCGTCACTTTGTATTCTGTCTTGGTTGGAAA TACCATCAGCCTTCC
WI-17519	55	T	C	GTTGTCCTAGC TAATGAATGC A	AATTATTATT TGCAGGCAATA CTC	TTTTTAACGAAATCTCACTACTGCAAATGCATTGTTGTCCTAGCTAATGAATGCA[T/C]AGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAGAAGCTTAGAACAGTACATGGTGCATAG
EST25356 3b	95	C	G	...	...	TCTTTGATACAGGTAACCAGTTTGTAACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG[C/G]TATAAGTCAACATCAGGATTTCTTTTT
EST25356 3a	26	A	C	...	...	TCTTTGATACAGGTAACCAGTTTGT[A/C]ACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99	C	T	...	...	GGGTGACGCTCCAGAATGGGAGACAAGCCAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTTGATAATGATAGAACCCAA[C/T]TAGGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86	T	C	ATTCAACATT ACTACCAGTT ATTTGATAA	CGTCAATGTAA ATTGCGCCT	GGGTGACGCTCCAGAATGGGAGACAAGCCAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTTGATAA[T/C]GATAGAACCCAACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86	A	G	ACTTCCTTGTG TAAACACTCC	CATTCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAGAAGGCCTACT TCCTTGTGTGAAACACTCCC[A/G]TATTGTCGGATTTCTAGCTATAAGAATGGGCCCACTAAGTGGGTC

ID	Pos	A1	A2			Sequence
WI-17623	46	T	C	---	---	TGTGGTTTAATTTCCCATATAATTAATGGTGGCACATT[T/C]GCATGTGCTTACTGGGTC ATTCATATATCTTTTGTGAAGCATCGTCCAATCTTTGCCTGACTTGGAGTTTTTGGT
EST264191b	46	T	C	---	:::	ATTTCATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGA[T/C]GGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGGTAAATGTCATGGCTGGTTCGGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGGACAGAGAATG
EST264191a	35	C	A	ATACAAAGGC AACTATGTGC AG	CAAGAAGTTTG GACTGCCC	ATTTCATACAGAGATACAAAGGCAACTATGTGCAG[C/A]AACAATCTGATGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGGTAAATGTCATGGCTGGTTCGGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGGACAGAGAATG
EST267805	69	G	C	---	:::	TCAGCTTTAATTTAAGGGACATGTAAATAAAAAGATGCATTTGACAGGACAGCAGACTAGTTCAAGC AG[G/C]AGGTTAGACCAGTAACAACAACCAAGAAAGCAAAGTGCTCGTTTCCATCTCTGGCTTTACCA CACTTACAAACTGATACCC
EST269007	39	A	G	---	:::	TACTTCAGTTTAAGGCAAATTCCACACAGAGACTGTCTC[A/G]GAGACGGGCACAGAACCAGACACC GTAGAAACACCCACCACCATGCTCATGACGGGGAAGCAGAG
EST271521	101	C	T	---	:::	CAAAGGATTTTATTTGTTCCCTAAAAGTAAAATCTAGAAAAATAGCAACCCACTGCAAGAAGAGTT CTATACTAAAACATTTCAATCATTCTCTCTTC[C/T]TTCACATGGTGTACTCTTTCATGTACACAT CATCGGAAAACAGACTGA
EST275040a	33	G	A	GCACTTTGCAA CAATTTAATA ATTT	GCTGGTGTGAT GCTACTGTAAT G	TTTTTGCACTTTGCAACAATTTAATAATTTATC[G/A]CATTACAGTAGCATCATCACACCAGCAGTCAAT AATGCCACTTAGGCAAAGTCTTTCAGTATTTCTGTTACACATTCTGTTAACAAGAACCCATACATT GGTAAAATTCATTCT
EST276624	51	C	T	CACATTCTGTT CTCCAGTCTTG	GCTTATGTAAC C	TTATGGAAATG ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTCTGTTCTCCAGTCTTG[C/T]AGGTTACATAAG CCATTCCATAAATTCTATAGCCTTCTTCTTAGAGTAACACACTCTTGTTTGAGGAATGTTC
EST277883	100	A	G	---	:::	ATTTTATTAGGCGGTACAATTCCAAGGTGGTAAGGGTGAAAGGAAAGGCGAAGGCAGGCAAATACAT TATTGAGCTGAAAACAACTTTACATTCAAGGAC[A/G]GCTTCCAGACAAGCCATGTAGAACCAGCAT GCCTTGGGACTGTGTGGAT
EST278284	58	G	A	GGAAGTCATC AGAACCCCAC	TACTCCAAGTA C GTGCAGAGAGG	TCTTCTAAAACTTCCTTCTGTTGGATCCCAGTGACGTGGAAGTCATCAGAACCCCAC[G/A]GTACTT GGAGTACCTCTCTGCGACCAAGATAGCTGGCTGCTGATTTCTGCTCAGTCAGTCACAATTTTACTTGAA
WI-18369	58	G	A	AATAAATTTC AATCTGTCAC ACAATC	TCAAGAAGGCC TTATCCATTT	TAAAAATTTGAGATACATTCCCCAATGTAAACAATAAATTTCAATCTGTCACACAATC[G/A]AAATG GATAAGGCCTTCTTGACAAATTTCTGCCACCTCCGTTTAACGCATCAGAACTCAATCTTTATCTC
EST280364	37	T	C	---	:::	TCCCGCTTCCAAAAGCTTTATTGGCAAATAATATGCTCTA[T/C]AAAAGAATGATCAATCCTGTTGCCTCT AAGTCAATGGAATGAAGAGAGCGTGTCCAGGGACCACCACCGCCGTGCTGAAGGAGACTGCTGTGTGTG TCCACCTCTTATTCATAG

Clone	Pos	Allele 1	Allele 2	Flank a	Flank b	Flank c	Sequence
EST284837	31	T	A	TTAAA	GGAGTAAAAG GTGTTTCTTCT	TTTCTCGCATT TATTTTTATAC CA	CATTGGAGTAGTAAAAGGTGTTTCTTCTTAAA[T/A]ATGGTATAAAAATAAATGCGAGAAACATTAAC GGAGAATGTACAGACAACAGACGAAGAACATGAGTTGTTTCTGACTGTGACACATTGGTGAAA
WI-17724	50	T	C	TGTC		TGGGCCCTCCC TGTC	AGAATTGGTCTAGTAATCGTTCAGGATTCGGTGATGGCCCCTCCCTGTC[T/C]GGACACTGCCAACC CACAGCTGGAGGGGCACTTAAGGCACGTCATTTTTGTGATTAGA
WI-17730b	68	T	C	...			TGAGCCTGGGGAGAAAGACCACAGAAGTGAAGTGCTATTAGTTACATCATACCAAGTGTACATACTG T[T/C]CACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTAGTAGTGTGTCA
WI-17730a	39	A	C	ATT	GACCACAGAA GTGAAGTGCT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGGAGAAAGACCACAGAAGTGAAGTGCTATT[A/C]GTTACATCATACCAAGTGTACATA CTGTTCACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTGTGTCA
EST290415b	53	G	A	CA	GGAACAAACA CATTAAGCAT	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTCATGAGGAACAAACACATTAAGCATCATTGTCACT[G/A]GCTAACTCCT CAAATCAACAATACCCTTATTTTTAGCCATGAAAAC
EST291284	58	A	G	...		...	CTTTTAGAAGGACACCAGTCTTGTTGGACTTAGGGCCTACCCTATTCCAGCAGGTGCC[A/G]TTATTT TCACTTGGTTACGTCTGTGTAAGGACCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTTGCTGGGGACACT
EST299123	103	C	T	T	TCTGCCAGCTT TCATTCTTCTG	GCGTAAGTGTC	ATTTATTAGGTATCTGCGTGTTGGGGGTGGGGGTGGGGGAGATTGTTTGAGATACTGCAACAGACACAAA AGCAAGAAAGAAACATTTCTGCCAGCTTCACAGGCT[C/T]ACAGAAGAAATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST299368	121	G	C	...		...	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGAGTATTAAATCTTAAAAGTAACTCACCATGAAA TTAACCTTCTGTACTGGCTTCACTGATGAGGCAGTAAACTACATAGGGATAAA[G/C]AGCTCAGTA TCTGGAATCATGCTTCCTG
EST302232	99	A	G	...		...	AAATAAATACATGGGGAATGGGATATCCATCCCCTCAAGCATTTATTCTTATTCTTTGAGTTACAAGCAA TCCAATTACACTCTAAGTTATTTAATATTCC[A/G]GGATTTAATTTCTTCCTAGTTCAATCTTGGGA GG
WI-16260b	86	G	A	...		...	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAGACCAGA GTTCACAATAGGTAGC[G/A]ATAACCAGGTCTCACTTCCCGTGAGAACTTCGTGGGAC
WI-16260a	59	G	T	A	TGAGGTGGATT CAAGAGAAAA	CTACCTATATT GTGAAACTCTG GGT	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAA[G/T]ACCC AGAGTTTCACAATATAGGTAGCGATAACCAGGTCTCACTTTCCCGTGAGAACTTCGTGGGAC
WI-17835	30	G	A	TG	ACAGGAAATA TTGTGCTTTCT	TGGGGTATAGG AAACAGGC	AAGAGAAAACAGGAAATATTGTGCTTTCTTG[G/A]GCCTGTTCTATAAATGTTCAGCTTCAAATTCTTTGCTTAATCAATCCAAATGAATTACCTGAATT TTCTCCTCTTGTTCAAAA

ID					Full Sequence
EST31951 4	87	C T	GGGTTGTCCAG CCAACA	CCCACCAAAAT CACCTCC	ACAGCCATTTATTATGTTTACTTGGTAATATCAGAGACTGAAACATTTCACTCTTTTAGCAATGACA TCGGGTGTCCAGCCAACA[C/T]GGAGGTGATTTGGTGGGGAATTCTTATCACAATTATTCT
EST31968 8b	95	T G	---		CGAATTGTCTCTCTTATTTGTGATTCTAGTAATCCTAAAAGATTGGGGGGCGGGTTACTATAAGT GCATTTTATAAATGGGGGATTTTCTGCT[T/G]AACTGCCCACTGATTCTTACATGGGAAAGGTGCAAAG ACAGTGGTACTGCTCCC
EST31968 8a	75	T C T	GCGGGTTACTA TAAGTGCATTT .	TGTAAGAATCA GTGGGCAGTT	CGAATTGTCTCTCTTATTTGTGATTCTAGTAATCCTAAAAGATTGGGGGGCGGGTTACTATAAGT GCATTTT[T/C]ATAATGGGGGATTTTCTGCTTAACTGCCCACTGATTCTTACATGGGAAAGGTGCAAAG ACAGTGGTACTGCTCCC
EST32063 2	103	C T	---	---	TCCATGGATGAACAGACGCTACCATGCCACATCCCCACTTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCCCTTCCAGACCTAGCTGGCTTTGTAGT[C/T]GTTCAGGCCCATTGAAAATAGCAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65	A G	---		AAGGCTTCCAAGCATTCAAAGGCACTTGGGTGTTGTGCTCTAAGTTTCTGGTCACTGCAGCCCC[A/G] [TCTGTATTAGGGAGCACCCCAAGCCCAGTAACAATATGGTTCTTGCAG
WI-17800	29	C G	TTTCCTACAAT TAATCCCAGTC TT	GGGAGCACAA GAGAAACTCA	TGGACACATGGGAGCAGCACAAGAGAGAAACTCACT[C/G]AAGACTGGGATTAATTGTAGGAAATATTCACAG TTTCCACAAGTCAGAGAGAGCTAATCCCAACCCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34	T G C	CCTAAAGTCTG GGATGACTTTC C	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCATTCCTAAAGTCTGGGATGACTTTCCT[T/G]ATTCTACATCAAGTAGAACCTAAGCCAAT TCAGAATCAGAATCCTTTTGTCCATCAAATTCCAGCTAACTCCAAGCTGAATTAAATGTTCATTCT
WI-17860	121	T A	TTTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGAACAAAATCTTTA TAGTGTCCAAAGATAATTAATTCTTGGTTTAAATCTTGCCAGCAAAGCAAATA[T/A]CCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17866	43	A T	TTTTATAGCCT ACTTCTCAAA ATTGTT	CAGCAACCTTTTTTGTTTATAGCCTACTTCTCAAAATTGTT[A/T][T/T]TGTGTGATTAGTGACAACG GGGGAATCTACACATGCTCACATCAAGTAAACTACCA
EST33301 4c	80	G A	---		GAAAAAAAGTCAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCTCCACACAAGCATGATC AATCGCCACGAGA[G/A]ACTGGATGCCAAAGAGTATGG
EST33301 4b	63	G A	---		GAAAAAAAAGTCAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCTCCACACAAGCAT[G/A] ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	44	G A	AGCGTGGTTTT CAATACTAAA CA	CTGTATTATT GTTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTGCAGCGTGGTTTTCAATACTAAACA[G/A][A/T]GTAAACAATGCAAATATT TAACAATAAATACAGTGATTAAATAAGCCATGGCATATCCAGTTGATGTAATACTTTGCAA

Marker	Pos	A1	A2	5′	3′	Sequence
WI-17904	50	A	G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAATGAACACA[A/G]TACGGGAATTAC TATTAACATAAGCGGATAACATCAAAACATCTGGTAAAATGCAGTAAAACAACAACAAATGA
EST341495	69	A	G	TGCCAAATAC TCAAGTGTGA GAT	AACTACTAGCG CG	GTTTTTCTTGAGTGACACAAGCTTGTTGTTCATTTTGAGAAAAATGTGTGCCAAATACTCAAGTGTGAA T[A/G]GATTTTATTAGTTGTTCTCGCTAGTAGTTTTGGTATTCTATGAAAAAAAGCAGCTAGTTCAGC TTACAAATCACACAAGT
EST343438	95	C	A	---	---	TGGGAAAACATAAGTTAACTCAAGAATATATTCCAGTCTCTTATGTTGTTACTAAAACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCT[C/A]TACAAAGATTAAAGAAACTTACCATCAAACACTTC CAGTGCATCAA
WI-17982	98	C	T	GGACCATG ATATATAACT CCTAAAAGC	CAGAAATTATG TGATAATAACT CCTTCC	GGTACACAATTTAATGGAAGGAACCACACAGGTATGTTGAAAGAACATCAGTCAGTACAGCTGGAGACAGG GAGGGACCATATAACTCCTAAAAGC[C/T]GGAAGGAGTTATTATCACATAATTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17993	118	A	C	---	---	CTCAGTAACTCCGGTGTATAATCTGCCATTTATTGATTTATTTATGATAAAACAACCTCTCATTGTGA AAAACAGCTAAGGGTGACATCTCCAGACCCAACCACTGTCCCTGTAATGT[A/C]CTGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17996	84	A	G	GTAGAGGCGA AGGGAACAG CAGC	AGGCACATGGG CAGC	CCCATCCAGAAACCCCAGTGTGATGGTGGAAGCAGCATGAAAÁCAACATCTCCCAGGCCTCGCCAGT AGAGGCGAAGGGAACAG[A/G]GCTGCCCATGTGCTGTCTCTAAAGACGCCACCCTCAGGTTGATGT CACCTGTGGGAGACCGGGT
WI-17136	33	C	G	---	---	ATTCTTTATAAAAACACCATGTCCCTAAAATGT[C/G]ATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAAGACAGAGAAATGTGTCCT
WI-18041	24	A	C	---	---	GCCACTGAAAAAAAGGTGCTCTTCC[A/C]GTTCTAACTCCCTGGACTCCCTCATTGGAACTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTAAAAGGCAGTGTTGATGCTCCAGGAT TCAAATACTTAATCA
EST351648a	57	A	G	CACAGCCCTGC CCCC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCTTCAAGCACAGCCCTGCCCCCC[A/G]TCTTGA GATTCAGAATCTCAAGAGGGTGCTCAGTCCTTGGTTAGGTGCTTCTGTGACATTTCCTCTTG
WI-18052b	67	A	G	---	---	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTTCTTTCATGTACGAATCTTGGTTACACATCTTAG[A/G]ACAGCAGAATCTTCATTGTTGTTTAATGTCGTATGCCTGCTCAGCACAGTGCTGGC ATGGCCCATCCATGCTTT
WI-18052a	50	T	C	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTTCTTTCATGTACGAATC[T/C]TGGTTACACATCTT AGAACAGCAGAATCTTCATTGTTGTTTAATGTCGTATGCCTGCTCAGCACAGTGCTGGC ATGGCCCATCCATGCTTT
WI-18054	46	G	A	GGGAGTGGGG GAGTAAAA	CGTCACCCTGC TTCCA	CTGTTGTGCTGAGAACAGAAGGGGTCAAGGGAGTGGGGGAGTAAAA[G/A]TGGAAGCAGAGGGTGACG CATGCAGGAGTCCAGAACGAAAGACGCAAAGACGGGTGATTTGCTCAGGTTGGTAGCAACAGAGGTAATG

ID	Pos	A1	A2	Flank A	Flank B	Flank C	Sequence
WI-18064	54	G	A	AGA	GTAGCTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAACCCTGTGGGTAGCTGCTAAGCTGTATTCAGA[G/A]GAATGTCAC AATCATACCACTGGGGAGAAAGAGTAAGCACAGTGTGCTTATTAGGTGCCAAACTGGGTACCTGGGAG GCAGAAA
EST35347 2	97	T	C	AA	GCATAAAATT TCCAGTTGGT	CCCTCGGCACC TGCT	TTTAGCACCATTCTTAGTGGAGCAGGATTCTTGATCATGGGGTGGAATTTGTGTATCTGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAG[T/C]AGCAGGTGCCGAGGGTCTGGATCAGAAAAAAAGG CAGGCA
WI-18070	28	A	C	AACCCACTAC TTACTCAGAGT GTGTAT	AAAACTAATA AGAAACTGGA GGTTTTT		AAACCCACTACTTACTCAGAGTGTGTAT[A/C]ATATTAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTTCTTATTAGTTTTGATATTTTCTGTACTCAGAAGCATTTAGGTTGCAAAGGATATAA
WI-18080c	80	C	T	...	...		TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTGTAATTAAAATCTACTATGCCGTG TTTGACTTTTAT[C/T]TCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTGGTGTAT
WI-18080b	65	G	A	...	...		TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTGTAATTAAAATCTACTATGCC[G/ A]TGTTTGACTTTTATCTCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTGGTGTAT
WI-18080a	41	T	C	GCAAATATCA ATATCAAACT AGTCTCTC	CAATTTACATA AGAGATAAAA GTCAAACA		TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCT[T/C]TTGTAATTAAAATCTACTATGC CGTGTTTGACTTTTATCTCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTGGTGTAT
WI-18086	63	G	A	...	...		GTGGGCATCCTATAAAAGCAGCCATGTGTTGAAACAAATGATATGCACAGAAAGCATACTTCT[G/A] TGGCTTTGTTACACGGGTTTCTTTCAAGAGGAAGATGACTCAGCCCTCCCAGCTCTGCAGTCTAGC TTAGGGAGAGGTGTTTGAA
WI-18115b	71	C	T	...	...		AACTACATAGTATGGTGCCTGCCTTAGAATCAATGGGTAAAAGCCTTTAGTGTACCTTTGGTATTCCC TTC[C/T]TTTGGTATGAAAGACACCTCTGCTGGAGGACTCATTACACATGTAAAGAAAGGGGTGAG TCAGT
WI-18115a	70	C	T	TTAGTGTACCT TTGGTATTCCC TTTCATACCAA A	AGAGGTCTGTC		AACTACATAGTATGGTGCCTGCCTTAGAATCAATGGGTAAAAGCCTTTAGTGTACCTTTGGTATTCCC TTT[C/T]TTTGGTATGAAAGACACCTCTGCTGGAGGACTCATTACACATGTAAAGAAAGGGGTGAG TCAGT
WI-18136	78	A	G	...	...		TTTTGAGAAGCACTCTGTAAGGCAAGGATGCATTCAAAAAATGGCTTTGAGGATTAATCTTCTCTTTA GGTAATTTGC[A/G]TAAGAAGAACAATAAAAGCATTTTAAAAGTCCACTGCCGCCTTAGAAACT
WI-18169	115	A	G	GAAGCTC	CCATCTTCCG GAGTTCTGCTT GTGCTCCA		GGCAAAATATTTTTACATCACACCTGGAATCTGCCCAAGTCTTTCCGGAATGAATGCGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAAGCAGCCATCTTCCGGAAGCTC[A/G]TTGGAGCACAAGCAGA ACTCGGTGGGTAGAGTGGA
WI-18190b	26	G	A	...			TGAAAGAAGTCGCACACAGCGGACACTTG[G/A]TCATAAGTGGAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGAGAGGGACAAAATCAAGAATCAAGAGAGCTGGAGACATTAATCCTGGCGA

Marker	No.	Allele 1	Allele 2	Seq A	Seq B	Consensus sequence
WI-18190	62	G	A	...		TGAAAGAAGTCGACACAGCGGCGGACACTGTCATAAGTGGAACAAAGGATGGAAGCTAATCATGGA[G/A]GCAAGCTCCCTGGAGAGAGAGGGACAGGGACAAAATCAAGAATCAAGAGCTGGAGACATTAATCCTGGCGA
WI-18181	100	A	C	CGTTTTACCAT TTGTTAAGCTT TTG	AAATATATAC AACACTCCCTT CAGATC	GACAGTGAAAACATTGAAAAACACAACAACAAAATACAACAACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAAACGTA TGTGTGAAAAATATATACAACAACTCCCTTCAGATC[A/C] TGTGTTCTTGAAC
WI-18215	78	G	A	CCTCCCTCTCT CCCCC	AGCAGAGTTC CTGCCCTC	ATTCATACAAGCATTTCCTGAGTACAAACTAGGGACACAGGTATTTCACAAAACAAATAGAGCAGA GTTCCTGCCCTC[G/A]GTGTGCGGGGGGGAGAGAGGGGATTCAGCATTTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18232	60	T	A	AAATAAAGGT TTTCAGGGGTT C	TGGTGTTGATT GTGATACACTT AA	CATTTCCGAAAATCTGATAGTTAAAATATCCGTCTGGTGTTGATTGTGATACACTTAAG[T/A]GAA CCCCTGAAAACCTTTATTTGAAGTTTTTGCTCAGAAACTGGGCAGAACTTTTCACATTCTG AC
WI-17892	76	T	C	CACAGAAGTG AATAGACTAGT GAGACA	GGAAAACTTG AGTTTGGAGATC CACA	TTTAAAAATGCTTAGATTTCCTCAGTATTTTATCAATAGTGTGTAAGCTGGAAAACTTGAGTTTGAG ATCACATAT[T/C]CTGTCTCCACTAGTCTATTCACTCTGTGTGGGCATTTCGGCAGAAGTGGC
WI-18242	30	G	A	GCTAACACTTC CCCCAAATGTT TACTGTAACAG CTTTC	AATCGTAACA	AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTGAAGTGTTAGCAAAAT TGGATGCCACAACTATCTCACCATTCCTTCAAGCAAGTGAGGGTCAGAATGTTTCTTGCCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119	C	T	...		GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAATTGAAAAGTGTTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATCCACAAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124	T	C	...		GCATCAGACATCACCACTCCTGAAAAAAACCTTCTACAAGAATTGAAAAGTGTTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATCCACACAT[T/C]CGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97	C	T	TTCATGCATCA TTTGTGCA	AAATAGGAAA TATGGACTATC TTCAAA	GCATCAGACATCACCACTCCTGAAAAAAACCTTCTACAAGAATTGAAAAGTGTTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGCACAAATGATGCATGAATCCACATTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73	A	G	GGAGAAAAGG GAGCAGAAGA	GCTGTCAGCTA TTGTTATTTCA AA	CTGAGCCTCTTGGATATGTGGTTTAGTGTCTATCATTAATTTGGAAAGCTGTCTCAGCTATTGTTATTC AAAT[A/G]TATA
WI-18330b	66	A	G	...		AAACATCTCACAGCTGTCTTAGGCCATCCTGTAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGGG[A/G]TATGTAGGCAGTGAGTCAGGACTATGCAAAAATCCATAAAATAAAGAACATAATTTTTGTTGAT TCACA

Clone	Pos			Flank	Sequence
WI-18330a	49	G	A	AAGA	AAACATCTACAGCTGTCTTAGGCCATCCTGTGTAAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGAGGGATATGTAGGCAGTGAGTGCAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTTGTTGATTCACA
				TCCTGTGTAAGA AATCAGGGAT AGTCCTGACTC ACTGCCTACA	
EST375645	85	T	C	AGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAATACTGCATGTTATTTAAGCTAAAATTC AAGCCATCTACAAAGAT[T/C]TCTCATTGAGGCCTCCATAGCTGCAAACACATCAAAGGCATTAC TGTACTGGAGAGGACTGAG
				AAATTCAAGC CATCTACAAA CTATGGAGGCC TCAATGAGA	
WI-18327	104	G	A	TT	CAAAGGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGCAGTTTCCCAAAGCAGTACCTC CCAAAACAATGGTGAAAACAGCTTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATGCGGGAGGCAGA GT
				AAACAGCTTT CGTTAGGCTAG CGCATACAATG GCTCAGC	
EST37626b	102	G	A	---	GTGGCAAGAGCAGCTAAAACACACTCATTTGCATGAACTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCCTCTGCGCTGCTCTCTGGACG[G/A]TTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCATTCC
EST37626a	58	C	T	---	GTGGCAAGAGCAGCTAAAACACTCATTTTGCATGAACTCCAAATACGAACAGTGCA[C/T]GCTGA TGGCCTGCAGTCCTCTGCGCTGCTCTCTGGACGCGTTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCATTCC
WI-18357	89	C	G	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAAAGTCCTACCGTGCTGAGGTGGCCATGAAGCCAAGCCCATGGAGAGACATTTCAGA TAATCCCAGCCCCTTAGCATCAA[C/G]TCATCTTCAGTCTTTGAGTCGTCCTTCCAGCCCAGGTCCAAGCTT GTGGACCAGAGACAAGCC
				CCCAGCCCCTTA GCATCAA	
WI-18012g	117	A	G	---	TTTTATCTGGGTCAGCTCCTCTTAATGGCCTGAAGGTCATCTCCTTTCAACTTCCAGACTTGGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCTTCGTGAG[A/G]TGTTCCTGATACA CGCTGACGTTCGAGGG
WI-18012f	113	G	A	---	TTTTATCTGGGTCAGCTCCTCTTAATGGCCTGAAGGTCATCTCCTTTCAACTTCCAGACTTGGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCTTC[G/A]TGAAGTGTTCCTGATACA CGCTGACGTTCGAGGG
WI-18012e	112	C	T	GCCACTTTTGC CCCTT	TTTTATCTGGGTCAGCTCCTCTTAATGGCCTGAAGGTCATCTCCTTTCAACTTCCAGACTTGGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCTT[C/T]GTGAAGTGTTCCTGATACA CGCTGACGTTCGAGGG
				TCAGCGGTGTAT CAGGAAACA	
WI-18012b	46	T	C	---	TTTTATCTGGGTCAGCTCCTCAGCTCCTCTTAATGGCCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTGGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCTTC[C/T]GTGAAGTGTTCCTGATACAC GCTGACGTTCGAGGG
EST383904	75	A	G	GCAAAAAGGA CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCCAGAGTAATTCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTGT[T/A/G]ATTAAGTTTATTAATCAGCTGACTTTAGCTGGAGATTATTCTGGAT
				GCTAAAGTCAG	

EST	Pos					Sequence
EST38512 7	91	T	G	TGACGATGCC AATACTTCG GGGAAGC	CACTGCACTCT	TAATAAAAACTGACCCAATTGGTAAACTGTGTCTGGACTGAGAGAAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACTTCG[T/G]GCTTCCCAGAGTGCAGTGATAACTGTTATAGCC
EST38519 0	24	C	T	CCTGCACCTCC TAAAAGATCT T	TCTGTTAGGAC TTGGGGGA	CCTGCACCTCCTAAAAGATCTTTT[C/T]TCCCCAAGTCCTAACAGAATGGTATATTCCTCTGGAAAA AGATGAACGTCATCAATGGATTGTGCTGCTCTCGTTTCAGCTTGATTTTTGTCCTTGAGAACCTTG TCCTCCCTGCTGATTT
EST38575 1	66	T	C	GAACATCCCA TGTTTCTGTTT AA	AGGGAAGGTA GTATAACACAT AAGAGA	AGTGGTCAAATGTAAAACTAATGGGAACACCAAGCCTCAGGAAGAAGAACATCCCATGTTTCTGTTTAA] T[C/G]TCTCTTATGTGTTATACTACCTTCCCTTTCTCTTCTTATACACATAGATTTTCCTTAATTGCAGC CCA
EST38616 9	101	C	G	CCTGCTCCGCC CTTC	GAGGAATGGAT GGTGGC	CCATCTAGGCAGGCTACCTGAGCTCTCTGTGCTCCCAGAGTGGGTGCCTCACGCCCGGGGCCCCGGTGG AGTCTCCGCGGCCCGCCCTGCTCCGCCCTTC[C/G]GCCACCATCCATTCCTCCAGGGG
EST38652 8	59	T	C	TCTGAACTGGG CATTTCAA	TTGCAAAAATG AAAGGAAAAA	TATAGTAGGTACTTTCCTTGCTGCAGCAGGAATTATTCAGTCTGAACTGGGCATTTCAA[T/C]GCGTG GTATTTTTTTCCTTTCATTTTTGCAAGTAAAAAAATCAT
EST38654 5	42	T	C	AATGGTCATTT TAATATATCA GTTTTACA	CAGTGATGGTC CTTAATCTTCT ATC	CTCAAGCTGAGAAATGGTCATTTAATATATCAGTTTTACATA[T/C]AGATAGAAGATTAAGGACCAT CACTGAGGTCACATAGCTCAGAGGCAGAGTTAAGATTTGGACCCAGGCAGGTTGGTTCCAGCATATA
EST38707 9	75	A	G	---	---	GGATCCTCACTCACCTGGGACAGCCTGAGAAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTTCCC[A/G]AGGCCAGCGGGATGGTGTGCCCCTGCTCCCTCTCTTCAGGAACACGAGG ATTCTTGCTTTCTGGAAA
EST38759 2	86	A	G	TGTCTCCCTGA GGGTGATATGG GACTTAAGG	TCACCATCGTG TAGCAGCACC	TGACCTTGTATTCTTCACTAGAGGGGGAGAAGAATCACCTACCTTTTGGATGCCTCCCACTCTACTTGT CTCCCTGAGGGTGATATGG[A/G]CCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAAATTCTTGCC
EST38775 1	40	T	C	AATCAATAGG AGAGGATTGG C	GGCTTTGCTCT GAATTCAAA	GACTCTCAACCAAAGAGAAAATCAATAGGAGAGAGGATTGGC[T/A]TTTGAATTCAGAGCAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCTTCCAAATGCCCCTTTCATGAGTTAGGATCTCCTAAGTGGTAC AAACAAACCAACATGGTGG
EST38815 4	91	C	A	TGTTTATGAGA ACCCATTACA CA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTTCACTTATGTGTTCATTCAACAAG TGTTTATGAGAACCCATTACACACA[C/A]AAAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38858 4	98	C	T	CACGAGTAAA AAGAAACTCA TGAC	GGAGCGGAGTCC AAGGAGAA	TCTTTACTGTGCTTACAACTTCCTCCAAGTTTGCGGTGGTTCCATATTGTTATTGTTATTA TTCAACACGAGTAAAAAGAAACTCATGAC[C/T]TTCTCCTTGGACTGCTCCTAAGTGGTAC ACCGACTGCCACTGTTG
EST38865 2	72	T	C	GCTGTGTAGAATT CTGTGTCGATGC AGGACACAG	GGAAGGACGG	CCTTAATGGATTTTACAGCTCATCTGAGTCTGCTGTGTTCTGTGAGGAGCTGTGAGAATTTGTGTCG ATGC[T/C]CTGTGTCCTGCGTCCTTCCCCAAATGAGCACATATGCAGGGCAGGCAGGAGCATGCTGGA TTTGTCTTAGTTGTTAA

EST38878 9	47	T	C	CCTTCAATAAA TCTCATGTCCT CA	AAACATCATT ACTAGCCTAG ATCCTAA	CCAATGAGAACCAAGTAATTAAAACATCATTACTAGCCTAGATCCTAA[t/C]CTGAGGACACATGAGATTT ATTGAAGGGAAATCCTCAATTAATATGAACACATTCTTTATTTATTTGTTTCACTTCTCAAATATCGGATTGTTGC
EST38882 6b	113	G	C	...	...	TTATTCAATGTCATCTCACACATTCTTTATTTTTA[t/C]TTGTTTCACTTCTCAAATATCGGATTGT TCATGAGAATAATGGCTGAGGGAGCTGGCACGGCAGTCTTCTCA[G/C]GCTCCCTGGATAGCTAAAT TTA
EST38882 6a	35	T	C	TGTCATCTCAC ACATTCTTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	TTATTCAATGTCATCTCACACATTCTTTATTTTTA[t/C]TTGTTTCACTTCTCAAATATCGGATTGT TGCTCATGAGAATAATGGCTGAGGGAGCTGGCACGGCAGTCTTCTCAGGCTCCCTGGATAGCTAAATT TA
EST38909 5	47	A	G	GCACAGCATG GCTAAAAACG	GGTATTGTTG ATTCCCATCTT T	GCACTAAACTAACTTTCATTGTGGATTGCACAGCATGGCTAAAACG[A/G]TAAAGATGGGAATCAA CAAATACCATTGAAGATATGGAGCAAAGAGAACTCTCACATACTGCTGGAGGGAATATAAATT
EST38911 9	85	A	G	ACTTATAAACCT GAAACAAGCG	TGTTGTTTGT CAC	AACTGAATGGCAGTGAAAACACTACACATCAAAACTTAGGGAAATGTGGTTAGTGTGGTACGTTGAG GGAAACTTATAAACCTCAC[A/G]GCGCCTTGTTCACAAACAACAGACAACAGAGAATTCCAACTC CAGCAATGACAGAGGCTAGGG
EST38955 5	30	G	C	TGAATTCCCTT GGTTGGG	CACTGCAATCT CACCCCC	TAAACATTCCCATTGAATTCCCTTGGTGGG[G/C]GGGGGGGGGTGAGATTGCAGTGCTCAAGATAAA TATCCACAAATATATCAAAAACTTCAAATTGTCTATGCATTCACACACTGACACTGAGCCACAAACATT CCTTTCACAGGGACTGTAC
EST39002 0	42	G	A	GGACCCTTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCTGGGCAGATCCCGGACCCTTCGGTGACC[G/A]CAGGCTCCCTGCCAGGGCTTGG CCCCTGACCGGCGGTCGGCCCCCAGCTGTGGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79	T	G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGGC	CACGTGGCCCCCTAAGTTTCCGGGTCTTCCTCCAGTCTGGATGGCTGTGTGTGGAAAAAGCTTGGTGGTAAG GCCTAAGGAAT[T/G]AGGGGCAGGGGGCGATGCCGCCGAGATGGTCCTGTAAGCCTGTGTGGGTC AAAGACCTAACTTCTGGA
WI-16398	90	T	C	TCCCTATTATT CCATGATATTT TCA	GAATGGTTTGT GAAAAATATA TTGATAT	AAAGATAAATGTCATCACAACGCAACATAGAAAATAAAGAAAATAAAGTATCCACCTAAAAT CCCTATTATTCCATGATATTTCA[t/C]AGCAACTAGTATATTTTCACAAACCAT TCAGTTACAC
WI-16403	69	T	C	CCTTTGTCCTC AATTTTTAAC ACT	TAAGGGCTAAT TCCCTATATAA AAAG	GGTTGTCTTCATGTATTTTTCATTCCTATCAGGTTCTGGTCCTTGTCCTCAATTTTTAACACT[T/C]CTTTTTATATAGGGAATTAGCCCTTAAACTGTGGTACTGCTGCCAAATTTCCTCCCAGTT
WI-16406	24	C T		GCTTTAATGGC TACAGAAAGA AGG	CCAGAACCAG ATGTGTTTAAA AA	GCTTTAATGGCTACAGAAAGAAGG[C/T]GGTTTTATTTTCTTTTTAAACACATCTGGTTCTCTGGCAGC AAGTTATATATGCATTTAGAGCAATAGGTGCCCTGAA

ID	Pos					Sequence
EST392360b	57	C	G	GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCATCTGAGA ATAAACTTCCT / TCCTTTTATTCATGATGATTTGTTCATCTGAGAATAAACTTCCTGTCTCTAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGTCTC TTT
EST392944	63	G	T	GGATGCC	GCACAATTAA ACATAGTACCG / CCTGAAACAG	CAAACAGACCTTTGGTTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGGATGCC[G/T] TTCTCGGTACTATGTTTAATTGTGCTGAGCCAGCAACCCTGAGTTACCGGCCTTTACCCCACGCC
EST393662	72	T	C	GGATAA	AGAA	AGCTCTGCTTGTCTGCAT / AGAAAACATTCTGTCTGATCAGAGAGGAAGATGTATGTAGAAAAATCAGAATCTGACTGAATTCCTAAA ATCTATT[T/C]ACACTGAGAGGAAAAATGGAAAAGAAAAATGTTGCATAAAGCTTTTCCCTGACTCTCA GAGGGGTTCAGA
EST393719	86	A	G	GCGTGAGAGG / CATTTGGATTA ATTTCACATTT TT	TGATTTGAGAC / AAAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTTATGTGTGTAAATTCCCAGTTGAGCCATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAAATGTGAAATGTCTCAAATCAAATGCTTCCTTCTAAAGATTA GACATTGCCCAACCCTGC
WI-17177	23	A	G	---	---	ACAAGTGACATATCCAACCAACC[A/G]TCCATCCCCACCTGTGCCCTATTCTTTCTTTGTGTTCTTT AGAGCCCTTTTCAGCTATTTCCTGTGAAGCAAAACTGCACGAAGGCCTCCCCGTACTCCTCCCCCTGGAA G
EST394288	31	C	T	AITTTTGATT / GCTCCCCACA AGCCACC	GGTCCCTTATG / AGGTTCCTGGTTGCTCCCCACAATTTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTCTGCATT TTCTGGGTGGGGCCTAGGTAATTCTGTTGCCCTTTGGTCCCACAGAGCACAATTAAAGAGATCAGGTCT GGCTGTTGC
EST394302	45	A	C	TAACTGATGTT C	GGCAGAGGAA CAGGGGTCGGG GTATTG	AATTTAGCAGAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTTC[A/C]CAATACCCGACCCCTGA CCCAGTACCTTCCCTGGGACTTTCCCTGCAGGCCCAGGCTCCGGTGGAGGAAGTCCGGTGGAGGATGTCCTGGG
EST394467b	117	C	T	GAGTAA	TCCTGGAAAAC TGACATAAACC	AAAGCCCTGTAAACTGAAGCTAGAACAAGTCAACTTTGGAAGAAAAATAACAGGAACCTATTTATAT ACGTAAATCACTTTCATACCTGCCTACTGACATAGGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCCC
EST394652	80	A	G	GGGTGGC	CAATCTCGGCC CCTCT	ATGGTGTCATTAGAGGGGCCACAGGGGATGGGGGAGTAAAAAATAACATAAACGAACTGAACAGAAA TGCAGGAGGGGTGGGC[A/G]GAGAGGGGCCGAGATTGGGGTGTTCAGGGCGCAGAGAGGTGGAAGACCAG
EST395010	81	A	G	AACATTAG	AAAGATTCCT GTAGACATCT CACTTGCAATT CTGAAGGCT	TGCTTACAAACCCATAACCATAGGCCATGTGTTCAGACATTCTTGACCAAGCCTAAAGATTCCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAATTGCAAGTGCAAGTTCAAGTCAAGTCAAGTCAAGCCAATTC
WI-18387b	84	A	C	---	---	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCATACATTTGTGGTCA CATGCTTTAGCCATAC[A/C]CATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAATGTGCGATG GCTATGTAGAGACATAAAGA

Marker	Pos	A1	A2	Flank 1	Flank 2	Sequence
WI-18387a	57	A	G	CCTTACTTTGG	GCTAAAGCATG	CACAAAAATGGGACTGCTGAAGAGTGGACCTTACTTTGGTGACCCATAC[A/G]TTGTG GTCACACATGCTTAGCCATACACAGTGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAATGTGCGATG GCTATGTAGACATAAAGA
EST406019	78	A	G	TGACCCCAT	GCGTGGAACCT GAAACAC	TCCCAGGATGGTTTATTCCAAAGCTGTGGACGGTGAACATTAAGACGAAAGAGAGTGACTCGCGTGGA ACCTGAAACAC[A/G]GACGCCTTTCTTCCAAGAAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32	A	G	AGTGTATCAC ATCTTCAGGAT AGGT	GCACACCCTTC ACACTGTTA	TCCATTCAGTGTATCACATCTTCAGGATAGGT[A/G]ATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTGAGTAGAGGAGTCTTCCCGAGAGTAGCAGTGTTGA
EST43091	28	C	T	CATTCTGGTCT TTATTTTGGA CTA	AAAACTGATTT GTTAAAACATG CTAC	ATGTCATTCTGGTCTTTATTTTGGACA[C/T]GTAGCATGTTTAACAAATCAGTTTTCATAGGCAA CCTTTTGAAACATCAAAAGAAATACAAATATATTTCACAAATTTCTCATCACTGTAAATTCA
WI-18420c	108	T	C	TTCCATTAAAC AGGAAGTTTC C	AAATTCTCAGC ATTGCTATAAG C	AGAGAGACAACAAGAAGAATAAGGGAAGAACAGAGTGAAATTAAAGCAAATCTTGGA TTCAGATTCCATTAAACAGGAAGTTCCTCAAAAAAAATCAAA[T/C]GCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38	C	T	GAATAAGGGA AAATGGGGAAG TC	CCAAGATTTGC TTTAATTTCAC AA	AGAGAGACAACAAGAAGAATAAGGGAAGAA[C/T]AGAGTGAAATTAAAGCAAATCTT GGATTCAGATTCCATTAAACAGGAAGTTCCTCAAAAAAATCAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101	T	C	...		AGCTGATCAGCTGTCGTGTTACTGTGTTTTATGTGGCCCAGGGAAGCCAAAAGATCAGACACCCTGTC CTAGACAGATTCAATGCACACAACAACAGGAGG[T/C]GGGGGGTCACACGGGCGGGAGAGCCAAAGAC TAGGGC
WI-18425	81	A	C	CACCCTGTCCT AGACAGATTC A	CCTCCTGTTGT TGTGTGCA A	AGCTGATCAGCTGTCGTGTTACTGTGTTTTATGTGGCCCAGGGAAGCCAAAAGATCAGACACCCTGTC CTAGACAGATTCA[A/C]TGCACACAACAACAGGAGGTGGGGGTCACACGGGCGGGAGAGCCAAAGAC TAGGGC
WI-18449	129	C	T	CTTTTGGCTCT AAGTGGGACT	CTCCCCTGACT GTATCCAGA	AAATTGAGGTCCGGGTGGAACTATAAAAGGAAAGAGAAGTAATCAAGGGAGGCCAAAGTG GGAAGCTGTATTGCTGATCTAACGTGCTGTCCAGTTCCTTCTTTGGCTCTCAAGTGGGACTA[C/T]TTC TGGATACAGTCAGGGGAG
WI-18457	120	T	C	...		ATCGCTTCATTGAAGCCTGCTGCTTAATTTCTCTCAGTCAACTGGTGCCCCCAAGACATTATTTTATTCTT AAATGTCCAATATCTGCCTGATGTCTGTGTGCACATTGGGCCACAG[T/C]AAATAGGCTAAA AGGCAGTCCCACCTGCT
WI-18462	39	A	G	CCACAATGGC AGAGGTGA	TTTAGGGCTTTG AGATGGTTTCT	GGTGCTATAGCTGCTTGTACACCACAATGGCAGAGGTGA[A/G]TAGAAACCATCTCAAAGCCTAAAA TATTTACCATACACATCCCCTCACACAGCAAAGTTTGCTAATCTCGGGTTTAGGGACTCCATTGAG
WI-18476	60	C	T	GGTGGGGGTGC GTGACC	GCACGATGGGA GAGG	TGAGGACGTTGTGACAAGCTCCAGCAGGGGGTGGGGGTGCGAGGG[C/T]GGT CACTCCCCATCGTCGTCCCTGCCCCTCCACTCCACCACCTGGCCCACCACCTCTCCCAGTCCACGTTGAGGT

ID	Pos	Allele	Seq 1	Seq 2	Sequence
WI-18491	109	G / A	AACAAATGGT AGGTGGTATT AATACTATT	CGTGTGCATTT TCTTGTAATCC CGT	CTAATGAGATGAATACATGGAAGGCGTTTAGCACAGTGCCTAAAACACAGTAAGTAACCAACAAAT GGTAGGTGGTGGTATTAATAACTATTATTATTAAATCCCAGAATGAC[G/A]GGATTACAAGAAAAATGCACA
EST50757 b	79	C / T	GAGCTCGAGG CTGCTTCT	ACCCTTCACCC GCCC	AGCCCCCTCCACTCCACTCTGCTTCCACAAAGTCGGCTCCCGAGAGCTCGAGGCTGCTCTCTTTTATATT GTGCAGGGCC[C/T]GGGCGGGGGTGAAGGGTCAGAGA
WI-17675	103	T / C	GGACATTTGG ATGGTGACTT	GGGGAACCACC CAGG	GATCTTGGAAAGCACTAGAAACTAAACATCTTCACCAGGTGCTGAAGAAAAGTGTCTTCGTTTAAT TGCCAAGCAGGGGATGTGGACATTTGGATGGTGACTT[T/C]CCTGGGTGGTTCCCCATAGATTCACCAT TGCCCTCTAATGGTGTCTA
WI-16543	67	G / T	AGATAAACTA CATTTGGGTTT TGG	GATTCATCATT ACAGGGGACTT	GATCCATTACCTAGGGTAAAATTCTCCTGAATGTCAAACAAAGAGATAAACTACATTTGGGTTTTGG G[T/]AAGTCCCCTGTAATGATGAATCAAGAATCCTCAAGTCTGTCTTGCCACCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	C / G	GCCAAAAAGG TTGGGGAA	TTACTTTTGTA CCGACCAGCA	ATCTGAGAGTGGAAGAGTTCATCCCAAAACCATCTCCCCCTGACCCCCAGTCCATGGAAAAATTGTC TTCCACAAAACCGGTCCCTGGTGCCAAAAAGGTTGGGGAA[C/G]TGCTGGTCGGTACAAAAGTAATT G
WI-17690b	79	A / G	---	...	ACAACACATGTGAAAGAAGAGATATGTTGTCTTACTCACAGTGGAGGCATTTTCTAGCTGTGTGTTTGATTT GGCTTCCCTAT[A/G]GATTCAGGACCCATAAACTCTGTTCTCCACTCATCTGCTATGCTGCTG
WI-17690a	63	G / A	AGGCATTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCCTGAATC	ACAACATGTGAAAGAAGAGATATGTTGTCTTCTTACTCACAGTGGAGGCATTTTCTAGCTGTGTTT[G/A]A TTTGGCTTCCCTATAGATTCAGGACCCATAACTCTTGTTCTCCACTCATCTGCTATGCTGCTG
EST51717 b	128	C / T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAATCTCAGTGTCTAACTCATCATCCCAGATTATTCTGGGGAGAGGCAGGCGGAAGACAGTGAGCGAGTGTTCGAG TGGCAACATCACCCACTCGGTTTTCTGGGGGCC[C/T]GGCGTGGGCAGGCCACTGGGTTTACATTCTCTGT CTGGATTATTGCCTCAAA
EST51717 a	39	C / T	...	...	GATCCAATCTCAGTGTCTAACTCATCATCCCAGATTATT[C/T]TGAAGTGGAAACCACCCTCCGACCC CAATGGCAACATCACCCACTACCTGGTTTCTGGGGAGAGGCAGGCGGGAAGACAGCAGTGAGCGTGTTCGAG CTGGATTATTGCCTCAAA
EST53012	97	C / T	TGGTCACTTTG GGGGCC	GGCTCTGCCCA GGCC	TTTCCAGGTTGACAGGTTTATTCCACCCCCTTCATCCCATGGCCACCCCCAGGCAGGAGGAGGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGGCC[C/T]GGCGTGGGCAGAGCCCACTGGGTTTACATTCTCTGT GGGCAGGTGTGGACAC
EST53349	96	A / G	TGTTGAAAGC AGTCACAATG TAC	CATCTGGATAT CTTGTCACATT TT	AAACTGCAAATAACAAAACAAAACAGAAGTCCAAGAAAGGCTAAAGTCTAAGCTATAATTACACATG AGTATATGTTGAAAGCAGTCACAATGTAC[A/G]AAAATGTGACAAGATATCCAGATGTTTAA
EST53389	74	A / G	GGAGACCTGC AGAACTTAAA	GCCCTTTCTAA CAATAAATGCT C	TTTCGAAATGTCCTCCATGACTTGACGACTGAGAGCCAGCCAGCAGGAGGAGGAGAACT TAAAACAC[A/G]GAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAAATAGTTTTAACATGAAC ACATTAAAGGGAGATGGCC

EST	pos				flank		Sequence
EST53477	61	T	C	...			TTTGAGAGGTTGTGCAAAACTACTGTATTACAAAAAATGGCACAAAAGTGAATTCAACAGT[T/C]AATGCACATGCATACTTCATTCACACATTCTTCAACAACAAAAGGTATTCTAACTCTACAGAACTGAATATTAGCTTCAACGGCAGCTGTT
EST64622	91	T	C	CGAGATTTTCT TCTTTATTTTA TATTTTCA	A		GGGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAAACTCCCGAGATTTTCTTCTTTATTTTATATTTTCATTTTCATCCTAA[T/C]TTACTGAAGCCATTTCTTGGTTAACTTTAGA
EST67268 a	77	C	T	TGTGTATAGCA CATACTTCAGG C	ATGGGGTGGTG CCGC		CTCATCTTTATTAAATGCATCGTGTGTGTGTGTGTGTGTGTGTGTATAGCACATACTTCAGGC[C/T]TGCGGCACCACCCCATAGAGATGGTGAGGAAGTAACTTCTGCTTCATTGAAACTGTAGATCCATCGGGGA
EST78503 a	26	C	T	ACGACGCCGG CGAGT	GCATTTCCGCG GCAC		GAAATGCAGAACGACGCCGGCGGCGAGTT[C/T]GTGGACCTGTACGTGCCGCGGAAATGCTCCGTTAGCAATCGCATCATCGGTGCCAAGGACCACGCATCCATCCAGATGAA
EST80253	92	G	C	...			ATGCACTTTATTGGCTCCCAGGGAGTGGGATGCAGAGTCAGAGTGGACACGCGCAGGGGGCTGGTGTGGGGGACAAAGCGCCGCGGGCCTGCCCG[G/C]GACCCTGGTTCCCTGAGGACCAACGTGAATGGGGGCCCCACTGGAAAGATGCTTG
EST91254	73	T	G	...			TATTCTGTAGGGAGGAATAACCATGCTTGCTTATGGACTATCCATGGATAACTTGGTTTTTTGTTGTTGTTGTT[T/G]TTTTAATTATAAGGAATAATATGTGCTCATCATATATGTGACTTACGGAAACAGGTCACTGAATATACCTGG
EST91332	100	T	A	...			TCCAAACTGAAAGGAGGAGGGTGGGGAAAACAAAACGCATCATATGTAAAGCACTGAGTCCAGCCTGGCTCTTAGTAAGCATTTAATCACCTTCAAAAATTAA[T/A]TGTGACTTACGGAAACAGGTCACTGAATATTATT
EST91495 b	58	T	C	...			CTGACTCAAAAGACACTCCTGAAAGCAGGTCCATCCTGAGCAGCAGCTTGTATTACTT[T/C]ACAAGTCAGAACCTGTTATTAAGACGGACAGCTGGCATTTAAATCAGGCTGTGTCACACCCATCCTGGGTCTTTGTTCTGGCTCCTATGGTGCTGGCTGAGGATCTCAAAGACATTCCACCACATTGAATCTTAGGCTGGAGGACATTTTCGTATTCTTCAGTCAGGAATAGCACACTTCCTTCATGAAТAGCAGCTTTAGGG[A/G]TTATATCATGAGGTACAAATAAAGAGGCCCTCACC
EST91921	114	A	G	...			ATAGCCAAGATTTGGAAGCAACCGTGACCATCAACAGATGACTGGATAAATAAA[T/C]GTGGTACATGTACACTATGGAGTACTATTCAGCCATGAAAAAGTCTAAGATCTTGTCATTAGCAACAACATGGATGGAACTTGGGAACACTGT
EST92026 a	56	T	C	...			TTTCCATGAGGAATAAATTTGTGTTTATATAAAACCTG[C/T]AGATGAATATTTTTTTAACAGCATGATTCACAAATGCCAAAAACAATGCAAATGCCCTTCAACACATGAATGGATTAACAGACCGTGATACATGA
EST92040 b	38	C	T	...			GAGTCTTGCTATGTTCCCAGGATGGTCTTGAGCTCTGGTTCAAACAATCCTCCTTCCTAAGCCTCC[T/C]AAAGTGCCAGGATTATAGGTGTGAGTCACA
EST98276 c	69	T	C	...			

ID	Pos	A1	A2	Seq A	Seq B	Sequence
EST98276 b	61	A	C	...		GAGTCTTGCTATGTTTCCCAGGATGGTCTCCTGGTTCAAACAATCCTCCTTCCT[A/C]AGC CTCCTAAAGTGCCAGGATTATAGGTGTGAGTCACA
EST98276 a	22	A	C	GTCTTGCTATG TTTCCCAGG	AACCAGGAGCT CAAGACCA	GAGTCTTGCTATGTTTCCCAGG[A/C]TGGTCTTGAGCTCCTGGTTCAAACAATCCTCCTTCCTAAGC CTCCTAAAGTGCCAGGATTATAGGTGTGAGTCACA
EST98800	53	A	T	...	...	GCCTCCAGCTGCATGACTCCTAAGCCATCATTCGAAGATTTGGCTAATTG[A/T]TAGTCTTACAA AGGCAGTCTAGTTCACCAGGCAAGAAGGGGGTTTGTGTTGGGAAAGCGCTGCTATCTTTGTTCAAAC TGTAAAGCAAGTTCCTC
J02931	138	G	A	CAGCATTAGTC ACTTTGAAAT GTAA T	TTGGAATTGGT TGTAGTAGTACCAT T	AGAGGATAGAATACATGGAAACGCAAATGAGTATTTCGGAGCATGAAGACCCTGGAGTTCAAAAAA CTCTTGATATGACCTGTTATTACCATTCTGGTTTGACATCAGCATTAGTCACTTTGAAATG TAAC[G/A]AATGGTACTACAACCAATTCCAAGTTTTAATTTTAACACCATGGCACCTTTTGCACAT AACATGCTTTAG
L41680	88	G	A	GAGAAATCGA CTACCAGCTG A	TTTAGAGCACT TTGCAGGTATT T	GGATCCAAAACACGGCTGGGTTCAGCATCCACCAATGAACTGAAAGGTGAATAAAGGACGTTCATG AGAAATCGACTACCAGCTGAT[G/A]AAATACCTGCAAAGTGCTCTAAAAATTAAATATTTGACTTT AAGGGGTCCTAGTAAGTGCCACTTCCACTAAGAATACAGTTTGAATGTATAATCAGTAGTGTTTACAA GATCCAACAGTGCACTCA
M15796a	84	C	G	CAAATTTGTA CCTCTAAGTAC ATTG A	TTGGACTTTAT TCTTTAAACAA GCAGTTT	CTTTTCTGTCACCAAATTTGTACCTCTAAGTACATATGTAGATATTGTTTCTGTAAATAACCTATTT TTTTCTCTATTCTCT[C/G]CAATTTGTTTAAAGAATAAAGTCCAAAGTCTGATCTGGTCAGTTAAC CTAGAAGTATTTTGTCTCTTAGAAATACTGTGATTTTTATAATACAAAAGGGTCTTGACTCTAAAT GCAGTTT
M20472	103	C	T	GTTGAGTTCTT TTGGACCAAA C	ACAATGAACA ACTCTAAAGAC AAAAA	AGAGCCACCCTGTGGAAACACTACATCTGCAATATCTTAATCCTACTCAGTGAAGCTCTTCACAGTC ATTGGATTAATTATGTTGAGTTCTTTGGACCAAAC[C/T]TTTTTGTCTTTAGAGTTGTTCATTGTTTG TGATTGCATGTTCCTTCCTTCCTCAACTGTGTTCTCCCTGGCATTCAGAGAGGAGGAGGAGGAAGA
M32315b	129	T	C	GCCTCTGCTGC GGGACAC CATGG	GCCTTCCGAGA G	CCCTCTGACCTGCGCAGGCCAAGAGCGAGAGGCAGAGCGAGTTGGGGAAAGCCTCTGCCATGG[T/C]GT GTCCCCTCTCGGGAAGGCTGGCTGGGCATGCGGTTCGGGGCATGCTGGGGCAAGTCCCTGACTCTCTGT G
M33875a	131	C	T	GGTTACAGCTG GAGGTGTGT TTAT	ACCTTTGTTAA AATTTAGGTGG	TTCCCAGGAGGAGCAGCAAAGGGGCCTGCTGAGCTCTGGTTAGGTTACAGCTGGAGGTGTGTATATACA CACACACACGTGTATATACACATATATGTGTATATATATGTATATATATGGCTTT[C/T]C AATAACCACCTAAATTTTAACAAGGTTCCTTCAAGTGGTAGAAGCTTGGGGTGGTATTTTTACCTTC CTTCT
TIGR-A003M18 a	29	A	G	TTTTTGTAGAG ATGAGGTTTTC CT	GGCAGACGGAT CACTTGA	TGTCTTTTTGTAGAGATGAGGTTTTTCCT[A/G]TGTTGGCCAGGATGGTCTCGAACTCCTGACTTCAA GTGATCCGTCGCCTTGGCCTCCCAAAAGTGCTGGGATTATAG

ID	Pos	A1	A2	Flank	Sequence
TIGR-A003P30	117	C	G	---	ACAAGTTCAAAAGGAGAACTTCCTTGTTTAATGCAGCTGTGTCTCAGAGAGCCTGTGATTCCTAGGA AACCATCTGGGTTAGCCCATTAGAAAAATGCAGTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCTTGGAGATACT
TIGR-A004S34	156	C	T	CCAAACCTCCT CATTCCTATAAA A / TGTAAACAGCT AACTGTTTTTG TTAAA	GCTTGTCTTTATGTTTAGGTTCGGGGGAAAGGAAGGGGCTGACAACCGCAGACATCTGGACACCAGC AAGGGTCCAGGGGAGGTTGCAGAACTTCTTTGTCCTTGGCTAACAGTCTGTCATGTGACAATAGCCA AACCTCCTCATTCCTATAAA[C/T]CTTAACAAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTT TACATG
TIGR-A004T44b	97	A	C	---	AACAACAGTGTAATCTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCAAAATGAT TGAGTATGATAAAGAATTTGCATGGCGATT[A/C]AATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAAGAAACAATATGACTTAGCAAAGAAACAATATAG
TIGR-A004T44a	69	G	A	GGAAGATAAA CCAAAATGAT TGA	AACAACAGTGTAATCTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCAAAATGAT TGA[G/A]ATGATAAAGAATTTGCATGGCGATTAAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAAGAAACAATATGACTTAGCAAAGAAACAATATAG
TIGR-A004V08	60	T	C	CAGGAAAACA GGCCATTCTCTT	CCTACAATCCTATAATTGCAAGGGTTGGGAAGGATGCAGGAAAACAGGCATTCTCTT[A/T/C]GCC TTTTGTGGGAAGGATCAAТTGGGTGCATGGGGACAATTTGGGCAGTAGCTGTCAAATTTC AGTAGCTGTCAAATTTCAAA
TIGR-A004V26	125	A	G	---	TCTAGCTATAAGACCAGATTTAATATTCTAGATATAGAATTATCCAGAATAATTCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAAATATGCATTATCTTCACATGA[A/G]AAGGT TTCAGTTTATAAATGCTAAATACTGTATATTTGCTTAAATACTGTATCTATTGG
TIGR-A004V28a	29	A	G	TGTTGTGGGTG CGGAGGTTGCA CGATCTC GTGAGC	CCAGGGCTATAATGTTGTGGGTGCCGATCTC[A/G]GCTCACTGCAACCTCCGCCTCCCAGGTTCAAGCAA TTCTCCTGCCTCAGCCTCTTGAGTGAGCTAGCCGGGACTACAGGCACCCGCCACCTAACTAATTTTTG TATTTTTTAGTAGAGACATTGTATTTTTTAGTAGAGACAGG
TIGR-A004X20	25	T	C	AAGTTTTCCTT CTCTTCTGTAG GA / TTTTATAGTTG ACTGTAACATG GAGAC	TAAGTTTTCCTTCTCTTCTGTGTAGGA[T/C]GTCTCCATGTCAACTGTTACAGTCAACTATAAAACATGGCTCATGT TCACTCTGGCCTTCGGCTTCCTTCAGAGGAGTTTGATATTTGGAAGTTGGTACCTTTGTTGTGTGTGTTTCA GACCAACCGCTTCTTCCTTCCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCCTT
TIGR-A004X30	26	T	C	TTTTGAAATCTT AGAGTAGAAC CCCAC / TTCTTTATGGA AGTGTTTAAAA CTATTTT	TTTTGAAATCTTAGAGTAGAAACCCACT[C/T]ACTCTAGTAATACTTGTAATAAAATTAAAATAGTTTT AGTGTTTAAAAAACACTTCCATAAAGAATTAGGGGGTGCCCAGCTCCTTGATTTCCCCTAGGGATAAAGATATCCAT GTTAGGGGATAAAGATATCCATGTAC
TIGR-A004Z04	102	T	G	TTCATTTGGGT ATGCAAAACT CTTATAATTAG AAATTTCATGA AAGCAA	CACGGGTATATGCCTTATATATAGGTATATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACT[T/G]TTGCTTTCATGAAATTTCATTTAGTGATTTAAGACTG ACTGTTGCTTCTTCCATATTCAATGACAATTACAAAAATACAGTCTCTTTAGTGATTTAAGACTG TCTTTAGTGATTTAAGACTG

TIGR-A004Z19	85	C	T	GCAGCATTTT	GAGAACAACT	AAGATGGTCAT CGGGAAGA	TAAGTGGAGACAAGTTTATTGGAGGAGCTTGACACCCCTCCTCTGCCCTAGCTTGAGAGAACAACTGC AGCATTTTTCTTTTTC[C/T]TCTTCCCGATGACCATCTTTGGGCTGGCGGGCCAGGCCCTGGGTGTC TCCCATATCGCTGTCTTTAGTGAGACTGAGGATCTGGTATAAGGAAACAGATC
TIGR-A004Z42c	89	C	T	AGGAGACT	TTGGGGGAGGT	CAGGGCTGCCG GTCC	GTCTTAGCAGAGGAGATAACTTTGAGGGACACCCCCAAGGCGGCCAGGTAGCCTTCAGGGGCGGGGCA GGGTTGGGGGAGGTAGGGAGACT[C/T]GGACCGGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTT CATCATCTGTGTCTTC
TIGR-A005D17c	81	T	C	---			TATGGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGC[T/C]GTCTAGATTCTTC[T/C]GGCCTCCTCTGTGCAGGATTCCTTCCTTCTGGGCAC GGGGTGGGACCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAACAC
TIGR-A005D17b	79	G	C	AGCAAG	GGGGAAACCC	GAAGAATCTAG AC	TATGGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAG[G/C]C[C/C]GTCTCTCTGTGCAGGATTCCTTCCTTCTGGGCAC GGGGTGGGACCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAACAC
TIGR-A005D44	97	G	T	CTGTTACAC	GAACTTAAAA	TTAAAGCCAAC AAAA	CATCAGTAACATATACACAATTGGTCATCAACTGAACTTTGCCTCCAATATATTCTATACAATACTT AACATTATTGAACTTAAAACTGTTACACT[G/T]TTTTGTTGGCTTAAATAATAGACAATGATTTTTG TCTATTACTTAGTGATAGACAAAGTGATTACTTTGTTAGACAAAGTGATTACTTTGTTAC
TIGR-A005E31b	27	G	A	---			GGAGTTCAAATTTATAACCAGGCCTCT[G/A]CTCACAGCTGTACTGGCTAGGCAAAGCTTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTCTTTGCCTGCTTGCCCCTACAAAGCCACCTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR-A005E39	182	G	C	---	AGTAAGGTTA		CTCAGTGTAAAAACTTTGTTTAGGGAGGAAAAAAAAAATCCAATGGATATATGGGAAGAGAGAAGTG CCAGGCTGGATGGTGCTGAGACAGAATGACCCCCTTGGCCTCCTTATTTGTTCTTTCAAACAGGACC CCCACAGATATTTGCGGTATGTCATGGGGGATGTCTATTG[G/C]GGATGTCTTCTATTTT
TIGR-A005E42a	42	A	G	AGAG	GGAAATTGAG	CCTAAATCAGG	GCTGAGTTTTGTATCTTAGTAAGGTTACTGCACCTTACTGCACCTTACTGCACTAGGTGTAATAAAAATGTTGTATTTAAGAGAATCCCACAAG CTTGGTATAAGGCAGAAAAATAAATGGTATAAGGCAGAAAATAAATAG
TIGR-A005E46	76	A	G	CACCTGACTCG GTGCTTTAC	AGGTAATGT	CCCTGGCTGTG	ATGACAATGATGATGATGATTAGCCTACCCGTTTGCTAAGCACCTACTGCGTATCCAGGCACCTGACTCGCGG TGCTTTAC[A/G]TACATTACCTCACAGCCCAGGGTTGGCAAATGGTCATTTTGACAAATGGTCATTTTG ACAC
U20979	24	C	T	A	GCAGGGGTGA CGTATGTGAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTGAGAA[C/T]GCTTAGGGTGTCCTCCCCACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGCACTTTGTCCTGCTTCACGGACCTCCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTTCCTTTGATATTTGTAAAAATTCCCCAAGAGCCGCCATATGAATCTGCCC

Accession	Position	Alleles	Additional sequences	Sequence
X57830	106	G C	CT; AGTGGAACCA ACGATCATAT; CATTGACAGAA TAAAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTCACCTATCTGAGAAAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAACCAACGATCATATCT[G/C]TATGCCTCATTTTATTCTGTCAAT GAAAAGCGGGGTTCAATGCTTCACAAAATGTGTGCTTGACAGCATTTCAGCTGTGAG CTTTC
X74070b	72	T G	TGGATC; CTTTTTAAGAA ATTTTTGTTTA TATTAGAGATC TAGATTT; GGGCTTAAAAA TATTAGAGATC	AACCTGAAGAAGTTACTGGGAGCTGCTATTTTATATTATGACTGCTTTTAAGAAATTTTTGTTTATG GATC[T/G]GATAAAATCTAGATCTCTAATATTTTAAGCCCAGCCCCTTGGACACTGCAGCTCTTT CAGTTTTTGCTTATACACAATTCATTCTTTGCAGCTAATTAAGCCGAAGAAGCCTGGGAATCAAGTT GAA
Z48804	44	C T	---	ACTGCCGAAGTGTGAGCCCCCAAACCTTGCTCTCATCACCAG[C/T]AGAGCTTCTTCCCGAAGGG CCTTAGGATAGGAGAAAAGGGTTCATGCACACACGTGTGAGAATGGAAGAGCCCCCTCCAGACCACT CTACAGCTGCTCTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCGTGTAAAGTAAGTGTAAGG TCCA
D28513b	133	A G	---	ATGACCAAAGCCACCACATTTAGAACTTTGGCGTGCCTTTGGAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCCAGAGGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTTTGATTGACTGCATGGAATGC[A/ G]TGTGCGTGCAAGCATGAACCTTGTTAAATCAAGAGGCTTACATAATTTAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A G	---	CCACTCCATCCTGATGCCCCAAGTTATCCACAGCCTCCTTCCCGACCAAGACCCTATCCACCTGGACC TCCATTTTCCCTGTAA[A/G]TTCTCCAACTGATCCTCCACCCCAAATATGAA CAACTGCAGCAGGTGCCACCACCACCACAAAGACACCACTACCCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A G	---	CCACTCCATCCTGATGCCCCA[A/G]GTTATCCACAGCCTCCTTCCCGACCAAGACCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATTCTCCAACTGATCCTCCACCCCAAATATGAA CAACTGCAGCAGGTGCCACCACCACCACAAAGACACCACTACCCTTGTAACTACTGCTTCTGCTAC
D31762	82	G A	---	CTCCCTGCCTCCTCCTTCCTGCGTGATGCTCCGTCTCAAACAGCCGAAACCTGTCTTGCAATGGGGG GAGGGGGCGTTTC[G/A]CTTTCCTTGGCTTCCTCTTATTCTTCCACAAACCATTCTCAATAAA GCCAAAAATCTTTCTCTTCTTCTCCCCTCCAGCCACTCCACCTCCTGTCCTGTGCCTGGCTTTT CTGGA
D37931	64	T C	---	ATTATCGCGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTG[T/C] CCCAGGCTCTGTCTCCTCAGCTCATTCCTACTCTTTTCTCTATTAACTCATTCTATTAAAATACATT GCACCAAAGAGATATGGAGACATAAACCTGTAATGAATGAGGCTGGGCTTTTCTGTAATAAGCTTCC TTT

ID	Pos			Sequence
D63807	101	C	T	CAGGCCAGGACTTCAGTGTCAGTATCCCTGCCTTCAGTCTTCTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGGGAGGTGTATTTTCCTGTTCCA[C/T]GAAGAGGACTTTTGTTCACAATTGGATCAC AATGCAGAGGAGTCTGTTCCTCCCCGTCGGCTTCTCGGTCTGGGAGGGGTGACCTGTCCCAGATGAC
D90145	21	T	C	TGGGAACATGGCGTGTGACCTC[T/C]CACAGCTACCTCTTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGTGGGACTCTCTTCTTAACTTAAATTTATTTATTATACTATTTAGTTTTTATAATTTATTTTGAT TTCACAGTGTGTTTGTGATTGTTGCTCTGGAAGTTCCCCCTGTCCCGTCCCTCCCTCACAGTGTG TCTGGTG
EST14035 1a	59	T	C	ATTATCACTCTCAAAAAATTTGGTGTGTGTTAAGTACTTCTTCTTATTTATGAGCCCCT[T/C]GAGGA CCAGACATGTTATTATCAAGCCCCTTATATACCATCTAAT
EST16668 5	71	C	T	GCATTTAAAATTCACATTGAATCATTATTTACTATTTATGATGTTTACATAACAATTCAGTATCATT ATG[C/T]TGTAGATTTCAGATGTTAGGTCGTCAATACTGAGCACTTATCT
EST16904 7	57	C	T	ACAGACTATCGCCAACTTATAATGCTTAAACTTTATGATCAATAGTAATAAATTACA[C/T]GAGATA TTCACACTTTATTATAAAATAGGGTTTGTGTAAGATGATTTTTCCCAACTGTAGGTTAACAT
EST21863 9	49	A	G	TTTTAAGTACCAGAGGCACTGCTGGAACAGGAGTGAAAACTGATACACC[A/G]GTTACTTACTACTC TTCACTCTTCAAACTGATTCCCCTAAAGACTTCTACTTAGCAAA
EST21885 6	80	G	A	GGCTGTAAGTAGAATCAAAGGTTAAGAACACATTTATGCACTTATTCCACAAACATTTACTGAGCATA CTAGGTGCTGTGGGA[G/A]TGTGACAGTGAGCAAAAAACACAA
EST22623 8a	26	A	G	ATTTTAGTGCAAATGACAAAGCCCAA[A/G]AGAACAGAGGATCAAATAAGATTGAAATGTATTACC TTCTCATAAGTATACGAAGTTAACACAAGTATGGGAGT
EST22644 2	98	A	G	AAAATGATTGAATTCAGCAAGTAGTACATTATTGATCTATCTACATTGTTAAAACAGCACTAAAAATAA AAATTTTAAAATGATTATCCATTATTATTTACAG[A/G]AAATGTGGAAAAGATGGCTTTAAACCC
EST23587 1	31	T	A	CCTCATTTATTTAAAAAGACGGACATAAAAAA[T/A]TATACAACAAAAAAACCCAAGTCACATTTCAG GAGGTAAAAACTAAAAAAGTCTGATATGAAAAATATGGTGG
EST24246 7	106	T	C	AAAGATCTGGCATTATTCACATCATCTCAAATATTTGTAATTACTTTTTCCATGAGTATTTTTTCA TGTCCAAGCATTTAACTACTTCATTTAGCGTAAATACC[T/C]GAATAACCCATAGTTACAGAATTGG GTCTGTGTAACCTCAATT
EST24308 3	45	A	G	TAGTTTAATTTCTGAACCTTGGCTTATAAATTTTTCTCAACTT[A/G]CATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACATGAAAATATAAACCTCGTTC
EST24435 6	73	G	A	CTTGAACTTCTGGTCTCAAGTGGTACGTCCGTCTCCCAAAATGATGCGATTACAGGCATAAG CAGCC[G/A]TGCCTGACCCACATTTCTTTATCCGATCTGTTGATGGACATTCAGGTTGTTTC
EST25089 6	25	T	C	TATTGTTGCATTATCATCAAAAATGGTTAT[T/C]AGTTTTCAATTAAAACTGTAATTGATTTCTATGTATAAA ACAGCTTTGAAGTTGTAAATGTAGTTTCCAATCGTTAGTTAATGCTACATT

EST254769	33	G	A	...	AATGATCTTTATTTTCAGACCTGCTCCTAAAA[G/A]CTTTCTCCTCCTCCTAAAAAACCAAACACA AGAGGTCCTCTGCTGCCTTTCCATGGACTGTGGCGGCGTGTGGACCGTCGTGCTGA
EST261832	70	T	A	...	AGATAATGCATTAGAGCCTGCCCTCATTGTATCTTGATTAACTTTGTAAAGATTGATCTCTAAATAAG AT[T/A]ACATTCTGGGGTACTGGGAGTTAGAACAAC
EST272311a	28	T	C	...	AGAAAATAAGGTGCTACCAGAACTCATGT[T/C]GATAGCGCTTTCTTTTAGGCACATATTATAGCATT CAGATGAAAGTTCTGTAATCACACACACTGTGCCTCTAACAAACACGGTGACTCTGA
EST278165a	26	T	C	...	CAACTCAAGGTACAAGACAATTGCATT[T/C]TAACATTGTTATAAATAAAAGGAACATCAGATCAAT CATTAAGGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST285880	78	A	T	...	GTTTAATTGGCGTATGGTTCCACAGGCGTACAGAAAGCATGAGTGGCTTCTGGGGAGGTCTCAGGAA ACTTACAAATCA[A/T]GGTAGAAGGCAAAAGAGAGAGAAGCAGCATCTCTTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGGAT
EST302265	25	A	C	...	TACTCACACCGACATACATATCTCA[A/C]GTAGAATTAGCTATACTGCATACTAACTTCATTGTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAAACAGACAGACTCATTTCCTTTGA G
EST309359a	59	C	G	...	AGCTATGGTAGAGCAAATTCCAGTGGTGGTAAATCAAGAACTCTAAAGTTCAGTAGAGA[C/G]AGGT GTTTTGAATGTCAAGGAAATCACTGAGGTAGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST325157	25	G	A	...	CCGAATATAAGGAAAAAAATGGTGGC[G/A]TGCCTCTAAAACCTGTTGAATAGAATAATGGCCAAAT ATTACAGTTTCTCACTTCCTATGAATACTGGCACTGTGTTTATTTCATGTTTATATGTGAGTTTCTATGC ATAAAAATCCCAGTAAGA
EST332744	27	T	C	...	TGCTTTGTTTCCCTCCAAATCCTAAAA[T/C]GTGTGTCTTCAAAGAAATTCGTGGAAAGGACTTTGAA TACGAGTTTGTACCATATTCCAAGTATTCTGAATACAGAGTTTCAGATAACTATGGAGATGATACCATT GGACTAGGTA
EST333527b	75	C	G	...	TACACATTATTCAAGAGACCCACCTGACATGCCATCTCCTCCGCAGAATACATTCGTCCTCTCTTAGAGA AGTTTAA[C/G]GGCACATAGTATTATTATTACTAAGAGAATATCTTCTTGGTGTCATATCTAGGGG
EST334241	126	A	C	...	ATTTTCCCACAGCAGCAGAAGTATATTTATTGTCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAAGTGTTCACAAAGATTTACAAATCTCAGTCATTACACACTGAGCAAC[A/C]AAA CAAAGGTGTTGAATCCTCTT
EST334887	90	A	G	...	CCTTTGGGGGAGTGTTTAAGCCAGAAATGTGACAAAGTCACTTACAGGAAGGAAGACTGGAATGTAGCCATAG TTGAACTCTAACATCGTCTATAG[A/G]ACCATTCCCGTCTCCAGTTGACGTTCTAGGCATACTAAGCT GCTC
EST335081b	45	C	T	...	AAAAACATGCTATTTGAACAAAACTTTTTATAAAGAATAAGTTGA[C/T]TGAAAAGCAGTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA

EST33508 1a	36	A	G	---	AAAAACATGCTATTTGAACAACAAACTTTTTATAAAGA[A/G]TAAGTTGACTGAAAAGCAGTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA
EST33863 4	77	C	T	---	ACAACATAGGACTGGTTATTCTTGGTTTGAAAAATTATGTTGCCACTTCCTATTGTTTTAAAAATGA TCATTTAAC[C/T]TCTTTGAACTACAGCCTGAATCCCCC
EST34739 3	97	T	A	---	GAAGTATCCTTCCCAGTGGCAGGAACTGAAGACTCCAGATCAACCAGGTGGACCTTTCGTTGATGA GCTGATAGCTCTAGCCTGTGGGGAACCTC[T/A]GGTGCCTTACAACTCCAACTACTGCAGAATTTCT TGTTGTGCCTCATAAACA
EST34792 6b	104	A	G	---	ACCTGACTGCTTTAAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GTATTCAGGAATTCTTAGTCCTATTACA AAGATTTTGTTGCTGTG
EST34835 9b	93	T	G	---	GGAAAATGTTCCCTTGCAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTTGTGCTTTCTGG[T/G]GGCCTTAAAAGAAACAGACAAATTTGTGCTAAAGAT
EST34835 9a	82	G	A	---	GGAAAATGTTCCCTTGCAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTT[G/A]TGCTTTCTGGTGGCCTTAAAAGAAACAGACAAATTTGTGCTAAAGAT
EST35230 0	93	G	T	---	CACAAAGGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACACATGAGAGCATAAAAGAGGTTCTC[G/T]GCCTTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33	C	T	---	TCTTTTCAAATTTTTGATGTAGGCATTAATG[C/T]TATAAATTTCCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTGGGCATGTTGTGTTCCATTTTACTTAGTTCAGAACTTTTCAATTTCATCT
EST35708 9	32	C	T	---	CTGCCCCAAATTAACTTTTAGGCAAATGGAAA[C/T]AGACTTACTGTATGGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTCATATGCAGCGTGTTGCTCCCCTCTGAGGTTGCCACCTTTCCTGTGTG ATGTGCAAAGTGTGGCT
EST35747 9	51	C	G	---	ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAAACGT TTCCCAACATCAACCTAATACAGTGACACAGCAACACCTCCCTCCTGCCCCCCTTCCAGTAGGGTTGAGATT G
EST35751 9	89	C	A	---	TGGTCCATTATATTAAAACTGAGGGAACAAACGGTGCTGACATGGCAGACATTTATTTCAATGGAGA AGTTCCTCCCCATGAAACCAAGA[C/A]CTTGTCCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAGGCCTGTGA
EST36301 4	93	C	T	---	CACCTGTTGTTCATTGGTTCACTGGGCTGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGCTCAGCCTACAGC AGTCAGGAGGCAGCCATGCCCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GCCATCAGCCCACCAAAGACATGACCAACGC[G/T]GGCCCCTTGCACCCATACTACTGGCCTCAGCAC CTAAGACTGGACAACTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTCTCTGT CACAGGGGGTCTTAGTCGT
EST36519 0a	33	G	T	---	

Clone	Position			Sequence
EST36620 6	50	G	A	GACTTTATTAGATAAGGGGGTTTCGGCTACCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCCTTATTTAAATATGGGAAATAAAATACAAAAGGGCCACACCGATGCAAAGACTTT
EST36690 0a	89	C	G	CCTGTGATGTGCATGGGGTGCCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCACGTATGTCAGGA AAGGAAGTCTGGGGATTCCTA[C/G]GAGGGGACATATCACACATATTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTTCA
EST36729 9	62	C	T	GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCTCTCCTCCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACTTTAGCTACCCTGGACAATGCTATCAAGTGTGCTGGGAAGGGGAG
EST36823 6	103	A	T	ACTGTCTGGCCGGATGATTGGAGCTTGAAAAAAACTACCATGCCAGATCTCCACCCCAGACCAATTAG GTCAGTATCTCTGGGGGTGCTATTCAAGCAACAATT[A/T]TCTTTTATGTTCCTAAGCTCATCATGAG TTAA
EST36987 4	126	C	G	ATGATCGCTTATGTAATTGAGGGCGAACATGGGTAATGGGAGATACCCACAGGAGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAACTGACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88	T	C	GGTCTCACTCTCTTGCCCAGGACGGTTTGAAACTCCTGAGCTCAAGTGACCCTCCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACCACCACCTGGTCCTTGGTTTAAAGTAACCACTGAA C
EST37269 3b	105	T	G	AATAGTCTATGGCTACGGGCCCGTGGGATGTTAAAAATTGGGATTTAAATTAAGATTGTGAACATG CAAACCCAGCAAATTTCTCAGCTTATATTTTGAAAGTC[T/G]CAGGAGAAAAAATGGGGTCC
EST37284 2	93	G	T	AAAAGACCTTTCTCAAGCAGTAGTAAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCAGGAA GCTCTCTGGATAATGTCACTCTAGGAA[G/T]AGTAAACAGGTGTTAAAACCCTGAGATAGCAACCCT CTTGGCTTGCTTGAGGAATA
EST37315 2a	90	A	G	AGATGGGGTCTTGCTGCTAGCTTGCTCGGGCTGAACTAAAGATATCCTCCTGCCTCAGCCTCCCAGGTAGT TGGAACTATAGTAGGAGTATCT[A/G]CCCTGCCCTGCCTAGAACTTCAAGTTTTGATGGGCAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45	C	T	CCTGCCATGATAATGTTAAAACATATCAAGATCCTCCTCAAACTT[C/T]AAGGGTGAAAAGCATACC ATTCCATTTAGTTGAAATATTCCTTCACACATAGCCAACACATTTTTCAAGCACTCTAGCTACTACACA GGA
EST37376 8b	101	G	C	GTGACATCATGTCTCTTCAATGCCCTTCAATTAATAGTAGTTGAGCGCGCTGGGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCACAGTGCTGCTGTCCTGCA[G/C]GCTGTCCTCCAGGCAAGTTGCTGACTTCTCTG TGTCCAGG
EST37376 8a	41	T	C	GTGACATCATGTCTCTTCAATGCCCTTCAATTAATAGTAGT[T/C]GAGCGCGCTGGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGCTGCTGTCCTGCAGGGCTGTCCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST	Pos			Sequence
EST373789	63	T	G	ACACACAAAAAAATGGTGGCAGAAAATCTGGAAAGATTCTAATAACCTCAATTCGTGAAAACT[T/G]AACATGCCTCAAAAAAGAGGGGAAAAAACTTTAACAGAAACACTGTGCTGACATGATTAGCTT
EST374524	46	G	A	AAGACATAAATCTGCAATGAAATCAGTTATGAAATATTAAACCTCT[G/A]CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTAAAACACCCTTAAATCAATGACGTAGAA
EST376136	34	A	G	CTAGGCATGGGGCTTTACAGTCATTTATTTACC[A/G]GTCATGAATTCATTAAAACCACAGCGGAT ATAGCAATGAGCAAAACAGACCCTCCCCCAAAATCACCCTGCCGTTCATGGATCTTCCATTCTAA
EST380254	56	T	G	TTATTGAGTAGTACACTGTGCCAGAACTAAGCTTACATGTTTATATCACTTA[T/G]TTATCTCA ACAATCTTGAAAGGGTGGTATTATTTCCCCGTCTTATAGGTGAAGACTCTGAGGTTCAGAA
EST380686	57	C	T	TCTACCAGGTCACCAAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACTTA[C/T]CGGCATGG AAGAACGCTCTCCTTTAATTCCCTAACTCTCTTCTTCTTCTGGGAAGACAGAACGTGCACAA
EST384206a	100	T	C	TAAATCAAGGCCTCTTCTTCATTACCAAAACAAAACAAAAAAAAGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTCATCCTGACT[T/C]GTCCCTGCAGTGCCCATGGGTCCCGTGCCT TATTCATTCTCCTCTCA
EST389505	25	T	C	TTTATTTGCAAAAGTAAGCAGCCGG[T/C]TGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAAATACTTGGGACTTACATTTGACACAGGCTAAAAGTATGGGATGAGAGAGGAACAAAAGCTT ACAAACAAAGAGCAGCCA
EST390536	90	T	C	TTTTTGTTACTCTGTAGCCAGTCATTAATCTGAAGGTTAATATATCATTTATTGGGATGAGATCA TAGTCTTTACACAAATGCTATGT[T/C]AAACAAGTTACTGAATATTTTCACCTCGTGGAGTTG
EST393311	70	G	C	TCCTTCTTGCTCTCTAGCACTCAGACACCACCAAAGAAGACCTGGAAGACCAGCCATGGAAGGAAAGTA TGC[G/C]GTGTTTTAGGGAGAGCTGGCACCTGGCACCTGTAATCTTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST405447	31	C	A	GTCACCATTGACCTTACATAGTGCCTCTAGT[C/A]ACCTATGGAGGCACTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST405484	37	T	C	TTCTAATAGCATGCCCTGTGACAGGGAAACTAAGCTC[T/C]TCAAAATAACTGAAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCCTTTGTAGTTTTCTCCAGAAGGCTCAAGGTGTTC AATAATCTGTGGGACTCA
EST405491	42	A	G	TGTTTCTCTAGAGAACCCTGTGTGATGTGATACACTAGGCATGGCACA[A/G]ATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTGTTACCACCATTTCTCACTTGAACCTAGCTCCCTGCAAAGCACCTTCTA CCCTGCACTTTGGGGAG
EST405791	81	A	C	TGTGAATTACACATCAGTAAGGCAGTTTACAGAATTTCATTCTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAAA[A/C]GGACTTGGAGACAGCGGATTTAAATACGAACAAGGTCTTCCAGGAAG
EST405843	68	A	G	TTGTATGGTTGTGAGGAATTTGGGAAGAAGAAATTATCTGTGAAGGAAATTTGCCACTGTAATGCACACCC A[A/G]GTCTGTACTCCCACAATATCCTATGTTTAAGCT

EST51340	51	G A	...	GATCAAACTGTATTGCCCAGGCCAGCTCCTGAAGAAACTATGAAC[G/A]TCTCAGCCTAGA AGGATAAATGTGACCTTCAATTGCACACCATCCATTGTCTCTTCAAACTAAGAGCCCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134	T C	...	CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGGCCTCTCACAAGCAGGAGAAAACATAGAACTCAGAGCCAGATCCTTTATCCAACTCTCGA[T/C]TTTCCTTGGTCTCCAGTGGAAGGGAAAAGCCCATGATCTTCAAGCAGGGAAGCCCAGTGAGT AGCTG
K01506	63	T C	...	CTGAAACTCCAGCTGCCCTACAAACTCCATCTCAGCTTTCTTCTTCACTTCATGTGAAAACTAC[T/C]C CAGTGGCTGACTGAATTGCTGACCCTTCAAGCTCTGTCCTTATCCATTACCTCAAAGCAGTCATTCCT TAGTAAAGTTCCAACAACAAATAGAAATTAATGACACTTGGTAGCACTAATATGGGAGATTATCCTTTC ATTGAGCCTTTATCCT
L18877	69	T C	...	TGAGTCTGAGCACGAGTTGCAGCCAGGGCCAGTGGGAGGGAGTCTGGGCCCAGTGCACCTTCCAAGGCC C[T/C]ATCCATTAGTTCCACTGCCTCGTGTGACATGAGGCCCATTCTTCACTCTTTGAAGAGACGCAG TCAGTATTGTTAGTAGTGAGTTTCTGTTCTATTGGATGACTTTGAGATTTATCTTTGTTCCTGTTGGA ATTGTTCAAATGTT
L31848	36	T C	...	GCTATTTTACATATCCCAAGCCCTTTAGGGCTACAG[T/C]CTCTTCTTGTCCTGGACCCTGTAGGGTGCCA TTTGGAGTTCACAGCCTAGAAGAAAAAGGCTTTGGGCCTGGTGGTGGCCATAGGCCTGTAATCGT AGCGGCTTTGAGAGGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTCGAGACAAACCTGGGCAAT GT
L38517	137	G C	...	GGGTCCAGAGAGCCTCTCAGCCAGCAGGAGGGAGCTGCCCTGAAGGAGACCTGAGCTGGGGGACACTGGC TCCTGCCATCTCCTGCCATGAAGATACACCATTGAAGACTTGACTGGGCAACACCAGCGTCCCCCAC CC[G/C]CCGTGGTGTTAGTCATAGAGCTGCAAGCTGAGCTGCGAGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123	T G	...	ACTTGAGAAGCAGAGCTCGCGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGGACAGGGCAACAAAATACAGTAGTTCTTTGTATTTTGTATAT[T/G]CGCCTGA AGATCATCCCGCCAAGGCAGGCTGGAGGTGCCGGTGGGCCTGGTGTTGCTGGGGATTTTAGTCTGTGCTGG GAG
L41268d	173	G A	...	CAAAGTTGTCTCCTGCGCCCATGAGCACCACAGTCAGGCCTTGAGGGGATCTTCTAGGGAGAGCAACAGC CCTGTCTCAAAACTGGGTTGCCAGCTCCAATGTACCAGCAGCTGGAATCGTGAAGGCGGTGAGTCTGCAT CTTAGGGCCATCGCTCTTCCTCACCACCAAAATCTGAAC[G/A]TCCCTCTCCCCTTGCTTACAAATGTCT AAGGT

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L48728b	111	T	C	---	AAGTGAACAGAAAGCAAAGATGGATTGTGTTCCTATAAAAGCACATAGTTATGTTTACTGGTATCGT AAGAAGCTGGAAGAAGAGAGCTCAAGTTTTGGTTACTTTCAGAA[T/C]GAAGAACTTATTCAGAAAG CAGAA-TAATCAATGAGCGGATTTTTAGCCCAATGCTCCAAAAACTCATCCTGTACCTTGGAGATCCA GTC
M18079	52	G	A	---	GCGCACAGTCCAAAATACAAATTGGACAGAAGATCTATATTGTACCAGAACT[G/A]TTTATTTCACC CCATCAAGTATAAGGTTACTGATTGATTGGTCCTTTATAAACATTGGTATATTCCATTCATGCCAA AGCAAAGAAGAAGTAAAAGCTAA
M19169	113	T	C	---	TAGGGATCTGTGCCAGGCCATTCGCCACCAGCCACCACCCCCTCCCACCCCTGTAGTGCTCCCACCCC TGGACTGGTGGCCCCACCCTGCGGGGAGGCCTCCCCATGTGCCTGT[T/C]GCCAAGAGACAGACAGAG AAGGGCTGCAGGAGTCCTTTGTGCTCAGCAGGGCGTCCGCCCCTCCTCCTTCCTCTGCGCTTCTAATA GC
M21539	114	T	G	---	TCACCTGTTCCACAGCTCCACCTGCATCTTCTCATCAAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCCCTTAGCCTGTGATCTGCCCATGATGCCCGACAGCAAAAT[T/G]TTCCTTTCTGAGGCTG CCATGCTGCCCACTGTCCAGGTGGGAGACTGAGCAAAGGAAGTCCTCAGCTGTACCGGCCTTTCAGAGCT TCTCTTTGGGTGC
M26041c	173	A	G	---	CCTAGCATTATTTTCTGGCCCCATTATTCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAAATTGCTATATCTGCTCAGAGCTCACAAATGCCTTGAATTATTTCCCTGACTTC CTGATTTTTTCTTTTCTCAAGTGTTACCTACTAAG[A/G]GTGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157	A	G	---	CCTAGCATTATTTTCTGGCCCCATTATTCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAAATTGCTATATCTGCTCAGAGCTCACAAATGCCTTGAATTATTTCCCTGACTTC CTGATTTTTTCTTTTCTCA[A/G]GTGTTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45	C	G	---	CCTAGCATTATTTTCTGGCCCCATTATCATATCCCTTTTCTCCTCCCTTTCTCCTC[C/G]CAAATGTTTCTCCTCTCACC TCTTCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAAATGCCTTGAATTATTTCCCTGAC TTCCTGATTTTTTCTTTTCTCAAGTGTTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57	G	C	---	TAAGGCAGCTGTCAGGGAGGCCCAGTCACAGTTCCAGCAATTCCACAACCACCTTGAC[G/C]AATGCT TGCCAAGCTGTTTTAAAGCCAAGAACACACCCTTTCTTGTTCCAAATTAACTCTTAGAAGAAACCCCA CAAATAAAGCAATTCAATC
M81695	34	G	A	---	ACTTACTTACCCTCACCTGTCAGGCTCAGGCTGACGGGGA[G/A]GAACCACTGCCACCGAGAGAGGCTGGG ATGGGCCTGCTTCCTGTCTTTGGGAGAAAACGTCTTGCTTGGGAAGGGGCCTTTGTCTTGTTGTCAAGGTTC CAACTGGAAACCCTTAGGACAGGGTCCCTGCTGTCTGTTCCCCAAAAGGACTTGACTTGACTTGCAATTTCTACC T

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U06641d	166	C	T	---	CTCCTCCTTATTCAGCATGGAGGGTTAAATGGAGGATCTCCTTTCCTGTGACAAAACATCTTTC ACAACTTACCTTGTTAAGACAATTTAAAAAAAGATCTTTTCACAACTTACCTTGTTAAGACAAATT TATTTTCCAGGCTATTAATACGTACTTTAG[C/T]TGGAATTATTCTATGTCAATGATTTTTAAGCTA TGAAAATACAATGGGGGA
U09607	39	T	C	---	GAGGCCTTATGAGGGTCCTCTACTTCAGGAACACCCCCA[T/C]GACATTGCATTGGGGGGCTCCCG TGGCCTGTAGAATAGCCTGGCCTTTGCAATTGTTAAGGTTCAAGACAGATGGGCATATGTGTCAG TGGGGCTCTCTGAGTCCTGGCCCAAAGAAGCAAGGAACCAAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82	T	C	---	GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATTCCAAAGGCCTCATCTGGAGCCTC GGGAAAGTCTGGTCC[T/C]ACATCTGCCCGGCCCTTCCCAGCCCCTTCCCCAGCCCCTCCTGTTTCTTC ATTCATTCAACAAAATTTGGC
U10694	20	C	G	---	GTGACATGAGGCCCATTCTT[C/G]GCTCTGTGTGTTGAAGAGAGCAATCAGTGTTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCATCTCGGGTTCCTGTGTCTATTGGGTGATTGGAGATTTATCCTT GCTCCCTTTTGGAATTGTTCAAATGTTCTTTAATGGTCAGTTAATGAACTTCACCATCGAAGTTAA TGAATGACAGTA
U13877b	162	T	C	---	AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGCTATCTTTGTGACCTTGCACAAGTTGTTTAAC CTCTTTGTTCAGAAATTTCTCCATGGAGTAACAATATCTAGGTGGGAGGATTAGTAGTGAAGTTACATGT AAAGCACAGAGGAACAGCCAAGAGAT[T/C]TTACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTTACCTTCAGCA
U15555	187	T	C	---	TTTCTGTCCACTTCACCTGGTTTTAATGACCAGCCAGTCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTGGAAGAATTAAATAAGCAATGCTGAACATCAGGAATTGTAGATATCCGTACAGAGAGT TCCAGTAAAATTTTATGAGTCCACGACCCCTTTCTAAGCAGTCTGGTCCATG[T/C]TGGTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122	T	C	---	TCCAATTATTGGTCCCCAAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAACGTCCACGGGATTAACAGAAGCGTCCTTGCGAGACTGAGCGATGACGACCACACT[C/T]TGTTTGG ACATTTAAATTCACTCTGCTGAATAGGAGGAAGCTTTTTCCTGGGAAAACAACTGTCTCTTGG AATTA
U18543	58	T	C	---	GCACATGCAGAATAGACTCAGCCTATGTCCTGATTCCAGCTGGTAGTTCTAGAACTT[T/C]AGAAG CTCCATCTTTAATGTTTTATTTGTTATGTCCCCTCCCGGCTTCCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAAATAGGACACACGATGTGTTGAGTGAAGTTGATTAGCAATTAGGCACTTCC AAGGCTTTAGTAGAGAGAGCC

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U25975b	164	C	A	TCACTGCTGTGGCCTCATACTCTTTTTCCATTTCTACAAGAGAGCCTTTAGTATATGAAAATTATTACTCTTTTGGGGTTAAAGAAATGGTCTGCATAACCTGAATGAAAGAAGCAAATGACTATTCTGAAGACAACCAAGAGAGAAATTGCAAAAAGA[C/A]AAGTATGACTTTTATATGAACCCCTTCTTTAGGGTCCCAGAAGGAATTGTGGACTGA
U25975a	143	C	G	TCACTGCTGTGGCCTCATACTCTTTTTCCATTTCTACAAGAGAGCCTTTAGTATATGAAAATTATTACTCTTTTGGGGTTAAAGAAATGGTCTGCATAACCTGAATGAAAGAAGCAAATGACTATTCTGAAGACAAC[C/G]AAGAGAGAAATTGCAAAAAGACAAGTATGACTTTTATATGAACCCCTTCTTTAGGGTCCCAGAAGGAATTGTGGACTGA
U25997	61	A	G	CAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTTAGGGGTGTTGACACACCA[A/G]TTTTGAGTGTACTGTGCCTGGTTGATTTTTTAAAGTAGTTCCTATTTTCTATCCCCCTTAAAGAAAATTGCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCATTCCCAACCAACAAATCC
U28413	29	C	T	ATTCCTGACAGCTAAATTAGCCCTAAATG[C/T]GGGTAATATATTTTCCTCATGTTTTAAAATGAGGTTAATATTTGCATAAAAATCCTAAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTTCCTTGATCCCAGATGTGTGGCCTGGGAAAGCCCTCATTGTGTAACAGTAACACAAGTCGTTGTACCTCAGTTG
U308884c	89	A	G	TAGGGGTAGCATTAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGTTCTTCTATTCCCACGTTAGCCA[A/G]TTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTATTGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACTGCCCACAGTTGAACACAAGTGCTGTCA
U308884a	34	A	G	TAGGGGTAGCATTAAGATTCAGGAGTCATTAGC[A/G]GTGATGATTTTGGGACCTGCCGTATAATCTGTTCTTCTATTCCCACGTTAGCCAATTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTATTGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACTGCCCACAGTTGAACACAAGTGCTGTCA
U31216b	78	A	G	GGGACAGCAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACAGGCCTGCAACCAAACAGCCGTCATCAA[A/G]CCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATACCAGCACCAAGACCCTTTACAACGTAGAGGAGGAGGATGCCCAGCCGCTTCGCTTTAGCCCGCCTGGTAGCCCTTCCAT
U31216a	70	G	A	GGGACAGCAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACAATGAGACAGGCCTGCAACCAAACAGCC[G/A]TCATCAAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATACCAGCACCAAGACCCTTTACAACGTAGAGGAGGAGGATGCCCAGCCGCTTCGCTTTAGCCCGCCTGGTAGCCCTTCCAT

U31416c	76	G A	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G/A]CCACAAATCTGGTGCCTCTCTCTCTGCTTAGCCACAGTTCTCCATTCACTTGACCCCTGCCCACCTCTCC GGAAAGAAAACACACTCCTTTGCTTAGCCACAGTTCTCCATTCACTTGACCCCTGCCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68	C T	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCCTCACGCCACCACAAATCTGGTGCCTCTCTCTCTGCTTACAAATGTCTAGGTCCCCACTGCCTGCTG GAAAGAAAACACACTCCTTTGCTTAGCCACAGTTCTCCATTCACTTGACCCCTGCCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U375519a	78	C T	ACGGGTCACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCAACTCACATTGTTCCTCC AGACCGCAGG[C/T]TCCCCCAGCCTCAGGTTGCTGGGAGCTGTCACATGACTCCTGCCTGCCAGG GCTGCAAAGCAAGGTCTTGCTTCTATCTGGGGGACGGTCTGCTCGAGAGAGGCCGAGAGAAC ATGCCAGGTGTCC
U37690	54	A G	GACCACGCTGAAACCCACCCACCCGCGTGTGCTGACCCATGGGCCCTGTGCTGAGCGTCCT[A/G]CCCCGAATTC ACGAGGCTGAGGGCATCCGGGAGCTGGCGTAATGCCTGGCCGCCAGTGTGTTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGTCTTT
V00540	39	T C	TGAAACCGTTTCAACATGGAAATGATCTGTATTGACTAA[T/C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCCTATAACCACCGCATGAGTTGAATCAAAATTTCAGATCTTT TCAGGAGTGTAAGGAAACATCATGTTTACCTGTGCAGGCACTAGTCCTTTACAGATGACCATGCTGAT A
X15943	106	A T	TCAAGAAGGTGACTGCCCTTGTATGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTAA AACCACTCTGAGCCTCTCTGAGACCATGTGGTTTAAAA[A/T]ATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCCAGTAGCTAAGACCCTAGAATTTGGATTCATCTCTGTTTTTCATGTCTCTCCTT GTAACCCTGAGATCATCAG
X52011b	148	C T	AGGAAGAGATCCCACCGACCCTTCCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAACATTTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTCACAAAGAAAAGTTGCGAAAATTGCG AAATCTGTTGTGCA[C/T]GCTCAAATGAAAACGCCCTTTCGGCTTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT
X52011a	118	A:C	AGGAAGAGATCCCACCGACCCTTCCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAACATTTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTCACAAAGAAA[A/C]GTTGCGAAAATT GCGAAATCTGTTGTGCACGCTCAAATGAAAACGCCCTTTCGGCTTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT

X54741	24	A	G	CAGGCCCACCTGTCTTCTCTCCCAC[A/G]TGCACAGCTTCCTGAGTCACCCTCGTGTCCAGCCAGCTCCT GCACAAATGGAACTCCCCAGGGCCTCCAGGACTGGGCCTTGCCCAGCGTTGTCAAATAGCAAGGCCAG GGCACAGCTGGGAGACGATCTTGCTGGCCAGGCCCTGGCCTTGTCCCCAGCCCCCACCTGGCCCCTTCTCC AGCAAGCAGTGC
X54869	99	A	G	AAGCATTTGCGTTTACAGTGCATCAGATACACATTTTATATTTCTTAAAATAGAAATATTATGATTGCAT AAATCTGAAAATGAATTATGTTATTTGCTCT[A/G]ATACAAAAATTCTAAATCAATTATTGAAATAG GATGCACACAATTACTAAAGTACAGACATCCTAGCATTTGTGTCGGGCTCATTTTGCTCAACATGGTA
X66924	147	G	A	GCCGTGTCCTGACACCTCCAGAACGCAGGTGCTGGGCGGCCGTTCTGCCTGGGACCCCGGGAACCTCTC CTGCCGGAAGCCGGACGGGCAGGGATGGGCCCCAACTTGCGCCTGCCCACTTGACTTCACCAAATCCCT TCCTGGAGACT[G/A]AACCTGGTGCTCAGGAGCGAAGGACTGTGAACTTGTGCCTGAAGAGCCAGA
X78932	62	T	G	GAAATGTGAAGAATGTGACAAAGCCTTTAAGCGGGTTGTCACACTTGATTGTATATAAGATAA[T/G]T CATACTGGAGAAAAACTCCCAGAAGTGTGACAAATGTGACAAAACATTTAATTAATTCTCATACCTTA TTGCACAGGAAAGCATTTATACTTGAGAAAAATTGTATAAAGAATGGAAAAGTCATTAATATATCTGCT CATATCTTAACATCAGCGAGTT
X80026	25	T	C	CTCAACCCCATAACCTCAACCACCATC[T/C]TATCCTCCACCCCACCATCCACCACTCCACTCCCATCC CCAACCCATCCTCATCCCCCAACTACAGCCCCAAAACCCAGACTAATCCACAGCCATCCCCAA CTCATCCTCCATCCCCCAACTGCAGCCCCCAAAACCCAACCCAGGCCATCCCCAAACCCATCCCCAAGCC AAACTCAACACCATCC
X80197b	99	G	C	ACCCCAACTCAAGTCCCAGGCCCCAGGCCATCTTCCTGCCCATCCAGTCCAGG CGCCTGGAGCAAGTGCTCAGCTACTTCTCCT[G/C]CACTTTGAAAGACCCCTCCCCACTCCTGGCCTCA CATTTCTGTGTGATCCCCCACTTCTGCGCTCTGGGCTCTGCCACCCCCAGTGGGAAAGGCCACCCTAGAAAG
X80197a	28	A	G	ACCCCAACTCAAGTCCCAGGCCCCAGGC[A/G]TCTTTCCTGCCTTGCCTTGGCCCATCCAGTCC AGGGCGGCCTGGAGCAAGTGCTCAGCTACTTCTCCTGCACTTTGAAAGACCCCTCCCACTCCTGGCCTCA CATTTCTGTGTGATCCCCCACTTCTGGGCTCTGCCACCCCCACAGTGGGAAAGGCCACCCTAGAAAG
X85106	150	G	A	GGCACCCCAGAGTGACCACAAGTCCAGCAGGGAGGCGGCGGCCTCGCCGTGTCCGCCGTGTCCCGCCGCTCT CAGCCCCCGGAGAGGTCCTGACCTGGGGCGTCCTCCAAGCCCTTCACCTTCACCCTCGGCGCCCACGCTCT CTTTCTCCCAAGC[G/A]AAACCAAATGGCGCCCCTTCACCTGCGGCGTCCCGGAGGGCGGGGGCTT CTTTCAGAGC
X87160	128	T	G	ACCACCAGCCACCATGGTCTAAGGACATGGATCGGGTGCCCCCAGACGTGTGCACAGGGACCCTCGCCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCTGCTTTAAACCGCAAGATGGGCGC[T/G]GGGGC ATGGCCAGGAGGAGCCATCGGGTACTACGCAGCAACACTGTCCACAACTGTCCAGGCTGAGATAAATCCC GGGA

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X87344	34	C T	CATCCCAAGGCACTGGTGGTGACTCTGCTTCCTG[C/T]ACTGACCAGGAGCCTCTGCCTGTGCACTGC AAGCTGTGTCTACTCAGGCCCCAAGGGGACTCTCTGTTCCATTCTCCCCCCAGAGACCTGTCAAGAG AAGCATGACAAACAAAATCATTTACCGACTTAGTGCTTTTTT
X87838	179	G T	GGTGGGCTGGTATCTCAGAAAGTGCCTGACACACTAACCAAGCTGAGTTTCCTATGGGAACAATTGA AGTAAACTTTTGTTCTGGTCCTTTTGGTCGAGGAGTAACATACAAATGGATTTTGGGAGTGACTC AAGAAGTGAAGAATGCACAAGAAATGGATCACAAGATGGAATTTA[G/T]CAAACCCTAGCCTTGCTT GTTAAAATT
Z14138	81	A G	GTTCTGCTGCCTCTACACAGGGCCCTGTACAGTGAATGGTGCCATTTCGAAGGAGCAGCAGTGTGA CCTCCTGTGTGACCC[A/G]TGAATGTGCCTCCAAGCGGCCCTGTGTGTTGACATGTGAAGCTATTTGAT ATGCACCAGGTCTCAAGGTTCTCATTTCTCAGGTGACGTGATTCTAAGGCAGGATTTGAGAGTTCACA GAAGGAT
Z18859	191	A C	TAATCCTCACCATTCCTCAGGTATAAGTTCTATAAACAGGCTTGGAATCTGGGTAATTAAAAACAGA AAATTATAGTACAATATACCATGACATGAAGAATGAATCCATTCTTGGAGATGGAGTATACATGACT GCAACTGTATTTCATACGTTCTTTCAAAGTGGGATAGCTATTGCAGCTTAAAGAGC[A/C]CAGGTTC CAGTACTGGTTTTCCAA
Z23091	159	G A	AGAACCTGACCAGATGTGGCTCGGAGGGGAATCCAGACCCGCTGTCTTGCTCTCCTCCTCCCCTCCC CACTCCTCCTCCTCTCTTCTTCCTCTCACTGCCACCCTCCTCCTCCTCCCCCCGTCTCTGGAAA CTCTGTGCTCTTCCATTCTCAC[G/A]AGGCCCGCAACCCCTCCTCTCTCGTCCCGCTGTCTCTGGAAA CTGAGCTTGACGTTG
11595b	125	A G	GTTGGCATTGTTAGTAAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTATCAAA GTGTGGTTTTCTGCAAGGGCAGGTTTGAAACCTGACCCTAGTTGTGCTCCAGGACCTA[A/G]GCGTGC TCACTCTACCTTGTCTTTGTTGTGGTTCCCATGACTGTTAAGTGACAAGTGCCATGG ATATCTACACCGTCACCAGACTAGATTGTTCTCAATGTCCTTGGCTTGCGAC
11595	125	A G	GTTGGCATTGTTAGTAAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGGTTTTCTGCAAGGGCAGGTTTGAAACCTGACCCTAGTTGTGCTCCAGGACCTA[A/G]GCGTGC TCACTCTACCTTGTCTTTGTTGTGAAGGAGTGGTTCCCATGACTGTTAAGTGACAAGTGCCATGG ATATCTACACCGTCACCAGACTAGATTGTTCTCAATGTCCTTGGCTTGCGAC
1241	131	G T	TATATCACATTAGTATGTCACTGCCATGGTAAGGACTTTGATCACTAGGAAAATAAGAACACTTTGAA TGGTCTTGTCCTTTCAATAAAAAAGAAGTGAACATGTGTTTTAGATAAAGGGCACTT[G/T]GCAGGAGTGTTTAGGATGAAGAAGAGAGATTAAGGAAGATCAGGAAGAAAAGTAGCAATGGGA ATGAAAATAGGAGGCCCTGAGATCCGATAATCTAAAAAACCAGAGAAAG

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1282	130	C	T	GTGCGGATCACCACTACAGTCTAATTTCATTACCCCTAAAAGAAATCTTGTACCCATTA GCAATTATTCCTCATTCCTGCCCTCACCCCCAGCCCTACTCTTTATCGCTATAGATTGCC[C/T]ACT TGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGCTTCTTTCACTGAGAATA ATGTTTTCAAGGT
6810	68	C	T	AGTATCACACATACTTAATATATTAGATATACACAATAATAAAATCACTCCCTACCTTGAAAACTTT A[C/T]AGAAGCATTTTAATTTACAACACAAAGCTCAAACGAACCTACAATAAGTCTAGTAGTCTG TTTACGTGCCAAAGGGATAAGGCTGAACAATAAATTAAACCCTTTAAAAATGTCTATGAACAAGTACAA TTTTCTTTTTGAGTTCTGCAGAGCAATGACCACTAAGAAATATTTTTAAAGGC
6817	118	A	C	CCAAGTACATTGGGTGAACGATGAGCTAGTCGTTCTCTAGTATTGCTTTTTGTAATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACTCAACATGTAGCTGCAGGGTAAC[A/C]TGTGGATACCCTG TGTGCTCTACTGGCCTCCAAAGGCATTCAGGGGATCATCAAAGATGTTGGACACCTTGTGTTCAAATC TTGGTTCAGGTGCGGCCGTGTCGCAGATCGGCGTTTTGGGTTGTCTTAG
6819b	212	C		CCATTTTATTTTCTCTAAATTTAAAATAGAAGACTTTAATGGAAAACATTAGTACCATCATCATGTCA CCCTGAATGCCAGCAATACCTGACTTTACACACGCAGGAAGCCTAGTAAAAGCCCCGTCAGTAGT ACACATTTCTCTCTATGGTCCTTCAACAGTTTGCATATACAAAATTTCTGCTATTTGCTTTAGCAAA CAGCAATAAACTTTGTGTTCCTATATGACACCTAATATCCA
6819a	166	G	T	CCATTTTATTTTCTCTAAATTTTAAAATAGAAGACTTTAAATGGAAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTGACTTTACACACGCAGGAAGCCTAGTAAAAGCCCCGTCAGTAGT ACACATTTCTCTATGGTCCTTCAACAGTTT[G/T]CATATACAAAATTTCTGCTATTTTGCTTTAGC AAACAGCAATAAACTTTGTGTTCCTATATGACACCTAATATCCA
681xx	39	A	G	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[A/G]TTATACTATGGCACCATTTGGGACA CAGATTATATATGTCAGACACCACGAATGTCCTTAAGATATGCAGCAAGCACAAATCTGTCATGGT TTAACAAAGAAATGAAACGTCTAGG
6972b	149	G	T	AGGATTCCCTCTTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCCTGGACTCTTTTGGTTGGTAAACTATTGATTATTGC CACAATTTCAGA[G/T]CCTGTTATTGGTCTATTCAGAGATTCAACTTCTTCCCTGGTTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT
6972a	122	A	G	AGGATTCCCTCTTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCCTGGACTCTTTTGGTTGGTAA[A/G]CTATTGATTA TTGCCACAATTTCAGAGATTCTATTGGTCTATTCAGAGATTCAACTTCTTCCCTGGTTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT

7598k	210	A C	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTATGTGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTTCCT CAATGCAG[A/C]
7598j	208	A T	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTATGTGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTTCCT CAATGC[A/T]GA
7598i	192	G T	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTATGTGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCC[G/T]ATTTT CCTCAATGCAGA
7598h	144	C T	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598g	142	C T	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598f	120	A G	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTG[A/G]GGATGCCTT TTAATATTTGATCCCATTATGTGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598e	83	C T	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGCCGGCTAA[C/T]CAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598d	77	C T	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAAATAAGC[C/T]GCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA

ID	Pos			Sequence
7598c	56	A	G	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCA[A/G]AGGAAC TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGAGATTTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598b	47	C	G	---	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACA[C/G]CAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGAGATTTTCCTGATATGTTATCTTATTTATATTTCCCGTATTT CCTCAATGCAGA
7598a	30	A	G	---	AAAGGTAAATCAAAGTTCCCTCTATAAATT[A/G]TGATTTACAAAAGACACCCAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGAGATTTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7998c	116	A	T	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCGTGTTCCTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAATGAATGGGTGTAGTCCTATCTTCTCAAGGTCCTA[A/T]CCTTGAGGTTCCT
7998b	94	A	C	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCGTGTTCCTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAATGAATGGGTGTAGTCCTA[A/C]TCTTCTCAAGGTCCCCAAATAACCTTGAGGTTCCT
7998a	75	A	T	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCGTGTTCCTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTT[A/T]ATGAATGGGTGTAGTCCTATCTTCTCAAGGTCCCCAAATAACCTTGAGGTTCCT
8071	119	A	G	---	AAATACAGAATTTTATTTAGAAACTGTTTAAAGTAGAAAAAAACCCTGTCAAGAAAGACCAGGTGG AAAATGGGTTCCCAATAAAATGGAATTTTAGGGCAACAAAAGTCTAAAGGCC[A/G]CAAAAGAGA AATAGCACCACTGTCATTGAACAATGGCTAGTTACTTGCCATTTTTGGCATTGTTAATCACTGAATC TGGGGTTTCCTCTCGAATTCCACACAGAGCATGCCACTACACAACATTTTTATCAT
8467b	93	C	T	---	AAGGCTTCCTCTCTAAACATCAGTCCTACGGAGAAAATCGGGAAAATCCTGGATATTTGGCTTATCACTT TGACGCAAAATCCACTTTGCTGTAA[C/T]GGTCATCCGAACTCCCTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAGTATTAAGGAAAAATTACTG
8467a	70	A	G	---	AAGGCTTCCTCTAAACATCAGTCCTACGGAGAAATCGGGAAAATCCTGGATATTTGGCTTATCACTT TG[A/G]CGCAAAATCCACTTTGCTGTAACGGTCATCCGAACTCCCTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAGTATTAAGGAAAAATTACTG
8498	84	C	T	---	AGGGTTCAGGGTTTGGTTTTAAATCAGGCTGCACACCTTTCAAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAG[C/T]AATACTTCATTCATTAAATCGAAAAGAAAAAAATTGCTTTAAGGAAAAAA AATCCAGTTTTAAGAACAATTAACATTAGTCTTTAAAATAAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCCTCAATACAGAACCAGGAATTGTAATTTCCTAACTCAG

Marker	Pos				Sequence
WI-18562	29	G	A	---	CTAAGGAAAAATTTAATGATGGAAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAAGTAGCTTCTCTATTTCACATAGCTTAGTTTGGGATAGAAATAGAACTAATGTTACAATGATTCTTACATTTAGCATTAATCAGAAACGA
WI-18618	51	A	C	---	ATAGCAGACTTTTAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCGTTACAATGAAGAAATGGTTTCCTTTCGATGCAAAGTATAATTGTAAACCACAGTGCTCGCACAGTTCAC
WI-18683	22	C	T	---	TAAGCTGTTCAGGACTGGACTC[C/T]GGTCCCTTTATTGAGACTGACACAGGCCAGTGGGTCCACCCAAACAAAAATAAATTTCTCTCCCAAAGCCTGCCTGCAGT
WI-18520	75	G	A	---	GACTTTGGTGATTTAATTGCTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTGTTCTTTACTACA[G/A]CCGGAGTGGTAAATACTACCTCCAACAAACACGGGCATCCACTCTGTCTTCAATGCCCTCTTCCGTGAGAC
WI-18563	94	A	G	---	AAATAAAGTTTATTGGCACACAGCCAAGCCCACTGGATGACACATTGTCCACGGCTCATCTTGCAATACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69	T	A	---	GTCCTATTTCAATTAGCTAGACCCATTTCATTCGTTGTTTAATGGCTACATTGTTTTTCATTGTGAGAC[T/A]GTGCCATAATTTATTTAATCAGTGCCATATTGAAAGACATTGGATCGTTCCCAG
WI-18723f	94	G	A	---	AACTTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTTATTTGGTGAATCTTCATCCTTGGTAACACAGGTACATAGGTAACCAAA[G/A]TATATAGCTTATTTGGTGAATCTTCATCCT
WI-18723e	71	T	C	---	AACTTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTTATTTGGTGAATCTTCATCCTTGGT[T/C]AACAGGTACATAGGTAACCAAAGT[A/G]TATAGCTTATTTGGTGAATCTTCATCCT
WI-18723c	96	A	G	---	TTTATTACAATATTTAGGTGGCACAATAACTAACAAGCTTCTGA[G/A]ACAGGAGGTAACATTCTCATAGACTTTGCAACTCAGCCAGAAGTAAAACTCGAAATA
WI-18619	44	G	A	---	TTATTCACAAAAAGTGATATTGCGAGAGGGTCTCGGGGGCTGTACATGGGCAGGGGCTTGGTGAGCTTTGTACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGGAAGGGTATTTTTTAATAAAAAAATAATGGAGCTACAACCACCCC
WI-18715	76	G	A	---	GTAAATAAAGTTTTATTGGCACAGCCACGCTCGTTCATTCATATGCCATTGACATCTGCTGTGCCCTACACAGCAGGGTGGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCCAACCTTCTGTTCCCCGTG
WI-18535	107	G	A	---	AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCCACTTAGTTTTTCAGTTCTCGGGCAGGTGACTTCATCTCTTCGAACTTCAGTTTCTTCATAAGATGGAAA[C/T]GCTATACCTTACCTCACCTCGTAAAGTCTGATGAGGAAAGAGATTAACTAATAGATGCATAGCAACTAACAGAGTGCATAGCAACTACACTGTTTTCAATAAATGCACCTTAGCAGAGAAGGTCGATGTGTCTACCAGGCAGACGAAG
D17525	107	C	T	---	

DWU-133c	313	A	G	---	TAATTGGCCACTGCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCTCATGAATGACTGACAGAATATTTGTTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTGGTTAAATGAATGTTCAGTTTTTGAATTTTAATAGTAACTCC AATTCAGTAAATGGTATCACTCGTTTAAAGATATGATTAGACT
DWU-133b	236	T	C	---	TAATTGGCCACTGCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCTCATGAATGACTGACAGAATATTTGTTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTGGTTAAATGAATGTTCAGTTTTTGAATTTTAATAGTAACTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTT[T/C]TAAAGATATGATTA
DWU-133a	199	C	T	---	TAATTGGCCACTGCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCTCATGAATGACTGACAGAATATTTGTTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTGGTTAAATGAATGTTCAGTTTTTGAATTTTAATAGTAA[C/T TCCAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTA
DWU-36	102	C	T	---	ATGAGATCCTTAAATCCTTCCATGAAACGTTTGTGTGGTGGCACCTCCTACGTCAAACATGAAGTG TGTTCCTTCCTCAGTGCATCTGGGAAGATTCTACC[C/T]GACCAACAGTTCCTTCCATTCGCC CCTCATTTATCCCTCAACCCCCAGCCCACAGGTGTTATACAGCTCAGCTTTTTGTCTTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAAGGATTCATGTGAATATAAAGAT
DWU-387	169	G	T	---	GTGTATAAAAATGCAACTGTGATTTCCTCACAACATGGCTCACAAATTCTATCCCAAATCTTTCTGAA GATGAAGAGTTTAGTTTAAAACTGCACTGCCAACAGTTCACTCATATATAAAGCATTATTTTA CTCTTTTGAGGTGAATATAATTTATATTACAAATG[G/T]AAAAGCTTCTTAATACTAAGTATTTTTCA GGTCTTCACCAAGTATCAAAGTAATAACACAAATGAAGTGTCATTATTCAA
DWU-447b	172	-	-	---	ATTTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAAGTATTCTGAACGTGCCCAGTCAGAT GGGCTGTTGCCATTAAAAATCACTGTAATTAATTAGTTTGATTAGAGCACAAAGCTTAGCTAATCAA CCATTATTTTCATTTTGTTCTTCTAAGAGGATTGANAATCAGTTTAGTTTAAAATGTCTTTTCTGTTAG GCCTTCTTCTTACAATGAAAGAATGATTCTTCTAGTTTATGGTTA
DWU-447	85	A	G	---	ATTTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAAGTATTCTGAACGTGCCCAGTCAGAT GGGCTGTTGCCATTAA[A/G]ATCACTGTAATTAATTAGTTTGATTAGAGCACAAAGCTTAGCTAAT CAACCATTATTTTCATTTTGTTCTTCTAAGAGGATTGANAATCAGTTTAGTTTAAAATGTCTTTTCTG TTAGGCCTTCTTCTTACAATGAAAGAATGATTCTTCTAGTTTATGGTTA
DWU-476	63	C	G	---	GTAAAATTCAGTTTTTTGTGCTGCTTCTCAATTAGCGTTTAAGGTGAG[C/G]AT AAATCAACTGTCCATCAGGTGAGGTGTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGGAGATTTTTT

DWU-505	67	A	T	---	TCATACTAGGGCAGTATCTCCTCTAGCTAGTGCCCATACAGAAAATTCTATCACCATACAAAAATTA[A/T]GCAGTATTATGTTTAAAGCACAGGTACCGAAAACTGTGAAAAGTCTGAATTTATGGGTTCTATGCATGCCATTTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTGAAGATGGATTAACTTTTGACTTTGAGCTTTAAACTTTTAA
DWU-512	131	A	G	---	AAAATCCAGGCATTTCGAATCTGTTTTCATGATTTATAGAGGGTTTACACAAAGTGCCACTTATTAAAGAGCTTCCACAGTGAAGATGGAAGGTGAACTTGCTTTGAATATTCCAGATGTGTTTGGTC[A/G]TGCGTATGGCAGTGAGCAGGTATGTTGTTTGCTTGCTTTGCACTGAAGTAAATTGCTATCAAGAGCAAACTATGAACGGTTTTTTATTCAAGATGTCTCCAGAGTGAAGATGCCGAG
DWU-525	97	A	C	---	AACTGCATATAGATAATTATCCAGGATGTGTGGCTCATTCTTTCAGCTTGTTCTATACTGTTTGTAATATACAGTTTTGTAACCATATGA[A/C]AAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACACCCAATTTAAAAAATAACAACATATTCTTGCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAATTCCACCAGGATTAATCTCTAAAATTCTAGTCTCTGATTTGC
DWU-59	94	C	T	---	CATTTCTTTGTGAAAGGTAATGGACTCACAAGGGGAAGAAACATGCTGAGAATGGAAAGTCTACCGGCCCTTCTTTGTGAACGTCACATTGGC[C/T]GAGCCGTGTCAGTTCCCAGGTGGCCAGACTCGTTTTTGGTAGTTTGTTTTAACTTCCAAGGTGGTTTTACTTCTGATAGCCGGGTGATTTTCCCTCCTAGCAGACATGCCACACCGGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68	C	-	---	CTTGATCATGGGGTGGAATTTGTGTATCTGGGCTTCATGGGATGCATAAAAATTTTCCAGTTGGTAAGCAGCAGGTGCCGAGGGTCTGGGATCAGAAAAAAGGCA
WI-19856b	63	C	T	---	CACACTGGCATCTAGGCCTTCGCCTGCATTGCAGAAGGAGAAGGAGAGCCAGGTCCCCCTCCTGGAGAA[C/T]GCTGCGGTTCCCCAGCCCCACACGGCTTTGCACCACACAGGCGTGTTGAGGCAGGAGGTGGGTAAGACGTAGCTGTAGACCCAAAGCAACCACCACCGCCCTGCGGGAGGAGGACACTTTAGAACATGGAAAAGTGTGGTCATCCCATCATTAGACAAGACACATCCTACATAATAAAAAGT
WI-18014	40	A	G	---	TCCATTTACATTGGTGGCATTTGTTGGTGCATTGGAATAGCTACAGAA[A/G]GAATGAAAGTGCACCATCAGAGTGTAATTAGGTCTGTGTGTGACCCAGGAAGTGTCGTTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCTA
WI-18036b	97	T	A	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAAACTTCTAGAAAATACAAAGAGAACATGATAAAATCTGATCACAGTGGAAAATTTTAATTCTTCATAA[T/A]CTGACAGGTCAAGTCAAGTAAGCTAAAGGAAACATATTAGGGATCTGAAGG
WI-18036a	27	T	C	---	TTCCAATGTAAGAGTCAAGTCAAGTACCAAGT[T/C]AAACTTCTAGAAATACAAAGAGAACATGATAAAATCTGATCACAGTGGAAAATTTTAATTCTTCATAATCTGACAGGTCAAGTCAAGTAAGCTAAAGGAAACATATTAGGGATCTGAAGG
WI-18046	72	C	T	---	TGTAAGGTGACTTCTATAAGCTTCCTAAACTGTCAAACTTCATTTACTGACGATTATTTCAGGCCAATGTGTTC[C/T]TTGTTGGGTCTGAGATTTGATTATCAGCTGGGTAAGTAACCTGTTCCTGTTTCA

ID	Pos	A1	A2	Sequence
WI-18063	105	G	A	AGGCTTTAAACTGATAACAATTGCCTTTAATCACATACAAAAACTCTGCCACTTTCATTCCTTCCTTCCCATGTTTTCTGATTTGATGTAAACTTAAAATTTGT[G/A]TCCTTTAACAATATACTGTAGCTGCA
WI-18078	86	A	T	AGTTGAAAGATCAGAGAGGTTATGGTTGGTGAGTAGCTGAAACTCAGATTCAAACCTGGTCCAGTGTGTTGTTTTTTCAGCATCAG[A/T]GTCCACTAGCCAAGTTGATCTCTGCAGTATCTACACTGTGGT
WI-18091	90	T	C	CCAAAGCTCACTCAGTATTTAATCATCTGCTAATTCATCCTTTGTTAATTCCATCAGACACTGTGGTTTTCATCTCTAGAAGTTTGACT[T/C]GGGCCCTTTTTTATACCTTCCATATCTCAACTTGTTAAGC
WI-18119	38	T	C	GCAATCTGTAACAGTTTGGTAGTGGTATTACAGAGGA[T/C]TTGTAAAATGGATTGGAGTACTTACCACTATTTCATCTGCTCTGAAATAGTTCACTAACCAAACTACTGACAACAGTTTAATTTTGGTTCTT
WI-18142	66	T	G	TTCAAGATAATTACAATTGGAAGGGGACCAATAATTCCACTTTTTAATCGAAAATAATCTATATAC[T/G]CCCAATAAACTCACAGTAAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAGAGGAAAA
WI-18178	68	T	C	GCATAGGGGTTGAGGGGTGTACAAGAGGAGAACCAGATTCAGTCCATGCCTGGAGGTTAGTCTGGGGGG[T/C]CGCGGGGATGGACACACAGACACAGACATCTGGCATCTGATAGCAGGGCATACAG
WI-18244	35	G	T	TCAATCTGAAAACTTGCTGTAAGCCAGCCAGCATGGGGT[G/T]GGGGAGGTGATTATGGCTGGGGAAGATGGGCACTCACCCGACACAGCAGCATCTAGCACCACACGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	G	A	ACAGATGTCAGTTGTTTGAATTGGCCCATTAAAGTATGGGGCTTTCTTGTTAAAAGTCATTCCAAAAGGCTTGGCAAGAGAGTTGCTATACAACGGAGGGACAGAGAAACATGA[G/A]CTGGGGGAGTAGGCTCTGACAGAGAAGGTGGGCTGTC
WI-18261	26	G	A	GATTTGAAGGGATTGCTTTATTTAAAC[G/A]TGAAAAGCGTGATAGAGGAACTGTTTAAGATAAACAACTTATAAAATACTCCCAATTGTAGAAGTGAAAGATTG
WI-18268	88	C	T	TAGGAGGGAAAAGGAGGGTGGGCTGCCTGGGCCCTCAAGACATGAGAAACGGGGTGGTGGCTTCCAAGCTTCCTTACTTCCCCATAGAT[C/T]CCTGACAATGTGCTGCAGAAGCCTCCAACCTGGAAC
WI-18299f	107	C	A	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTTTATCTATTTGGGTCTGAGAATTCCACAATTTTGCCAATTATTGACATATTCTG[C/A]TTTTGCCAATTATTGACATATTCTGCAG
WI-18299e	101	A	G	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTTATCTATTTGGGTCTGAGAATTCCACAATTTTGA[A/G]GAATTCTTTGCCAATTATTGACATATTCTGCAG
WI-18299d	77	G	A	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTTTATCTATTTG[G/A]GTCTGAGAATTCCACAATTTTGAAGAATTCTTTGCCAATTATTGACATATTCTGCAG
WI-18299c	67	T	G	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTT[T/G]ATCTATTTGGGTCTGAGAATTTTTGAAGAATTCTTTGCCAATTATTGACATATTCTGCAG

ID	Pos	Allele		Sequence
WI-18299b	52	G	A	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTG[G/A]TTTGCCAATTTTTTATCTATTGGGTCTGAGAATTCCACAATTTTTGCCAATTATTGACATATTCTGCAG
WI-18299a	48	C	T	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAA[C/T]TTGGTTTGCCAATTTTTTATCTATTGGGTCTGAGAATTCTTTGCCAATTATTGACATATTCTGCAG
WI-18307	76	G	A	TCAACTTGTACCAAGTTTAGCAGCAAGAGGAGGATACTTCCTTAGAGACTTTCAGTGGACTTAAACTCAGTTTCCGCTG[G/A]TGCTATGTAAAGCATCCACGATGGTTTTATTGTACTCTGCAATCTGCTTGGTCAC
WI-18324	72	C	T	TTTGGTATGAAATCTTTCTGACATTTACCAATCATCACTTAAACTCAGGGGGGTGGGGTACTGATTTATC[C/T]TAGATCCAAATAAAAGCATGCAGAAGTG
WI-18350	48	T	C	ATGAAAGTCACTTCAATCATCATAAGGGTCAAGAGAGAAAGAATGTTTTCAGA[T/C]TAAATCTATGAAAAGGTGTGTATCTGCTTGCAATTTAAGAAACAACAAGTCA
WI-18395	77	G	C	TCTTGACATGATCTGTGAAATAACGTGATTGTGGTTGAATTTCCTGAAAATTTGAAGAATAAATTGATTATTCAAG[G/C]TGTGCATTGGTTTATACATATCTCCTCTCTTAATGCAAAGCTATG
WI-18398	62	G	T	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAAAGAAAAAGAAAAACAACTCAAGGGTT[G/T]GATAACATTGCCAGTATAACCATAATTCAAAACAAGCAGCAGAATTGGAGGATAATTTGTT
WI-18396	21	C	A	CTCGTTGGTATTCTCTCATCC[C/A]TTCCTTTCGCCTCTTTCTAAAATTAAAGAAAAGCAATGGAATTTAAAAGATCATCTAAGAAATAAGAACTTACATTAACTTATCAACTTGTACAAGTCAATGAAAA
WI-18409a	20	C	A	AAGATGGGAAAGAGGAAATC[C/A]TTTTTCTTACTAGAGATTTTTTTCCCTTTAATCCTTTTCAAATTCAAAGGATCATCAAAGGAGCAGGTGCAGAAGCTCTGGGGCCCAGAGGCCCCAAGTGCTA
WI-18442	62	C	T	AAAAAGGAAAAAGAAAAGGATGGAGTGGAGTAAGAGAGAGAGACAGAGAGAGGAACAAAATAAGTTTCTGG[C/T]TTGGCTGATCTGGGTGATCAGGTGGGACACTATTATCCCAGAAGGGAAAACACAAGAGAAAAAAAAGGTTTATAGGTGGGAGGAAGAGGA
WI-18452	38	G	A	TTGATGTTAATACTGTCATTCTGGAGATCGGCTAAAAT[G/A]AAAGCATAGTTATTATTAGCTTTGGTATATTCTGCGACACAGATTTAAACAAGTAAGACATATATCAACCCTCTCATATTTTCCAACCA
WI-18489	102	A	C	ATATAAAGCTGGAGACTGTTGGGAGGGTGGGGGGACTAGCTGTTGAAGAGAATGTAGCAGTAGTAAAGATGAAAGACTGCAAAACA[A/C]GGTTATGGCAATGAAAGAAAGGCCATATAAA
EST5b	93	A		CTGGTGGGAGGGAAGAAACAAATTGTGTATATTCATACAATGGAAAACTCTTCAGAAATAAGAAGGAACAAACCACTGAATCACACAACACATGGACAAATCTCAAATCATTATGCTGATGGAAAGAAACCATTCATAAGAATACACAGTACAT

EST5	93	A	---	CTGGTGGGGAGGAGGAAACAAATTGTGGTATATTCATACAAATGGAAAACTCTTCAGAAATAAGAAGGAA CAAACCACTGAATCACACAACATGGACAAATCTCAAATCATTATGCTGATGGAAAGAAACCATTCA TAAGAATACACAGTACAT
EST6	48	C	---	TTAGCTACTTTCAGAATTGAAGGAGAAAATGCATTATGTGGACTAAGCCACTTTTCTAAAGCTCT GAACAAAAGCTTTTCTTCCTTTGCAACAAGACAAAGCAAGCCACATTTGCATTAGACAGAT GGACAGGACCTCTATTCCCGCCTGGTGCGCAGCAGCCCAGGGCTGATGGACTGAGGCCCCAGGGATACTGGGCC CTCTTCTCAGGGGCGTCTCCAGGACCCAGAGCTGTTCCTGCTTGAGTTCCCTAGAGCTGTGTGCGGCCA
EST8	158	A	---	GATAGCTGTTCCTGAGTTGCAAGCACGATGGAGATTGGAGCACTGTGTGCTTTGGTGGGGT TCCTCATTGTTGGGGATGATGAGAGAAAATGATTTGGGAAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAATCTCATTTACCATCATGTATCCAGTAGTG[G/T]ATAATTCATTTGATGGCTTCTATTTT TGGCCA
WI-18740c	104	G T	---	TCCTCATTGTTGGGGATGATGAGAGAAAATGATTTGGGAAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAATCTCATTTACCATCATGTATC[C/G]AGTAGTGGGATAATTCATTTGATGGCTTCTATTTT TGGCCA
WI-18740b	96	C G	---	CCAAAGTCTCCTGTTCGCTCATAAAGAAGTTTTGGGATGGGAGAGAATCCAGACCACCATCTTGGGGCA GCCAGGCGCCCTGCCCTTCATTTTACAGAGGTAGCACAA[C/T]TGATTCCAACACAAAACCCCTTCCCC TTTTTAAAATGATTTCTGTTCTAATGCCATAGATCAAAGGCCTCAGAAACCATTGTGTGTTCCTCTT
WI-18985a	105	C T	---	TGAAGCAATGACAAGCACTTTACTTTCACGGTGGTTTTGTTTTTCTTAT GCCAGCAGCTGAAGTGTCTCTTTTTCTCTCGGCTGGAAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGTGTACTTGACCGTTTTATATTACTTTGTAAATATTCTT[G/A]TCCACATTCTACTTCAGCT TTGGATGTGGTTACCG
WI-18746	114	G A	---	CCGTGTTCACACACACAATGGCAAGCATAGTCGTCGCCTGGTTACGGCCCAGGGGGAATATGCCAAGG GACCCCTTAATGCAAAACACAGATCAGTAGTGCTATCTCATGACAACCACAAGAAACCGACGACAAA TCTTTTGCGAGATTTTCTTCTAGTGGCTTAGAAAACATGGCTTTTAAGAAACACGGTGATATCTTTGAG GGTGACAAGGC[G/A]TCTCTTCAAACAGTTCCATACAACTGCTTGCTCTAG
WI-19112i	212	G A	---	TGGTGGCTGGCTAGCTAGTTTCTACAGAACACATAATTTGCCTCTATAGAAGGCTATTCTTAGATCATGT CTCAAATGGAAACACTCTTCTTTCTTAGCCTTACTGAATCTTGCCTATAATAAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCCTGAAATTTCATCTTGAATGTCTTTGTATTAAACTGAATTTTC
WI-19092	232	A C	---	TTTTTAAGCTAACAAAGATCATAATTTTC[A/C]ATGATTAGCCGTGTAACT
WI-19057i	175	G A	---	CCCATTTATTATAGGCCAGTGATGTGTCTCAAAGAGTAGAGGAGGCGTCTACTGTCTTCAACTCCTTCA GTCTTCTGACGGCGGGACTTACCGTGACAGCGGAAGTGGTATTGTACGTCCAGGCACCGCAGCCACTG TCTTCATGCAGGAACCACCACAGTGCCAGATCCCCACAGCTC[G/A]TCTTCATCTTGGTTTTGCCACA

Name	Pos	Allele	Allele		Sequence
WI-20103	168	C	T	---	TGGGACTTCCAACTCAGAGGATGTGGGAATCCCAGCTCAAATGATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGGATATGGGAGTCATGGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCCTGGGCTGGAAGCTGGGTCCTCCCCCA[C/T]TTCATTCTGCTCAAAGCTTCTTGAAGGAGC TGGTTTGACTTCAACTTGCTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111	G	A	---	GCCTTACCCATTTTGCACATATATACATATGCACCACCTTTGCAGTGGCAACATATATCCACACTA TAAACATACCACCATTTATAAATCTTGTAAGGACAAGAAATGGA[G/A]TTGAATAAGTACCCCCCAA CATATACAAGAAAAGTTAGCATACTTACCCCGTTTTCACTACATCAGAGGCAAAATAAGAAATCTTT TAAGAAAATCTCAAGACTGGCTCATGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116	A	G	---	TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAAGAACGT TTTAGTCTTTTTAAACTGAGTTTAAAAAAAAATAACAATGCAATTTTA[A/G]ACACTGTTTTGAAA ACTTAAAAGTGCAGCAATA
WI-20613c	165	A	G	---	GTCCTCAAGGGGGAGAAAACTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAAATGGCATGGGAGGAGGCAGTTAGAAAAAACATCTAAAAC AGCTCCTTAGAAGGGGCCAATAATAAAAGTTGGAA[A/G]AAAGGGAGTTCCACGCAGCCAGTGGTGAGC TGC
WI-20613b	156	A	C	---	GTCCTCAAGGGGGGAGAAAACTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAAATGGCATGGGAGGAGGCAGTTAGAAAAAACATCTAAAAC AGCTCCTTAGAAGGGGCCAATAATA[A/C]AGTTGGAAAAAAGGGAGTTCCACGCAGCCAGTGGTGAGC TGC
WI-19984	47	A	G	---	CAGTAAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAAATA[A/G]TATAAACATTAGAAAA GCAAAATTCTTTAACTTAAGGACAGAGCTGAACCATCAGGTATGGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGAGTTTTCCCACACTGGAAAATGAAGGCAGTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	T	C	---	GCCAGTTGGAATATGGCCTATACGAACCAAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTCCTTGGAACTCTGCACCGACTGTCCATGCTCTGTGTGGGGACTTACACATTCAAGTTTGACAG[T/C]TGAAAAACCAACTGAGAGCTGCTTTCCAAGAATGTTCGTTCCTTCAAATAGGAATTCCATG TTATTTCTTTCTTGCCTTAAGCTCTTATATCTTTCAAATGACCTAAGCTGA
WI-18846a	49	G	A	---	GAGTGCCATACCTTCTCCCCAGGCCTCTGCCCCAAGAGCAGGAGGTGCCT[G/A]AAAGCTGGGAGGCGT GGGCTCAGCAGGGCTGGTCACCTGGTCACCTCCTTCCCTTCCCTGTAAGACCTCCTGCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123	G	A	---	AGCAGTGGCCTATTGCATCCCAAACCACGCCTCTTGACCAGGCTGCCTCCCTTGTGGCAGCAACGGC ACAGCTAATTCTACTCACAGTGCTTTTAAGTGAAAATGGTCGAGAAAGAGGCACC[G/A]GGAAGCCG TCCTGGGCCGTGGCAGTCGGTGGGACGGATGGTTCGTTGCCGGTCGTGTTGAGATTCTCAAAGGAGGAGCAT GTCGTTGGACACACAGACTATTTTGAGATTTCTTTTGCCTTTTGCAACC

ID	Pos			Sequence
WI-20146	31	T	C	---	TGAGTCTCTCTGTAATTCATTGAGCAGTTAGC[T/C]CATTTGAGATAAAGTCAAATGCCAAACACTAGCTCTGTATTAATCCCCATCATTACTGGTAAAGCCTCATTGAATGTGTGAATTCAATACAGGC
WI-18922	74	G	A	---	TAGGAATTGGTTTCACGCCTGAGGCAATTAGACACTTGGAAGATGGCATAACCTGTCTCACCTGGACTTAAGC[G/A]TCTGGCTCTAATTCACAGTGCTCTTTCTCCTCACTGTATCCCAGGTTCCCTCCCAGAGGAGCCACCAGTTCTC
WI-18763b	53	A	G	---	TTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA[A/G]TATTTAGAATGTACCATATTTTTGTAAATTATTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAA
WI-18763a	38	A	G	---	TTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGA[A/G]TGACGATGATGTGAATATTTAGAATGTACCATATTTTTGTAAATTATTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCATGTGTTTTGCCAA
WI-18771b	75	G	A	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAAGATGTTGGGAACAGAA[G/A]AAATAAACTGAGTTTAAGGGGGACTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57	A	G	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAG[A/G]AGATGTTGGGAACAGAAGAAATAAACTGAGTTTAAGGGGGACTAAACTGCTGAATTCACCTGTGGA
WI-18820	70	T	C	---	GGGAAAAATTTGAGACGCAATACCAATACTTAGGATTTTGGTCTTGGTGTTGTATGAAATTCTGAGGCC[T/C]TGATTTAAATCTTTCATTGTGTATTGTGATTTCCTTTTAGGTATATTGCGCTAAGTGAAACTTGTCA
WI-18742b	51	C	T	---	ACAAAGTCCTGTAGCCCCCTCACCTTTCCTGTTTCACTTTTGCCAATGTA[C/T]ATCGGGTTTTGGTTTTCTTGTATATTTAAACGGTTGTGTGGTTCCTTTTCCTTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCGAGGAGAGTTTTACC
WI-18882	94	C	T	---	GTGTGTCCAAAAATGGGGTCTGCTCCTGCTACCTTGACCCTTCCCTTCCTCTGCTTCTCTCTCCTCATCATCATTCCCAACAACATCCTCTGCCA[C/T]ACACAACAAAACGTAAGTTTCATTTGGGCAAAAATTGAGC
WI-19970b	167	G	A	---	TATAAGCCCGAGTCACCAGGACGGCCCTGTCTGGGCCACAGACAGGGGCTGTGGAGCCTGCCCACCGGCCCCCGGCAGTGCAGTCCAGCGGGGGAGGAGGCTGCCCGGTTCCTCACTGCGGGGGACCAGCAAAGGCCTTCTCACTGGGTTGGTCAAAG[G/A]TAGTCACCTTGGCCTGGTGCATCCACAGAGGATGTTGTTCAAACCAGAAATCTTTAAACGACTGACCTTCCTTAAAAACAGA
WI-19970a	126	T	C	---	TATAAGCCCGAGTCACCAGGACGGCCCTGTCTGGGCCACAGACAGGGGCTGTGGAGCCTGCCCACCGGCCCCCGGCAGTGCAGTCCAGCGGGGGAGGAGGCTGCCCGTTCCTCAC[T/C]GCGGGGACCAGCAAAGGCCTTCTCACTGGCTGGTGCATCCACAGGTAGTCACCTTGGCCTGGTGCATCCACAGAGGATGTTGTTCAAACCAGAAATCTTTAAACGACTGACCTTCCTTAAAAACAGA

WI-19067d	202	T	G	---	TATTGCTGTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCCTGGCTGTGCACATTCCCTCCTGCTCCCCAGAGACTGCCTCCGCCATCCCACAGATGGATCTTCAGTGGGTTCTCTTGGGCTCTAGGTCCTGGAGAATGTTGTGAGGGGTTTATTTTTTTTAATAGTGTTCATAAAGAAA[T/G]ACATAGTATTCTTCTTCTCAAGACGTGGGGGGAAATTATCTCATTATC
WI-19067c	153	G	C	---	TATTGCTGTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCCTGGCTGTGCACATTCCCTCCTGCTCCCCAGAGACTGCCTCCGCCATCCCACAGATGGATCTTCAGTGGGTTCTCTTGGGCTCTAGGTCCTG[G/C]AGAATGTTGTGAGGGGTTTATTTTTTTAATAGTGTTCATAAAGAAATACATAGTATTCTTCTTCTCAAGACGTGGGGGGAAATTATCTCATTATC
WI-19067b	151	T	C	---	TATTGCTGTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCCTGGCTGTGCACATTCCCTCCTGCTCCCCAGAGACTGCCTCCGCCATCCCACAGATGGATCTTCAGTGGGTTCTCTTGGGCTCTAGGTCCT[T/C]GGAGAATGTTGTGAGGGGTTTATTTTTTTAATAGTGTTCATAAAGAAATACATAGTATTCTTCTTCTCAAGACGTGGGGGGAAATTATCTCATTATC
WI-19067a	57	C	G	---	TATTGCTGTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCC[C/G]CTGGCTGTGCACATTCCCTCCTGCTCCCCAGAGACTGCCTCCGCCATCCCACAGATGGATCTTCAGTGGGTTCTCTTGGGCTCTAGGTCCTGGAGAATGTTGTGAGGGGTTTATTTTTTTAATAGTGTTCATAAAGAAATACATAGTATTCTTCTTCTCAAGACGTGGGGGGAAATTATCTCATTATC
WI-19106	247	T	C	---	TTAATCCCAGCCCTACCCTTGTAGTTATTTTAGGAGACAGTCTCAAGCACTAAAAAGTGGCTAATTCAATTTATGGGGTATAGTAGTGGCCAAATAGCACATCCTCCAACGTTAAAAGACAGTGGATCATGAAAAGTGCTGTTTTGTCCTTTGAGAAGAAAATAAATTGTTGAGCGCAGAGTAAAATAAAGGCTCCTTCATGTGGCGTATTGGGCCATAGCCTATAATTGGTTAGAACCTCCTATTTTAA[T/C]TGG
WI-18944	147	A	G	---	CAAGGCAAAAATATCAGGAGCTTTTTACACACCTACTACTAAAAAAAGTTATTATGTAGCTGAAACAAAAATGCCAGAAGGATAATATTGATTCCTCACATCTTTAACTTAGTATTTTAACTTAGCATTTCAAAACCCAAATGGCTAGAAC[A/G]TGTTTAATTAATTCACAATATAAAGTTCTACAGTTAATTATGTGCATATTAAAACAATGGCCCTGGTTCAATTTCTTTCTTTCCTTAATAAATTTAAGTTTT
WI-18952	232	G	A	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATTGGAATAAGCCTTCATATAACATAAAGTTCTCTGTAATTACAACTAAATTATTATGCCCTCTTCTCACAGTCAAAAGGAACTGGGTTGGTTTTTGTTGCTTTTTAGATTTATTGTCCCATGTGGGATGAGTTTTAAATGCCACAAGACATAATTTAAATAATAAAACTTTGGGAAAAGGTGTAA[G/A]ACAGTAGCCCCATCACAT
WI-18932d	177	C	T	---	CACACCTCATGCTAGCCTCACGAAAACTGGAATAAGCCTTCGAAATGTCCTTGAAGCTTGTATCTGATATCAGCACTGGATTGTAGAACTTGTTGCTGATTTTCAAGTTAACTGTTCCCCTTGGTATTTGTTAATACCCTGTACATATCTTTGAGTTCAA[C/T]CTTAGTACGTGTGGCTTGGTCACTTCGTGGCTGGAGGTAAGAACGTGCTTGTTGGAAGACAAGTCTGTGGCTTG

WI-19042	193	A	C	---

TTTGTCAGTGTTGCCTCTCGCCAATCGCCTCCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATG
GATAAGGGAATAATAGGCACCAGACAAGAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG
ACACAATTTATACTGCGACAGAACTTCAGCATTCAGCATTGTGTAATTATGTAAATAACTCTAACCA[A/C]GGGCTG
TGTTTAGATTGTATTAACTATCTCTTCTTGGACTTCTGAAGAGACCACTCAAT

WI-18984	208	A	C	---

ATTGGCCCTGTACAGTTGCTTATTTATAAATTCATTAAAAACACTACAGGGTGTTGAATGGTTAAAA
TGTAGGCCTCCAGTTCATTTTCAGTTATTTCTGAGTGTGCAGACAGTCTATTTCGCACTGTATTAAAT
GTAACTTATTTAATGAAATCAGAAGCAGTAGACAGATGTTGGTGCAATACAAATATTGTGATGCATT
TATCTT[A/C]ATAAAATGCTAAATGTCAATTTATCACTGCGCATGTTTGACT

WI-18851	90	T	A	---

GCTTCAATTGGCGATTGATTCAGTGCCCACAATGTAAACAGGGTTGGTAGTTGTTACTCATTTTGAAT
ATAACCTTTTCCTTATTGTATTC[T/A]GTAATATAGGATCCTGGAAATGAGACCTGGTGGAA

WI-18821b	76	T	C	---

TCAACTGCAGTGTTGCTTCCCTGCCCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC
ACAGAGGC[T/C]GGGGGGTAGCCATTGTGCAGTCATGGCCCGGGGGAAACTTGCCAACCTTCGTGTCAG
GTGCTGTGT

WI-18821a	69	C	T	---

TCAACTGCAGTGTTGCTTCCCTGCCCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC
A[C/T]AGAGGCTGGGGGGTAGCCATTGTGCAGTCATGGCCCGGGGGAAACTTGCCAACCTTCGTGTCAG
GTGCTGTGT

WI-19021a	20	C	G	---

ACTCCTCTGCTGCTGTCCATC[C/G]ACTGTCCTTTTGAACCAGGAAAAGTCACAGAGTTAAAGAGAA
GCAAATTAAAACATCCTGAATCGGGAACAAAGGGTTTATCTAATAAAGTGTCTTCCATCACGTTG
CTACCTTACCCACACTTCCCTCTGATTTGCGTGAGGACGTGGCATCCTACTTACGTGGCATAAC
ACATCGTGTGAGCCCATGTATGCTGGGGTAGAGCAAGTAGCCCTGCCCCTGTC

WI-18908	70	G	C	---

TGGAAATTCCCTTCATCTGGAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAAGGGTCAGTA
TGG[G/C][T/C]TAGGGAAAACATTCCATCCTCCTGAGTCAAAAAATCTCAATTCTTCCCTATCTTTGCCACCC
TCATGCTGTGTGACT

WI-19037b	155	A	G	---

CACGGTTCTCTGCATCGTTACCAGAGCGCCCTTCGTGGTCCTAGCCACGCCCTGTATGACCGCGCAAATA
TCCCCAAAGCTTTGGGTCCTCAAGTCATGCCGGAATTTAGATGCTGGTCATTTTCTGGAGAGGGGTC
CCCTCCCCTTACGAACACA[A/G]AAACCCAGCCCACATGACTACACGCTGAGCTCTGCAGGGACCA
GTGCCAGGCACTGGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG

WI-19037a	47	C	A	---

CACGGTTCTCTGCATCGTTACCAGAGCGCCCTTCGGTCCTAGCCACG[C/A]CCTGTATGACCGCGCAA
ATATCCCCAAAGCTTTTGGGTCCTCAAGTCATGCCCGAATTTAGATCGTGGTCATTTTCTGGAGAGGG
GTCCCCTCCCCTTACGAACACAAAACCCAGCCCACATGACTACACGCTGAGCTCTGCAGGGACCA
GTGCCAGGCACTGGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG

WI-19064	66	T	C	---

TTGAGGGGGTGGGGTGAACTGCTCCTTGGCAGGGATTTGTGACACTGCATTGCTGGGCTGTGTTCC[T/
C]CGGGCCTCTTCTGGACCTTGCACCGTGGATACCACCAGCCACGTGCCATGTGATATTTGGGGTCCTGGGGGGG
TGGGTGAAATAAAGGC

ID	Pos	Alleles		Sequence
WI-18972a	112	A G	:::	AGGCCTGTGCTTATGTCACCCAACAGAGGGGTCCTGAGAAGTCTGGCTGCCTGGGATGCCCCCTGCCCCCTCCTGGAAGGCTCTGCAGAGATGACTGGGCTGGGGAAGCAG[A/G]TGCTTGCTTGGCCATGGAGCCTCATTGCAAGTTGTTCTTGAACACCTGAGCGCTTCCTGTGGCCCACCAGGCACTACGGCTTCCTCTCCAGATGTGCTTGCCTGAGCACAGAGCAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184	C A	:::	GTTTGCAAACCAACATGTGCTCTTTCAGTCATTCACTGTTTAATATGACATGGTAGAGAAGATAAGGTTTATGGCCAGGTAATTTTTGTAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTCCTGAAAACCTTAGATACATAGCCGACTGTATACACAGAGGTTCATCTCAA[C/A]CTCAACACTATTGACTTTTGGGGCTGGATAGTTCTCTGTTGTGTGGGGGTTTGTCTTGTGCACTGTAG
WI-19016a	161	C T	:::	GTTTGCAAACCAACATGTGCTCTTTTCAGTCATTCACTGTTTTAATATGACATGGTAGAGAAGATAAGGTTTATGGCCAGGTAATTTTTGTAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTCCTGAAAACCTTAGATACATAGCCGA[C/T]TGTATACAGAGAGGTTCATCTCAACCTCAACACTATTGACTTTTGGGGCTGGATAGTTCTCTGTTGTGTGGGGGTTTGTCTTGTGCACTGTAG
WI-20096	21	T C	:::	GGTTTTGGGGGCATTTATTTC[T/C]GATAGAGACTGGCACAAGCTTGGGCTAAGGACACCGCCCCCACCCTCATCTAGAAACAATCTCTCTGCCAGACTTG
WI-19591b	156	C A	:::	TGGGGCAATTTTAACAAACCAGGCAAAATATCACATATACCTGAATATAAGGTAACTCCAAGCCATGAGTATAAGATTAAGGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGTGCCCCTTAGGGTGGGGAGCTCTTCCC[C/A]CTACCACTCCCCACCCCAAGGCATCATTTTGGGAGAAAAAAGTGTCTTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45	T A	:::	TGGGGCAATTTTAACAAACCAGGCAAAATATCACATATACCTGAA[T/A]ATAAGGTAACTCCAAGCCATGAGTATAAGATTAAGGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGCCCCTTAGGGTGGGGAGCTCTTCCCCCTACCACTCCCCACCCCAAGGCATCATTTTGGGAGAAAAAGTGTCTTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125	G A	:::	TCCTCCAGCTCTGTCATCCTTGTCTGTGTTCTGAGGGTTCTGTGTTCACGGCCCCTCCAGGCATGGTTTCTTCATTTAGGTAGGAACAAAAGGCCAAAAGAACATACAAGCCCAGCTCTCTAGAGGCTCCA[G/A]TCAGAACTGGACCCCTTAACTACAAAGGAATCTTGGATGAATTATTTTAGCGGGGCTTCAGGAGCAGGTAGCAGAGCCAAAGTGCACACTCAGGCCATCTCAGGCCATCTTCCTCCCAATGTCCTCCCGGGGGG
WI-20860	224	G A	:::	CTCTCCCCTTAAGGAGCCTTGGCCTTGCCAGCCCCATTCAGCAGGGATGGAAGTCACAAGACAATGAGTGGAGCCCTCATGCCCTCCCATGGAGGAAGCCCTTAGTACTGCTGACATCTGCCCTTATCCTGTCTCTCCTCCCCAGTGCTGTGTCCACACTGTTGGGCAAAGCAGAGTGGTGGCAGACCCAGCCCAGCTCTTGTGTAGACCGGAAGGAAGGGGCGGTCATT[G/A]GGTGATGGCTTCTGGCTCTGGCTT
WI-19359a	39	T C	:::	GACGTGGACAAAGGAGGAGGTTTAAATGAATACTTTGTTTGT[T/C]CATGTTCAAAAAAAGAGTATTAATATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAAGCCATGTTTCCAACTTAGGTTAATAATAAGGCTATTTGTCCACCCACTCTTCGGGATTGCTGCAATATTCCTGGCCTCAAGTGGGGAGGCCCACGTGGGAACAAGGCCCTCAGAAAACAAAGGACATGCAGCCTCCCTGAGCCCAGTTCCT

ID	Pos			Sequence
WI-19766b	93	A	G	TGGCCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGGCAGGGCAGG AGATGAACCATAGGAGCCAAAAGTC[A/G]GACAAACAGAGAAGGCACACCAAGCCTGAAACCCTC CGGCAACAGCAGAGTTACCAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTC ACCCTCCTTCACCCTCGTTGGGCAGGCTCTCGGCAGTCATGGACTTAT
WI-19766a	31	G	A	TGGCCTCAATGACTGGTACATTGGAGAAGCT[G/A]TGCAGCAGCATCCTTTCTGTGGTGGGCAGGGC AGGAGATGAACCATAGGAGCCAAAAGTCAGACAAACAGAGAAGGCACACCAAGCCTGAAACCCTC CGGCAACAGCAGAGTTACCAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTC ACCCTCCTTCACCCTCCTACCACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126	C	G	CTTCCTCTGTTTGGCTTTGCATTTGTGCGATTTGGAAAAACCACTTGGAAGAAGGGACTTTCCTGCAA AACCTTAAAGACTGGTAAATTACAGGGCCTAGGAGTCAGTGGAGCCCCTTGACTGA[C/G]AAAGC TTAGAAAGGAACTGAAATTGCTTCTTGAATATGGATTTTAGGCGGGGGCGGTGGGGTGGGCTCACGCCT TATTAATCCCAGGCACGTTGGGGAGGGCCAACGCGGGGTGGGATCACCTGA
WI-20512c	59	T	G	CTTCCTCTGTTTGGCTTTGCATTTGTGCGATTTGGAAAAACCACTTGGAAGAAGGGACTT[T/G]TCCTG CAAAACCTTAAAGACTGGTAAATTACAGGGCCTAGGAGTCAGTGGAGCCCCTTGACTGACAAAGC TTAGAAAGGAACTGAAATTGCTTCTTGAATATGGATTTTAGGCGGGGGCGGTGGGGTGGGCTCACGCCT TATTAATCCCAGGCACGTTGGGGAGGGCCAACGCGGGGTGGGATCACCTGA
WI-19599	230	C	G	GGGCTTAAAATTCCCCTCTGTTTGGGACTGGTCTCTCCCAGTTACAGCAAAGGATCGCACCCTTTCC ATAACCCCTTCTACATTGGAAAGAGCACACCTTGTATACAGAATGGCTCCGTGAAGTCTTTAAACG GACAAAGGTAAATCACAGCTAACAAAACGTGATGTTGGCTCACACGTAACCAAACACCTCTTTTTCA GAACAGAGAGCGTTAAAAGTAAAAGTAAAAGGGCA[C/G]TTCCAAGAGTAACACTGCTA
WI-20679	82	T	C	TGTTTGAAATAAAAAATTTCCATGGTCTTAATTGAACTGTATGTTCTTTCTTTTAGAATATCCTTTT TTCATTAAAATAATT[T/C]TCTAAACCACTCTATGTTCAACCTTCTGTTTAACACTAAGATATGGGT TTTTGGAAAGGCCACAGTCACCAGCTCCATGAGTGGGCGAATTGGTCCTTGTTTTGGAAAGCTCTC CAGGGTGTTTCTCCAGAAA
WI-19909a	29	T	C	CCAGAAATAAAAGCCTGAAATATTCTCTTTC[T/C]TTAAAAAATATAATTTTTCCTTCTTTGCTCTTCCAA GTAAATCTTAAAATGAACCTGTTCTAGTCTATTTTTAATCTAGGCAATTATAACACTACCTAGGCGGGG TTTTTCTTTATACCTTGTTCTCTGTTACTGTGGAATCAACTAA
WI-20341	221	G	C	TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAAGTGCTTAGGGCATGAGAGACATTAGGAAG GCCACAATTATGAGTAATGAAATGTGGAGGCTGAAAAGCTACTGCTCCCATTGTTTAGCAGGA GGCAGGAAAAGTGATCTGGGGTCTCTGGCCAGCAAAAGCGTGTGGTAAATATTGGGTGACGTCATGC ATCCCCCATGCATTGGTTTTTG/C]ATGTCTCCAGTGAGCTGTTGGGCAAGTCT

ID	Pos				Sequence
WI-20113	60	T	C	---	TTCTGGTACACATGGTAAGTGCTCCAGTATTACTGAGTGAATGAGCAAAGACCTGAAATACTG[T/C]GGAAACAGTAAAAGCAAATTACCACACACAATTAGGAGGAATTATTTCAGACACATAGGATATTTAAAACATCACTCAAAATACTGGAGCATGATTCAGCAATAAATTCTATTCCATAAACCAGGTAGATAAATGTCACAGCTTTAAAATATAGTTAAGTACAGTTGATCCTGCGTTATTCATTGGATTCCGTATT
WI-20895	107	G	C	---	TGATGGCAAAGTACAAAGGCTCTGAAAGAACAGAGTAAACAGAGGCAGCGCAGTGCAGCGTGTGGCCACTTCCCACCAGGCAGAAACACTTGACTTCATTAAGGCAAA[G/C]CTTTACTCTGTTACTTTTCCTCCCACATAGTTTAACCCAAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAATATAACTGGTACTATAGGCAAACAGATGCA
WI-20721	72	T	C	---	CCTGCAATCACAAAAGTGGAACTAGTTGATATTTGAAATCATACTTGATTTAACCACCTTCAGAAATTTCTA[T/C]AAAACACTAGCAACTTCCTTTATCAGA
WI-19415c	161	A	G	---	CTGGATTTAATATTTCTGGCCTAATAACCAAATGTAATCAATAAAAATTTGGTCAATATCTCCACCTCATTTCTGCTAACATGTTTTGCAAGATTCCCTAAGTAAGGTATTGACGACTGAGACTAGTCCGGCAAAGTCATGAGACCCTTAGCTGATCTCAT[A/G]AAGTCCACCTCATGAAGGAGATGATTCAACATCTCAAGCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAGTTTTACACTTCCTG
WI-19348c	103	C	T	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGGTAGCAAGTACGATGGGCCATGCACTTCTGGCGGGTCGATGAAGAGACTGTTGGTCATGGCGGTGA[C/T]GTCCTTCTCCAGGCTCATATGGATGTCCTCGAGGGTGCACAGGGAACTGCTCTCGCTTGTGAGAAGCTTCTCC
WI-19348b	98	G	A	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGGTAGCAAGTACGATGGGCCATGCACTTCTGGCGGGTCGATGAAGAGACTGTTGGTCATGGC[G/A]GTGACGTCCTTCTCCAGGCTCATATGGATGTCCTCGAGGGTGCACAGGGAACTGCTCTCGCTTGTGAGAAGCTTCTCC
WI-19635	98	A	T	---	ATTAGTTCGTGTGTGGGCCACATTCAAAGCCATCCACACAGCTTCTTGTAGGCCATTGTAACACAATGTTAAAAGGTACAGTAAAAATACAGTATTAT[A/T]ATCTTATTGTTAGCACGGCTGTGAGGCTCATTGTTGAATGAAGCATCCTTAGGCAGCACGTGACTGCATGCAGATATGTGCTGCAGAAGAACTTTGCCTTT
WI-19641a	46	A	G	---	TCCAATTTCAGAAAACATGTTCCATGTTTATTGTGATAAGCACTAG[A/G]TATTATAGTCTCATGTTTTTAATTTATGAATAACGTCTGATTCATTTGATTTGTATTTGTATTTACAGAAGATGTCAGGGCTACTATCTCATTCAGTTATTAATAAATGGATCAGAGTAGTCAAGAATAAGTGCATAATGTGGTTAAATTTTAAAAAATACTCAGAATGAGGTAGTAGTATTTTAATTTTAATTCATCCACCACCTTG
WI-19642b	52	C	A	---	ATATAGAGTACCATCCATGTTTCAAGCATGGCCTGGACACATTATCCCCCT[C/A]GGGTAAACCAGGACTATTGCATGAGCATTCTTAATACGTATTTTGATGGACACAAGTTTCATGTCTATTA
WI-19673b	180	C	T	---	TCTGCCATGATCACATTGTCATGATGAAGAAACATGATGGTCACTAGGTAACTTTCTGTGTCATTGCCTTACTCTCAGTGGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGCATCACCACTGTAAATCTAATAGTGAAAAGGCAAATGATGTCTCAGTATCGTCAGTATCACTGTGAAAACATTTTTC[C/T]CTTGGACCAGCTGAAAGAATCTTGAGGAGCCTGAAGGCTTCAAGGTCCCACACGTCCACACAAAAAAACACAGCCC

ID	Pos				Sequence
WI-19673a	35	G	A	---	TCTGCCATGATCACCATTGTGATGAAGAACATGATG[G/A]TCACTACTAGTAGGTAACTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTGCATCACCACTGTAAATCTAAT AGTGAAAAGGCAAATGATGTGTCTCAGTATGTCTCAAGGTTCAAGGCTCGAAGCTTGAAGCTTCC CTTGAGGAGCCTGAAGCGTCGAAGGCTTCCACGTCACACGTCAAAAAACACAGCCC
WI-19724	35	A	G	---	TTTATTTGGGAAACAAAAGGATTGTAATTTGGGTAA[A/G]CTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAAACACGAGAGAGTTTTGGTTTTTCTCTT
WI-19307	196	T	C	---	TCCTCCTCCCCAACTAGATGTATTGATCACTCTGCCCACAAATGGTACCCCTTCAGCAAGAACTG CAAGCCCCTTCTTGGATTTGCCTTCATGAGAAAATGGTGGCTTGGGATGGAGGTGACATTCCTTGCTGT GGTGAACTGCAAAGAAGGAAACCAGGCAATGTATTCCATAGAGGCCTTTAAAGAGACCCG[T/C]TGG AAATGGGCCATGGTCTAATTTGGTGTTGAAATAAACTAACCTCTTTGGCTG
WI-19269	85	A	T	---	CTTTCCCTCATCCCCTCTTCCACCACCACCATCCGGAACAAGTGCTCCAGGATTCCCTGCCCACTGGC CATTTTTGGGAGTGTGTCC[A/T]TTGGGTAGCAATGTGGAAACCACCAGGGCCTTTGTGGAGAAAATGG AGGGGGTTGAGGAGGTCCCAGGAGGGGCCTTATTTGCTCACTTGCTCATAGGCGGAGCTCG ATCTCCTCATCTCTGGACAGGTGGAAGCGAATTCTTCCCGGGCGTAGGCA
WI-19946	122	C	T	---	CAATGGACTGAATGAGTGCGTGCTGGGTGGGGGCACACACCTTCAATACACGTCAAGGTCG CTTCCAGTTTTAGAAAAACAGAAATCTGCATCTCAGCCTGAGACGCCACAGAGAGGT[C/T]TCTTCCTG ACCCAGACGCACTCACGAGCCAGGTCCTGGTTTTCAAAACTGCATTAACCTGCGCGCCAGAGAGTTCAC CGTAGGCATCTCTTTAATAAACTAACTCCAGCAAACAAATGTGGGTACGGTTACTAA
WI-19956	141	G	A	---	CACAGCCATGGTGAAATAGCATCAGATTGAAATGAAAAGTTTGTAAATGCAACCATAAATAATTATA ATAAATATACACCAAGTAACTTACAGCACACATTTTAGGGCCAAGGTTTGGATCGTGTCTGGACCT CAATGT[G/A]CTCTCGGAGAAGCCAGTAAATCTATCTTGCGCTCCTGAAAAACTGCAGA GTGATGGCCAACAGAGAGCTTCTGAACTCCTCCTGGGGAGGTAGCTGACAAG
WI-19076	40	G	A	---	TTGGTTGGATACTTGCTGGAAAAAAAAAGCAGTTTTAAT[G/A]GTATTCAAAATACCTTTAAAAA GTATTCTAGCACAAGAGATTTTTCTGTAAACTAGATTATGTTGTAAACTTTTTCTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATTCCTATTCCAAATCTATCTTGCGCTCCTGAAAAACTGCAGA AAGGCACTTGAAAGCTGTTTCTTTAAGGATTTCTTTTTATTCTT
WI-20218	26	T	C	---	CCACACACTCTGGTTTTATAAAGCTA[T/C]AGGACAGAGCAGAGATGGAACTGAAAAAACAGGGTAG AAAATAACATAAATTGGAGGGGAACAGTGGGGATGCAGAAAGAATGACACAGCCACATGTGCCCCA GTCAAATACTTTTAGTCCCTGCGACAAGATGCCAACCAGTCTCTATACTGGCTGGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154	T	G	---	CAACCTTTTTGACAAGGGGACGTGAATTTCTGATGAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTCTTTAATATCTCCAGGCTGATTGGGGAGGGGGCTGGCCTCTACCCTTTCTTCTTCCA TCCAGTCTATTGCCAGAT[T/G]CCAGAGAAAAGCGCGGGAAGCCCAGCTCTCCAGCATAGCCACTGTGG GTCGGGCTTCACCTTCTGTCGACTCCTCGTCGCCATGCTGGGACTTGTCTTTCGGGG

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WI-20361a	192	G	A	---	CTGGGAGTGCTGACCTAAGTGACATTTTTTTAATGCCAAATACAGTAATCTCCAAGCTTTAATGGCTTATGCAAGATGACAGAATATGTGAAATCTGATTGTCCCAGAGTTACACTCTGCACTCCAAAGCTACAACAGTGCCACAGCTGAGAGGTTCCCTACTACTTCCTACTACTGTGACAATTTAGC[G/A]ATCCTTCAAATGGGAAAATTCCTAACTACACGAGACAATGGGTCCTACAGTAGGCCCG
WI-20572	75	A	G	---	GAGCCAAACCCAAAACAAAAATAAAACAGAACTCTTTTGTAAACTAAGTCATACCTACTTTCTTCTTCAGAATT[A/G]TCATAAACATCATCTTTACAACATGGAGAAGCGAGGTAGGCCATAATTGTTCAAATTTCATCTTTCTCAAATTTTAAAATTGTTTAATCCCAAAGGTGCCTATTGAATTCTTCAAAAATAAACTGCCTATCAGGTATCATACCTGCAAATGCTTCTAATATCTCTTGATTAT
WI-20588	133	G	A	---	CATGACAAAAGACAAAGATCAAGGAGTAACATAAATTATAAGTTGAATAAATAGTATACAGCAATCTTCACTTTTTAAGAAAAATGTGAGATCCTTTGTTGGTTTTTATTTCCTTAAGTACAAAATGCTAAAC[G/A]GGAGCCGAGCTCTTCCGCATTCAGG
WI-20593	79	A	G	---	TGACCTCATACTGTGGGTTCTGGTTAGAACACAGCCACTAGAACAAACTCCAGTCTTTTCAGTCTGTTGCTGTACTTCAG[A/G]TTTAAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAGAAAAGCTGTTAAAAGGAACTCAGGATGTGTTAGGAAGGGGGAGTGGATGCCAGGCCTTCACCAGACTATCCAGAAGCCATTCCATGGGGTATTGGTCTGCAAATACTGTGAGACACTGAGCT
WI-19765	57	T	C	---	TTCTTTGCCAAGCCTGTTCTTCAAGTTATTCAGAACGTGGGTGTATACCTTGTCCTCA[T/C]ATGTATCTTGTCCCTGCTGTCTTTAGGTTAGCAAGGTGTATGAATACTTTAAGTTTGTTTCTTTCCTCGTGGTATCAGTGAAATACTGATCTATTCTCTGGCTAGGGTCAATTTACAAAATTGCCATGGAACTGAGCAAAAGGCCCACGTGGGATAAAATCACTCACCATCGACGCCACCAGTATT
WI-19066i	239	A	G	---	TGACAAGGGAGGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAGCACTTAAAACCCATGAACCTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGCGTTGGTCACCCTGTGAATTACTTCTCCATATTCCGGATGCTCAATTACAGTACCATTGCAGGCAAAGCCTTCAAACTTTTTCTTAAACGCCTTCACT[A/G]TTTCTTTTTA
WI-19066g	184	C	T	---	TGACAAGGGAGGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAGCACTTAAAACCCATGAACCTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGCGTTGGTCACCCTGTGAATTACTTCTCCATATTC[C/T]GGATGCTCAATTACAGTACCATTGCAGGCAAAGCCTTCAAACTTTTTCTTAAACGCCTTCACTAGTTTCTTTTTA
WI-19066f	148	T	C	---	TGACAAGGGAGGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAGCACTTAAAACCCATGAACCTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTCCATATTCCGGATGCTCAATTACAGTACCATTGCAGGCAAACTTTTTCTTAAACGCCTTCACTAGTTTCTTTTTA

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WI-19066e	147	G	C	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAAACCTGAC[G/C]TTGGTCACCCTGAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGCGTTGGTCAAACCTTTTTCTTAAACGCCTTCAATTAC AGTACCATTGCAGGCAAACTTTTTCTTAAACGCCTTCACTTAGTTTCTTTTA ...
WI-19066c	100	G	A	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAAACCCATGAACCTCAGCTGATC[G/A]TCCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCTGAGCTGATCGTCCTTAGCCAGTCCAATTAC AGTACCATTGCAGGCAAACTTTTTCTTAAACGCCTTCACTTAGTTTCTTTTA ...
WI-19066b	87	C	T	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAAACCCATGAA[C/T]TCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCTGAGCTGATCGTCCTTAGCCAGTCCAATTAC AGTACCATTGCAGGCAAACTTTTTCTTAAACGCCTTCACTTAGTTTCTTTTA ...
WI-19066a	72	C	T	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA[C/T]TTAAAAACCCATGAACCTTCAGCTGTCCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCTGAGCTGATCGTCCTTAGCCAGTCCAATTAC AGTACCATTGCAGGCAAACTTTTTCTTAAACGCCTTCACTTAGTTTCTTTTA ...
WI-20660	105	G	C	TTTACAGCGAGTTTTCCGTCTCAATAAGTAGAATCTAAATAGATTAGGGTGAAAAGAAAATGTG TGTCTAAATAAAATCTCCCTTTTGAATGTATATTTGT[G/C]TTAATAAAGGGAAGCATTAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTGATTCCATTACTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCCGCCCCCCAAAAAATACTGTTTAACACACTATGTTTTAAGA
WI-18768	120	C	T	CTGCTGCCAGCTTCTCTCTCTTGGCCCTGCCTCCCGAGATGGCGGTCTCCTGGCAGCCTCCCCTCAGTCTTCC TCCACCCGCCTCTCTTCCTTCCCCAGCCTGGTC[C/T]TTCGGCTCCATCGCC TTGAAAGCTCTGAA
WI-19087	37	A	G	TTCCCAGGGTTCTGTATTGCAGCTAAGCTCAAATGT[A/G]TATTTAACTTCTAGTTGCTCTTGCTTTG GTCTTCTTCCAATGATGATGCTTACTACAGAAAGCAAATCAGACACAATTAGAGAAGAGCCTTTCCATAAA GTGTAAITTTAATGGCTGCAAAAACCGGCAAACCTGTAACTGCCCTTTAAATGGCATGACAAGGTGTGC AGTGGCCCCATCCAGCATGTGTGTCTCTATCTTGCATCTACCTGCTCC
WI-18790	49	A	T	GAAAGCCAGAGATTAGCCCGCATTCCGCATCTGTCAACCAGGACAGAA[A/T]GCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACTTTGGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACA CAGTGATTTGGGAATGCCT
WI-18987	35	G	A	AGGAGGCTGTTCCAGGAGTCCTGCCCAGCAGCCTC[G/A]GTGGCCAAGCCCAGACACTCACCCACCTT CCCCAGTGGCCCCGTGGATCCTGGCTGGACACAGGATTCAGAAAGACACCAGGCTGCACA GAAAGAGCCAGATGGCAACCTGAGTGTCGGTCACAGCCCCCTACACTCAAGGCTCGAGGCCTCAGGAA AGTCA

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WI-18919	26	C	T	---	TGGATGAAAACCACAGGGATTCCGGA[C/T]GCCAGACCCCATTTATACTTCACTTTCTCTACAGTG TTGTTTGTTGTTGGTTTTATTTTTATTTTTATACTTGGCCATACCACAGAGCTAGAATTGCCCAGGTCT GGGGCTGAATAAA
WI-18741c	64	G	A	---	CTTTCTGGTCAAGGCTTTGGACATCTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38	G	C	---	CTTTCTGGTCAAGGCTTTGGACATCTCTTCAGTCATCA[G/C]ACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23	T	G	---	CTTTCTGGTCAAGGCTTTGGACA[T/G]CTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170	G	A	---	TCAGAAGCAGACATGGCATCTGTTCCTTGCTTGCTTGTGGTTGTGTACCTTTCACGAGACCTGAATT TTAGAATTGCCCAGTGCTGCCCAGAGTGAGTGAGTGAATTCTCCTTTCAGGTAAAGATAGGCTATCTC AACACTGCTGAGTGATTCATAAACATATCAACCA[G/A]TAGCATTAACCCATTTATTTCCTGTCCTT AGTGTCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212	46	T	A	---	CCAAGTTGCATCCATGTTTGATTTCTGATGAGACTAGAGTGACAG[T/A]GTTTCAGAACCCAAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGGATTATGCAGATGGCCTATGGAAAATGCAGCTGC ATAATTAAACACATTATCAAAGTCCTCTACAATTTATTTCCGCAGCATGTCAGCTAAGTAGAGACCCA ATGGGGAGAGAAAAATGCCTGCTTCTTTCCCTCTTTTTCTGCACTGCCATAT
WI-19183	210	G	C	---	CTGTTGAAGGCTTCCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAAAGCACACATTGGATG GCAGCAGTGGGTTCTTCCCCATTTATGGGCATGAAAATATGTGTTTAGAATAAAGGAACAAGCATTATT CCTTTGCCAACGCCTCACTCTAAGAGAGGCTTTTTGCTGAGTCAAGCAAACACTTGCCTGCTCTGCCC CTTGGAG[G/C]TGCATTTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
WI-20014b	214	T	C	---	TTGAAATCCCAGTCTCCTGGCCCCCCAGGCAGGGTCTGTCCACCATAGAATGTCTTCCCTACTGGGGTC GTTCTGGCTTTTGTTAGAACTTGGTCTGAGATGTTCTTCCCCGTCCATTACCATTCGATGTTCTTT TGTTCAGAGCAATGTTTCTTGTATTCTGAAAACTGGAAACTGAACCAGTTGCCTTTCTCCTAGTCACC AAGCATACTT[T/C]TCCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198	T	C	---	GTCTCCCCAGAGTGCTTCTGCACCCCAGCCCTGTCCTGCCTGTAAGGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCCCAGGGGGTGCCCTTAGTTTGGACATGCTGGGTAGCAGGACTCCAGGGCGTG CACGGTGAGCAGATGAGGCCCCAAGCTCATCACACCAGGGGCCCATCCTTCTCAATACAGCGCC[T/C]G CCCTTGCCAGTCCCTATTTCAAAATAAAAATTAGTGTGTCCTTGCCTGTCTGT
WI-19135	20	G	A	---	CAGTTACCCTGCTTGCCTCTC[G/A]AAAGTTCATCATTGTAATTTGTAATTTAGTATTAACTCTGTAAAAGT GTCTAGGTACGTTTTATATTATATAAGGACAGACCAAAAATCAACCTATCAAAGCTTCAAAAACT TTGGGAAAGGGTGGGATTAAGTACAAGCACACATTTGGCTTACAGTAAATGAACTGATTTTTATTAACT GCTTTTTGCCCATATAAAATGCTGATATTTACTGGAAACCTAGCCAGCTTCAC

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WI-19236	54	G	A	TACACAGAGAGGTGCGCACTTGGACTCTGGAGGGTTGGGTGTGGAAGGGGGAAAGGG[G/A]GATGGAGAC CTGCTCCCCAGCTCTTCCTGTCAGCCGGTTTACATGGGAACAGGGTTAACATCTGTGTTAGGGGAAGGT CACCTTACCCTTTTCATAGGGGAAGAGTGTCACACTCCTGGCTATCTCCAGGGGGGAATGGGGAAAAG AATCTTTCAAGGGCAAAGAACTCGTGGGAGGAATCTGTCTGTTGTATGTAATACT	⁞
WI-19144	222	G	C	GTGCCAGTCTTCCAGAAAGCAAGGACTGCCCTTCATTCAGCCTTGCTGACCTCCCAGCCTTTCTAAGG CTCAGCCCCACGGGGACTCTGGTGGCTGCCAGCTTGGTGAGCTATCTATCTATTCATTCATAGCCAA ACAGGAGACCCCTTGCACGGACTTGCACACAGGGAGGCTGTAGCCAGGAAACCCTCTTCTTCCCTGGT CTGGCTCTGCTGGAGCGGG[G/C]TGGGAACCAAAACACCTTCAGTGCTGGTG	⁞
WI-19139b	110	C	A	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCTGACAGAGAGTGGGTTGGCAGACAACAACACTAG[C/A]ATTTTCACGGGGTGTGGGCAC ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGGTCTCGTGTGTGAAGCCACCGTGCTTCTCTTTGG GGGGCCCCGAGATCTAGCATCTCTGAAATCCTGGCTGTCGTGTGCGAGGCTTTGAAG	⁞
WI-19139a	66	C	T	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA[C/T]GGCAGATGCCTGACAGAGAGTGGGTTGGCAGACAACAACACTAGCATTTTCACGGGGTGTGGGCAC ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGGTCTCGTGTGTGAAGCCACCGTGCTTCTCTTTGG GGGGCCCCGAGATCTAGCATCTCTGAAATCCTGGCTGTCGTGTGCGAGGCTTTGAAG	⁞
WI-18910	112	T	C	GGCTGGGACCTTTAGGAAAGTGAAATGCAGGTGAGAGAACCTAAACATGAAAGGAAAAGGGTGCCT CATCCCAGCAACCGTGTCCTTGTGGGTGATGATCCACTGTGTGCTGCT[T/C]CGGCTCATGGCAGAGCATT CAGTGCCACGGTTAGG	⁞
WI-19235	173	A	G	TTCAGGAGGTGGAGTTCGTCGTGCAGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCCTCTTCACTGCCCCAGTATTGCTCTGTATTTATCAGCGATGCCCCTCTGT CACTCATGCCTTGCCTAATTGTTCACAAATGGTGGAA[A/G]GCTTCATGTAATATGATCAGGACCCACC TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCTGCGAGCACTA	⁞
WI-19222	179	C	T	CGTTTTCCCTAACTCACCCAGTTAGTTTGGGGATGATTTGATTTCTGTTGTTGTTGATCCCATTTCTAA CTTGGAATTGTGAGCCTCTATGTTTCTGTTAGGTGAGTGTGTTGGGTTTTTCCCCCCACCAGGAAGT GGCAGCATCCCTCCTTCCTCTCCCCTAAAGGGACTCTGCGAAC[C/T]TTTCACACCTCTTTCTCAGGGAC GGGGCAGGTGTGTGTGGGTACACTGACGTGTCCAGAAGCAGCACTTT	⁞
WI-19117	134	A	G	AAATAATGCAACGCAGGAGGAGGAGAAAGAAAATGCACTAAGACAAGAAACATTCTCTCATAGAACATTG ATCTGTTTTACAGGAAACAAACCTTGCCTTGAAATTTACACAGTGAGACTGTACATAATTGCATGAA A[A/G]TAGCTATTTTTTCCTAAGACATTTTCATTCATGAATATTTTCAAGTTTTTCATACTGTACA CATTTCTTAAAACACATGATACCAGCAACTGAAAATGAATGCCGAATTTG	⁞

WI-19134c	263	C	T	---	CTCCTGTTCGTGACCTGACACAGGGTGACACAGCCCCTTTCACACTCTGTCCTCCTATCTTCCTGGGTAGATGCCCTGGTGTAGGGCTGAGTACTGAAGTGCTTCCATCCCAGCAACAAGGGGGTGCAGCCCAGGGTCAGGCCCTTCAGAGCACAGGCCAGGGCTAGAGGGATGCACGGTGCACGGGCTAGAGCCACCCTGGGTGGGGAAAGGG
WI-19134a	162	T	C	---	CTCCTGTTCGTGACCTGACAGGGTGACACAGCCCCTTTCACACTCTGTCCTCCTATCTTCCTGGGTAGATGCCCTGGTGTAGGGCTGAGTACTGAAGTGCTTCCATCCCCAGCAAGGGGGTGCAGCCCAGGGTCAGGCCCTTCAGAGCCAGGGCTAGAGGGA[T/C]GCACGGTGGCTAGAGCCCAGCTGCACTATCCTTTTCAGAGCACTTCATCCACTTGCTCTCCCTCTACCCTGGCCACCCTGGGCACCCTGGGTGGGAA
WI-19224	112	C	T	---	GGTTTCACCAGTCTTTCCCAGGGAACTCCGATGAAGTGTTCCAACAAAATGAGCGAGTGAACCAAGAAGAGGATGACATTAGATCCAGGAGATACAACAGAGGAGATAATCT[C/T]CAGGATGCCTGTGAAGAAAGATCCCTGGATCCCAGGATGATTATAGGACAAGTTGTTCATAATCCAGCAGGCCAGAAGACTTCCAGGGAAACTCATTCAAGGAGGTGAAAATGATGAGTGACTCCTCCAAGATGAAAA
WI-19201	179	T	C	---	GCAGCTCCTAAGGACCACTGGCCATTAGCTCTTGCTTTTGATGGCATTCTCTTTCCACCTTGTCTTCTCCTTTGCTCTCTGTGTTAGTGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCACACTGCCCTTCCGCCCCCCCACACTTTGCCTGCAGGTCACCGAAAGGAC[T/C]TGGGGGATAAAATTCAAAAAAGTGTGTGATGTGCTGCTCAGAAGGTCAGAGACTCCATGTCTGCCTTGGCCTCAA
WI-19034	45	T	C	---	GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGGAA[T/C]ACTTCTATTACATTAAAGGCAACAGCAGTTAGTAAAAAGTTTTACAGTGTTCTGCTGTTGAAAGTGCAATATAAATTTTTGCTAGCCCATGATCAATCGACTTCTATTGTTGATATACACTTCAGCATTTAAGTTCTGTCGAATTGACATTTGCTACTTATAAACTTAGTCCCTAAGTCTTCTTATGCTGTGCTATATA
WI-19102	25	C	G	---	TGTTCCTGAGTCACGCTGAGGAGAG[C/G]CTTCACTCAGGAGTTCATCGTGAGATGATCATGAGTTCATGCGACGTATATTTTCCTTGGAAACAGAATGAAGCAGAGGAAACTCTTAATACTTAAAATCGTTCTTGATTAGTATCGTGAGTTTGAAAAGTCTAGAACTCCTGTAAGTTTTTGAACTCAAGGGAGAAGGTATAGTGGAATGAGTGTGAGCATCGGGCCTTGCAGTCCCATAGAACAGAAATGGG
WI-18548b	65	A	G	---	AAAGGAGGGAGGAGAATCTTTTTACATAAAATGCCTTGCATCATCCTCCAGTCCCCTCACTGGGGGAA[A/G]AAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62	G	A	---	AAAGGAGGGAGGAGAATCTTTTTACATAAAATGCCTTGCATCATCCTCCAGTCCCCTCACTGGGG[G/A]AAAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97	T	C	---	GGCAGCAGCTTTTTAATTGAACACTTTCTTCTGGAGGACACACCTTCAGTACAGTTAACAAATGGTTACACCTGAAATCTGCTGAGAGCAGAGCT[T/C]AAGATCCACAATTGCAAAGGCCACTGCTGCTCACTTCCTCACA
WI-18501	121	C	T	---	CAGAGGGAAAAGTTTATTGAGTCAGCCACCACAGAGGAACAGAGAAACAGACACAAGGAGGTTCTGTGTGCATGGAGGAAATCAGGGCGCGGNACAGCTGAACCCTGCGCCAGGACAGCAGGGGGGGG[C/T]GGGACAGCAGCGCGCATGCCCAAACATTCA

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WI-18017	87	C	A	---	ACAAAAGAAAAATGGAAAACTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGAGGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCATTAAAATTATATCTCTTGCAT CAGAGCTGGTGGAAAATCAT
WI-18148b	101	A	G	---	TTATTGCGTTCCTTCGATAACCTCTCTTTGGGACTATGAGATCATCCACCAGATGTGAAAACGAAAGCA GTGATTTCAGAAACCNTCGATTCTGAATATCCC[A/G]TGGGCGCATATGCAAAGGAAGATGA
WI-18254	64	T	C	---	TATACGGATCATGTATTTGTGACCACCACCACCAGTCAATTTGTAGAGCAGTTAAATCAC[T/C]GCCAAAATTCCCTCTGCTTCCTTGTAGTCAGTCCTTCCCAACCCCAGGNACTTGGCAACCTGTTT TCCGTTCCTAGACATTT
WI-18265b	117	C	A	---	CAAATGGGTGGACTGAGTGATAAAACGCATATTGAGAACAAGACGGCCTTCTGCGCCNCTCTGCGTCC AAGGCTGTAAAGGTCTCAGGATTGCTGCTAAGTGAGCCATGAACTGGCTG[C/A]GTTTTCAACCTTTC CTTGGGTGGTTTCTTCAG
WI-18295	40	C	T	---	ACCACACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TGGGAAGTAAAGGTTGATTACT TCCTCTCCAAGGATGATATGTTTAATGAATTCCCTTNCCTTAGCTTCATTCTTCATAATGCCAAA
WI-18459b	64	T	C	---	GGGCAAGAGAGACAGAGATTTAATTGAATAAAAACTCCAGGTGTGACACGGGTGGGAGACACAAA[T/ C]GAGTAATTAACACACATAATATTTANATGACAGTGCAATTAATTAACGTCCTGGGTAAGCCAGAG GGGGAGGGGCGGTCTTTCA
WI-22585	56	A	G	---	TTTATTTAAATTTGCATCCTGAGATAATAAAAATTTATCTGACAAGTGAACAATG[A/G]CAGAAGC AGCAGTGAAAGTTTCGGAGAGGCAGTGTATCCTTCATTTGGCACAGCTGTATATAGATTGA
WI-21155	36	A	G	---	GGGCTGTGGAGTAACAGAACTTGATGGAAAATTGGC[A/G]TCTGTGTGTAGAATGATTCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88	G	A	---	GCCTTTGCTCTTTGCTGTCCTCAGAGAGGCCTCAGATGGATACGCAGCAACTTCCTTTGAACCTTTTAT TTTCCTGGCAGGAAGGAAGA[G/A]GGATCCAGCAGTGAGATCAGGGTTCTGTTGCCACAGACAG GGAAACAGGC
WI-19888a	98	C	T	---	GGCACGGATTCAACCCATAACAGAGAAATAACTCCTTATTGGAAACAAGGTTTATTTTGATATGATG AAAATATTTTGGAACTAGAAAGTAGCAGTGA[C/T]TGGACAACGTTGTAAAGATATTAAATGCCACT GAACTGTTCATTTAAAATGGTAATTTCATGTTATTTATGAGANCATATTTATGTTGGAAGTGAACATGT CTTATAATTGTAAATTACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82	C	T	---	TGAGACCATCCTCCTCAACAAAGAATCAGTTCAGCACCTAATTTTCCCACACTGAAGTCTACG CAATTTTCATGCAGA[C/T]TGTGCACACAGTGCACAGTACAGTGCACAAATCCAGAGGGCAACACATTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125	T	C	---	TCAGAATTGCTTTCCACTGCCCAAACCAAAGAATTTAATGAATGCNCTTACAATTGAGATGACTT GAAGTAAAGAAAGGTACCTTCCTTGGAGGTTGCATGACAGGATTAGTCTTCTCTGTTT[T/C]CTTGGT GCAAGTTTGAACCAGTGATTATGTACCATTGCATCAGAGACATCGTTCCCTGTCGAGATCCCCAACTAG

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WI-20561b	94	T	C	---	CGTTGCTTATTTAAGAGATGGCTGTGTTATAAGTAGTAAAGCAGTTGAGCAACACTGATTGTGTGCATTATTG TACTTCAGATGAGAAAAATCCTTACACATG[T/C]GGAATCAATGTCTTTAAAATTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20561a	25	A	G	---	CGTTGCTTATTTAAGATGGCTGTGTT[A/G]TAAGTATAAAGCAGTTGAGCAACACTGATTGTGCATTA TTGTACTTCAGATGAGAAAAATCCTTACATGTGGAATCAATGTCTTTAAAATTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20116e	69	T	A	---	GCTTTCATTTCTGTCACCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT A[T/A]ATAAATCTATATCATATATTTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCCTCTCCCACTGCCACCAGTCAGTCTGCAATTCCCGAGATAA GAATTCAACAGAGTTGGTCTGCTGGCCATCAGTCTGCAATTCCCGAGATAA
WI-20116c	59	T	A	---	GCTTTCATTTCTGTCACCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGT[T/A]TAGAA CATATAAATCTATATCATATTTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCCTCTCCCACTGCCACCAGTCAGTCTGCAATTCCCGAGATAA GAATTCAACAGAGTTGGTCTGCTGGCCATCAGTCTGCAATTCCCGAGATAA
WI-20116a	22	C	G	---	GCTTTCATTTCTGTCACCCAC[C/G]CTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAAATCTATATCATATATTTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCCTCTCCCACTGCCACCAGTCAGTCTGCAATTCCCGAGATAA GAATTCAACAGAGTTGGTCTGCTGGCCATCAGTCTGCAATTCCCGAGATAA
WI-20466b	133	G	A	---	AAAGATTGCAGTCCTGGGACACAGTTGGAAAACACTATTTATAAGGTTGCACATATTACAAACAG NTCCCAAATGGTGAAACTGGTATTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGC[G/A]TGTGAACTAATGTTTAAAAAGTTTAGAGCTTGTCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACAACTACTTTATTTCTTTGCTCTTTTATCCCTTTCAGGTTCGATT
WI-21444	39	A	G	---	CTGGGCAGCAAGTAACCATTTTAAAGAAATACTCTCAAC[A/G]AGTTCTTTTTTTATGGGGTATTTCA GTTGTTAACAAAGTTAAAATACTTATTGGAACTAATCTTTGTATTTATTCGAGGAAGAAGAAATCT ATAAGATTGACTTACTCATTGTTGACTGGTTTTTGAAGCCTTACTGGGG
WI-21034b	148	T	C	---	AGAAATGGACAATGATGCAGATGATTTGTGAGCATTTGATGAGAAAGTGGTGATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTCATCTAGCTAACCTAATCTGTTTCTGTAGAATTACTGGTCATGG GAGATTGGATAGA[T/C]GCCTAACCTATCTCAATTTAAGTAATGTGAGCAA
WI-22091c	205	G	A	---	GGCGTGTATTTGATGCAATGTCCAACCAGTCAAGCTATCATTGAAATCCAAATATTTCCCAGTAGAG ACATGCAGAGCAATGTCAATGTCAATGTAACATACAAGCATATTACCTCCCCCTAAGTGACTCATAATTC ATTACTTGTCTGTCGTAGCTTTAAAGTTAAAAATGTGTAGCATTAAGTGGTATTACTTACTGAGGGCA ACA[G/A]AAATTACGGCCTTAACAACACACTAAATCATGAGGCTCAGGGATTG

ID	Pos	Allele 1	Allele 2	Sequence
WI-21805a	45	A	T	CAACTGCTCTGAGGTCTTCACTAGCTGATTTATAATCCTATATT[A/T]AAAAAAATCTATAGTCTG CAGTCTTTGACATACTTCTCAAGGGTGGATATGTGGTGGAATGCAGACTCCATCAATATGTGTGGTT TTGTTTGCTTTTGTAGCTTAACTGCTGTGTTTAGNAAATCCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATTCGAACAGTTGAAGGCTGTGTTTTGTTAATTGCTG
WI-21778b	155	T	C	AAAAATCCATAATTATTGAAACCCAAGTTACAGAGAAAGTTCGTAACTTTTTTATTGAATTATTGAC TCTGCCCGCCGGTGTCGTTCGTCGCTTCAACTCCAGTCCCCTGTGTAGGTGGGGTCCCCAG GTCCTGGGGCTTCTGAGGTCC[T/C]GGTAGAAGGAGGGGCAGGTGGT
WI-20907	241	A	C	TGAGTCAGTGGTCAGATGGGGCAGTTGCGCTCAGCTGCGCTCAGTCCCTGACTCCGGAAACACTGTGCCTCT CAAATGATCTAGAGCTCATCCTTGGGCGGTACATGAGGGGCAGTTGTTGTTCTAGTACCCATTTAGCCC ATGGCTCTTCAAGCCAATTCACACTGGGAAAAACACACCCTACAAGATGCCTATCCATTTGAGTTC ATACAGGTTTTAGTAGCTAGAACTAAACTAAAAACATTTTA[A/C]AATTATCTA
WI-21449b	222	C	T	AACAGCAGCAGTCACTTCCAAAATGCAAAAAAATTACAATTTTAGAATAAAATTATAATGTTTA TAATGCGGGTCAGAAGANTTGAAGGTACAACAGAATCAAATCACGCAGCACTGGAGGGGCTGGAG AAGCCAAAGCCCACTGGTCAGGGGTCCAAGCTGACAAGAAGTCCCAACCTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCA[C/T]TGACAGAGCCAGTCAGTGTCCTGGGTTAG
WI-21558a	157	G	A	GCTTACAAGGAAGCCTGTGGACAGGCGAGNTGGGTGGAACCGACTCCAGCCTGGAAAACCTGCCCTC CCATCCCCCTTAGCGCCCTTCGCGGCGCCTTCGCGATTTCTTCGACAGCAGTTCTGGCCAGGGCAAGG AGCTGTGGTGGGGGGCAGTAT[G/A]AGCCAGGAGGACTCCCTTCCCACAGATGAGGGCCTAGGGGCTGCAA AAGGGGCCCCGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI-22187b	178	G	A	TTTGCTGTGTGGAATCCATGAGAGAGCCGGAAGCCATCGTTGGGGCCGGCCGTAGCAGAGCTCATGGNGACCA GTCCTGGGGCCTGACCAATGGGTGATTACATTTAAAAACCAAAACCAAAACAAAATACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG[G/A]AAATTTCATGAAAATTTCC CCTAAACCATAACAAAAACTGTCCTCCTTACCCCAAAGTGCTGGAGGAAAG
WI-22187a	110	C	A	TTTGCTGTGGAATCCATGAGAGAGCCGGAAGCCATCGTTGGGGCCGTGGCCGTAGCAGAGCTCATGGNGACCA GTCCTGGGCCCTGACCAATGGGTGATTACATTTAAAAACCAAA[C/A]CAAAACAAAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGGAAAATTTCATGAAAATTTCC CCTAAACCATAACAAAAACTGTCCTCCTTACCCCAAAGTGCTGGAGGAAAG
WI-21609b	146	G	A	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAAACGTGCAGTCGGTTCACAAGCTGTAAA AACAAGCCCAAACCCAAAGACATCACAAGAGGCAAGACAGTCAGTGAGAAGGGAGCCTGTAAAG GATGTTTCAAAG[G/A]AGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTCGGGAAGTGGCAGAGGCTGGCAGAGGCTGAGACANTGGCCAAAGAGAGGAGTTGGAG

ID					Sequence
WI-21609a	42	C	T	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCCTGTAACAAA[C/T]GTGCAGTCCGTTCACAAGCTGT AAAAACAAGCCCAAACCCAAGACATCACAAGAGGCAAGACAGTGGCAGTGGGAGGGAGCCTGTA AAGGATGTTTCAAAGGAAGTGGGCAGAGGGTTCCCGGCTATGTGGCCACTGGATGTAGGCCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCACANTGGCCAAANGAGGAGTTGGAG
WI-22512a	104	T	G	---	ACATTCCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAAATCCCTGGTGCCTCCTAGGCTTCA GGGTAAGCCCTGACATCATGGTCCTTTGTGATCTGT[T/G]ACCTCACCCATGTCTCCCACCTNAGTTCC CACATTCCCCCACGTCTCAAGGGCAGGCAGCTACACTTGACTGCA
WI-21028b	139	A	G	---	ATCGGCAAGCTACAGCCTTAAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTCACATGAAAGGGTCGTGATTGAGCAATCTAGGGGATATGTGACAGGGG TTTC[A/G]TGCACTGGTACAGAACACAACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAAT CTACGG
WI-21028a	121	A	C	---	ATCGGCAAGCTACAGCCTTAAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTCACATGAAAGGGTCGTGATTGAGCAATCTAGGGG[A/C]TATGTGACAG GGGTTTCATGCACTGGTACAGAACACAACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAATC TACGG
WI-18829d	58	A	C	---	ACAAACATGCCTGTTCACAGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG[A/G]TTTCA TCATACAAGACAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCTTGAAA AA
WI-18829b	35	A	G	---	ACAAACATGCCTGTTCACAGGGGGAAAAATCCTAGG[T/A]AATAACTTATGTGTACTTCTTGATTTCA TCATACAAGACAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCTTGAAA AA
WI-20964	87	T	A	---	AGCCAACTCAAGGCCAAAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAAGCAAAGGA GCACAGGTAGTCCACAGAATA[G/A]GACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAATTAA AAGAATAACTAAGATTAGATGAACAACACTCAGAAATACTCTAGGAGAGCTGAAAAAGAAGGAAC AGATGTTAACAAAACAAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI-20059a	59	G	A	---	CTCTGAACTAAAGGGCCGTGAAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCA[T/A]ACAT TGGCTGGAATGAGGTGGTCAGGAAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGTAATAATTACAAAGACTGACCTGCAACTCTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGGATGAGGAGTATGGGCCTTAGGT
WI-22130b	165	T	A	---	TGTTTTTGAGGGGCTGTAGCAGACTACATAATGAGCGGTGAAAGCGGCTGCCTTCCCCTCTCCTGACAC CAGCAAGGGGGGAGGCCACCATCACCGGCCCTGCCCATCCATGCAATGCATCCAATGATCATGTCTGA GCCAACGGAANAGGACCCCGCGCTTGCT[C/T]GTGTTAATCCAGGTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAGTCCCTGTGAGTGGGAATGAC

(final row base columns: C | T)

WI-21661	117	G	C	---	GCTTAGTCTCCACCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGT CTTCCAACTTTAGAATGTATAAATAAGAATGACATTTAAAATAAAATA[G/C]TTTAGTCACAGTC ACACAAAAACTACCTTCTAAGGAAAACTGTCCAGTGAAGCCGTTAAATTTGTGCTTTCAGCTATGAAG GA
WI-21980a	25	T	C	---	TCAGTTTAAACACATTCATCAAGGA[T/C]AGATTAATTAATGTCAGGTGAGCATAAAAGGGAGATTA TAAACCAGAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTAATTCAT GGGTGAAGCCCCTGGGATAAAG
WI-21636	71	A	G	---	TGCTTGTATTAATGTGGTGTTACATTATCCTATTTCACAGATGGAAACAGAAAATACCAGCTTTTT AAA[A/G]TAGCAATATCTATTATTATTATAATAAATATTGAAATAACACCATAATAATATCACTAAGGA AGTAATCTAATTGTGTTGATTTGCAGAGGGAGAAAAACATTACCTCTAGAGCTGAGGCTATTGTGC TCATGCAAACTCCAATCTGAAGGTGGTAGAAACTAGGAAGGGACAGGGATTTC
WI-22457a	112	G	A	---	TTGCTATAATTTCCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCACTCATTAGA CAAACAGTAAACATACTGGACACGGTTTCAGGCATGAAGGATACA[G/A]CAGTTAATTAACTAAAG GAACAGAGAGTCCCTGCATTCCTGAAGCATAGGATGGGGAAACAGTAATGCAGATTAATACCTGGGGCC AAAACCCACTGAACTCACCCCAGCTGAAAACACTGAAGGATACTGGGTAAGGA
WI-21524b	97	C	T	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGTACGACCTTCGCGTCATACTTAT AATGGTTAATAACAGCATTCCTGTCTACC[C/T]GATGATGCTTCTCTCTGCAAATGGACTATTGCC CAGTTGCAACAGGGCTAAGATTGTCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTTCTTGACTTTCTCCAAGTTACTTCCTTCCAGGGGATG
WI-21524a	35	A	C	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT[A/C]GCCTGATGTACGACCTTCGCGTCATACT TATAATGGTTAATAACAGCATTCCTGTCTACCCGATGATGCTTCTCTCTGCAAATGGACTATTGCC CAGTTGCAACAGGGCTAAGATTGTCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTTCTTGACTTTCTCCAAGTTACTTCCTTCCAGGGGATG
WI-22652a	32	G	T	---	TTACCTTCCAAACCAGGCCACTTTGGAGAAATGCTATTAATCAATAAGCCAAGAC AATAGGGACTACCTGGGTAGACCAAGATGGGCAGTCACCATACACCATCATTCCTGCCACAGAACC TTTGCACATGCTGCCCTCCTACTCCGCCACTCACCTGTCTAATTGGGACCTGAAGCTTCAGCATCCCTT CTTTAGGG
WI-21703d	197	A	G	---	CAACAGGCTCATGGAACAGAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGGCAGGGCTC TGCATCCCCTTTCCTCAGCACAGCACCATCTTCACCCTCCTGGGAAAGCAGCATTGGAGCCTACACCA CTTGTGCTTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAA[A/G]G TGGGCAGCAGCAGCTAGGGGCAAGGACTTAAGGGAACTTGTGGGGGAAGAG

WI-21703c	134	A G	---	CAACAGGCTCATGGAACAGAGCCTAGGATCCAGGAGCATAGGAGGTGGTGCTGGGCAGGCTC TGCATCCCCTTTCCTCAGCACATCTTCACCAGGTAAGAAATGCAGGTATTTGCAGAGGGAGTGAGTCTGGGAAAG A/G[CTTGTGCTTTTCTCACCAGGCACAGCTAGGGCAGAGCACACTAGGGACTTAAGGGAACTTGTGGGGAAGAG TGGGCAGAGCACAGCTAGGGACTTAAGGGAACTTGTGGGGAAGAG
WI-22663c	139	G A	---	CCCTTGTCAGTCTGTGCCTCGGCGTTCTCACTGCTGCGGCAGGTGAGCCGGCCTCGCTAATCTTATTC CCAGTCTCGGTGAACATGGCTCAGTCTCTCCCGGCTCAGTGTTGGGTTTGCACTGGTGCACTTACAG GC[G/A]GAAGAGCTTCCTCATTTGCTGAGGGCTTTTCCTGAATCCGTGTTGAATGTGGGT
WI-22663b	55	C T	---	CCCTTGTCAGTCTGTGCCTCGGCTTCTCACTGCTGCGGCAGGTGAGCCGGCCTC[C/T]GCTAATCTTA TTCCCAGTCTCGGTGAACATGGCTCAGTCTCTCCCGGCTCAGTGTTGGGTTTGCACTGGTGCACTTAC AGGCGGAAGAGCTTCCTCATTTGCTGAGGGCTTTTCCTGAATCCGTGTTGAATGTGGGT
WI-22663a	38	C T	---	CCCTTGTCAGTCTGTGCCTCGGCTTCTCACTGCCACTGG[C/T]GAGGTGAGCCGGCCTCGCTAATCTTA TTCCCAGTCTCGGTGAACATGGCTCAGTCTCTCCCGGCTCAGTGTTGGGTTTGCACTGGTGCACTTAC AGGCGGAAGAGCTTCCTCATTTGCTGAGGGCTTTTCCTGAATCCGTGTTGAATGTGGGT
WI-22668	99	A G	---	TCTTTTATCCTGCTGCCTGCCTGAGTATTCTGGAATCCTACAAGGATTTGAGGAGCCCCTTGGGATT CCAACCTAACAAATTAGTTTCTGTAATATT[A/G]TTCTAGTCCATTTAGATTGTGTAAATGATCTAA ATGGGNGTAACCATTTAATATCAAAAGTATAAACAGCATTTAAGTCAGCTTTCGAAGAAACTTTATT
WI-22631a	52	T C	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGGCTTCAGTTCTGA[T/C]AGCACCATTTT CAAGTTTTAGGCAAGGTATTTAACCTCTCCAGCGCTCATTTCTCTTTGTAAAAATTGTGATAAATGGACC TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTT
WI-20258	157	G T	---	AATCCACACTTTCACGGAGGGGGACCAGCCTGCCCATGTCGTCCCCAGGCTCACAGCAGCGGCGGCTAC TCTGCTGGTGGTTTGGTGGCAGGTGGCAGGTGGGAGATGGTGACGGCGCATTGGAAACCGTAAGGCATGACAACG GGAGGGGCCCCGCGGGGTGTTTCAG[G/T]CGCCGTTGACGGCAGGTGCATGGCCAGGCGGCCTCTACAGA AGGAGGGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAAGTACC
WI-22714	212	C A	---	ACTACACATATGCTGATTTTCAACAGTAAAAATAACATTTTACATTTGTAGAGAGAAAATCTAGGGTCT ACTAAATAATCTAGTACTTGTTTCCACTCTCCTGCTAACTCTGACAGGAGTGTTGTGGGAAACGAAGT CTGAAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTT ACCAACCCCA[C/A]TGAGTAGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI-22734a	44	G A	---	TGGGGCTACTTTAGATGGGATGGCGTCAGGGTCTGGGAAGGCCT[G/A]TCTTAGAAGACATTACCCA AATGATGAGAGGCAGCCAGTCGTCGAAGCCATAGTTTGGATGGCGAGACTTTTCCGGCAGAGGAAAT AGCAAGTGCAAAGGCCTGAGGGAGGAGAAATGAACTTGGGCTTGTCCTACAGGGTGAAAGGCGGCGGT NTGGCTGAGGTTTAGTTGGATG

ID	Pos			Sequence
WI-22724	117	A	G	TGATATGATGTCTGAGATTTGCTTCCAAATATGCCTAGGAAGGGAAGAAGTGTTTAGAGATATAGGA CAAATCAAGATTGTCAAAATGTATAGTAACTGTTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTGGGAATT
WI-22750	48	G	A	TGTAACCTGTGTTTCCTGAAAGTTGAGGGAAAGCTGAGGCAGCTAAT[G/A]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATTCTGACCTGTGCT
WI-22775a	60	A	G	TGCTGTTTCTTAGTTCATGACGTTTATCACAATGTGCTACTGTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGAAAATAAACTCCCTAAGGCAGCAATAATTTCTGTCTTGAATCCTTCATTCAGGCAAA TATTTGTTGAGCACCAAGGCCAGATGGGAACTGAGGTATGTAGGTGTTGGGAGCCAGGAAAAGGAAG GGT
WI-22808	143	C	T	CTTTAGCTAATGAAACTGGCTATGTGTGGACTATGATAGACCAAGAAAGCTACCCAAGTCCTGAGGGAG CCTAGTCCTCCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCAGGA GGATGAAGA[C/T]AGCAAAACTGATTAAGAGAGTAGGTATAAGAACCAGGGAGAGTGGGGTCCAAAT ATC
WI-21016	207	G	A	TCTCTCGTGTCTTGAGCCCTCATCCCCACCCCTCCAAGCCCTCATGCCCACCACACCGTGTCCCACATT CCCCATCCTCCCCTGTCTGCTCCCCATCTCAAGTCCAAGGCCCAGAGCCCTGGCCAGCTTTCTG GGAGACAGCATGAAAAGGAGGGAGTGGAGATGGCAGAGATGGGGTGGAGCCAGTGCGCTGTGTGGGTC CT[G/A]TTGGGCGTGGTGATGTGGGGGCCAATCCTGAGGCCAGAGGTTCA
WI-21031	31	C	T	TTGAACACCTGACCTGCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCCATTTGTCTCCAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCGAGAACACTCAGTCTTCTTCAGCAGCCGAGAAAACACACA
WI-21314	122	A	T	CCAATATCCAGTCTTCTTGAAGCTTCTATTGACTTTAGGGTTCAGTTATTATATCCTTTATCACTAT GACTTTCATTTGATTTTTATTTGTTCTTCCATTTCTCTGTCAAACTTTC[A/T]TTTTTGTTTATAA ACTGTTTTCTAAACTTCACTTAATTCTCTATCTGTATTTNCTTGTAGTTCCCTGAACTTCTTTAGAGG
WI-21186	95	G	A	AGCGAGCATCAGAATCACCTAGAGGGTTGACTAAAACAGACTTCTGGACCCAACCCCCAGAGCTTCT GATTCAGTAGGCCTGAGGTGGGGCTTAC[G/A]AATTAGTATTTCGAAGGACCTTCCTAAGTGTTGCAG ATGCTGCTTGTCCCGGGGAACACACTTTGAGAACTATTGTTCTAAAATGTTCTCTCCTTCTTTTAAA GGAGAGACAGGAATTCCAGAGAAACTGCTAATTTAAGCATAAATGTATTGAAT
WI-21187a	94	A	G	CCACGATAACTATAAAAGCAGAAAATTAGCTTTGAAAATCAAATAACATATTTAGTAACACACATT CATTTTTATAAACACACATAAAGACACC[A/G]GGNTCTCAGTAATGCTCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCCATTTGCATCACCTAGGGAATTGCTAAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGCGGTGAGACCAAGCAACCTGT

WI-21190	39	T C ...	TTTTCCCCACATACCAATGCACCTGTTTGTATAAAACTATT[T/C]GTGTGGGTAAGCCCTTCTTTGGAGAC CAGTGACATAGACATGATTCCCATTATATATTATAACAAATAATTAATAATCTGTACTATTACTGC TTTAGTTATCTAGTGTTGTTATTGAGAAGGAGAAGTCAGCATAGTTTATTTTCCATGTAATAAAAGCTT AACACA
WI-19937d	186	G A ...	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCAANCTAAACTTGGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185	C T ...	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCAANCTAAACTTGGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCCTCAGCAAGTC[C/T]GTCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-21117b	227	C T ...	GAAAACGGGGTGCTAAACAAAGAAAAGTCTCAGATCCCACTGAAAATCTGTTCAGTTTCACAGGCTC TCTCCAGAAAAATGCATATGTACCAATTGCATGTAGCCTTCAAATACATTCTGGGG TCCAATCACATACTTCAGGTTCAGAGACTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTCTACAGTCTGTATT[C/T]TTCTACTGAATCTTGGGTGGGAG
WI-21122a	42	C T ...	TCACTTTTGATCATAATCCCCTGTAAAAGCTAAAGTTATTCA[C/T]TTAACAGGAACTCTGTTTTTCC TTATTCAAATGTCACAGCCTGACGCGTTACTGTACATATTGCTAGCAGGAGACAACTGGAAATACT AAACAAATACTGGAATTCACATTACAGACGAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTTGTGGGTTGCT
WI-21254	53	A G ...	CAGTTTTGGTACAGGAAGGGCCCATGAATGTGGGCGGGAACTATTCCCACAGGAG[A/G]CAAGGAGAAG CTGTTCTCTGG
WI-21054	23	G T ...	AAGGAAACTGCATGGGTACAAAT[G/T]TCCAATTCATACTTAACAAGGTGGGGAAACGGGGTCATTCT TGGCCTGCTCCAGAACAAGGGGCGAGTCTATGCACTCCTG
WI-21059b	181	T C ...	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTTCCCACTGAGCCTGCTGAA CTACAGCTGCCAGCATTTCCTGGGCTTGCATTTCCCAGCTTCGTCAATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAAGACATACTTCACTGAAGTCATTTCTCTATTC[T/C]ATTGTAGCCAGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
WI-21059a	63	C T ...	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTTCCCACTGAGCCTGG[C/T]T GAACTACAGCTGCCAGCATTTCCCAGCTTGTCACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCTATTGTGAGCCAGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT

ID	pos	a1	a2		Sequence
WI-20442	37	T	C	---	TCCACGTGAAGGAAGAAGAAAAAAANGGGGGGGGGGGCT[T/C]TAAGGTGGCACAATTTAAGAAAAT ACCATCCATTTTCTCAGTCTCAATCTGAATCCATACATTAAAACAAAAGTGCAAGTGATGAGACGAA CA
WI-21235	43	T	C	---	GTGACAAGAGGTGAAGCAAGGACAAGGGCAGCAGGGCCAGTC[T/C]CTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57	T	C	---	ATCAGAAACTGCAAATCTGCACATGAAAAGACCTGGGGGAATGCCTACATCTGGAATT[T/C]CATTAC ATCAAACGTTAAATTTGTCCGACCAGTTCTTCATTGCTGATCACTTTGATAATGACAGATCCAACAT GAAACTTCCTGAAGCAAATGAATATTTACCTTGCTTTCATGCAAATTAGGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACCAGATCTAAGGAATTGTGACAGGGATCTTCT
WI-21149a	167	G	A	---	AGGACCTGCTCTCACACGTTCCCTCACCCCCACCAGCTTTGGCAAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTTTTTTTTAACAATGACCTTATTTTATCTTTTAACTTTAACTGAGTCTTATATA CAGACCTGCCCAACTGGAAAGCTTTACAC[G/A]TGCTTCAGAATGCGGGCAGTATTGCACAATGGTT TGGGGCAGGTTCTGTTGGTTAAACATGGGAATGGAACCCCAGGCTCTACCTG
WI-21376b	188	A	G	---	GGTGTCAACTTGGAAATAATGGTTTAAAAACAGGATAAGCATTAAGGAAAAAACACTTTCAATGTGTC TTCCATTTGATGAATTGTTTTCTCTCTTTATCCCCGCAAGTGGAGTTCATGTCCTCGGTGAAACCA GACAGTGTGAATCTGTTCCAGCCCAAATCTGCAGCATTAGGGATGAGTTCTC[A/G]GAAGTGATTCT GAACTGAGCAGCACGCACTCATGTCTGCATGGGGAACTCTGGGGAGGAAGAGCCT
WI-21382d	125	C	G	---	CCATTGCAGTCCAGAGATGAGAAACTGACCAGAGGCAAATCATGAACAGAACGGGAGTCAAGAGA AGGGGTTTCTAAGATGGAGAAGTGGGGGCGGGGTTTGGATCCAGTGGGATNTGGCTTCCC[C/G]AGGTT GCAACCCCAAGGAGGTCTCTGGAAGCAGCACCAGTCCTGATGGGGGAGCAGAAGAGCTGCCATCCTC AGTCAGGGTCCGAGGTCAGGGTGCGAGGAGAGCTGCTCCATAGTCTCGCAC
WI-21437a	201	G	A	---	TCCCTGAGGTTGGAGTGCCTAGCATAGCTCCCCTCCCCCAAAGAGGGGACAAGGGGGTCAGGGGCAGAGC AAAAATCCAGTCTGCTTCAACCACGGAGACTGCCTTTGGGATGGAAAGTTTCTGGAGCTCCCTCCATT CTATTCCTGTGTGGGGCAGGAACATGCCAGGCGTGCTGGTAAATGCCAGGGGTCACCTTTACCAGGGC[G /A]CAGGCATAGTGTGTGGCCCCTGNCTGCCCTGGGGGCCACCCTGGGAACAGT
WI-21202b	156	A	C	---	CAAAATAGAAATTCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTTATGAACATGTATTTATAAAAATGGTCACAATATATTTTTAAGTTAACTGATTTATTATTGAGGG AGGAGGAGAGAGTTGACCAAGTTGACCAAGTCCTAAAAGCGTATCTCAAACATG A
WI-21202a	61	T	C	---	CAAAATAGAAATTCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATG[T/C]TGA TCTGTTTTATGAACATGTATTTATAAAAATGGTCACAATATATTTTTAAGTTAACTGATTTATTGA GGGAGGAGGAGAGAGTTGACCAAGTTGACCAAGTCCTAAAAGCGTATCTCAAACATG A

Marker	Position	Allele			Sequence
WI-21627b	153	A	G	---	GCATGAAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAA[A/G]TCCAAAGTCATCTAATATAAACCATATTTACATAATTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTGTTGCTTA
WI-21627a	106	A	G	---	GCATGAAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTC[A/G]TTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATTAAACCATATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTGTTGCTTA
WI-21399a	75	C	T	---	GGATTTGAGTCCCAAACTTGATCTCAAATTCACTTCTTGCATGTAAACAAGCTCATTCCCTCTAAAGTT TCAGTTT[C/T]TTCACCAGTAAGGAAAAGGTTGGACCAGACATGTTGGACCGTAATTGCTTGGTAA CTGCCTTCTGCATTGTCTCTGAGGTGTGTGTCCCTAGGACTAGGATCTCTCTTGCTTTCTGCC TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGCCCAATTCATACTTGT
WI-20329a	68	G	A	---	CGATGTCTGCTAAGATAGGAGGTTAATTCTTTACATGGTGAGTGGGTCACAGAGACAAGACATCAAT C[G/A]TCTGTTAGCAGCGGAGAGAGACACTTAAGTTGCCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTGCTGCTGGCTTCTTAAAAACAGTAAAACCAATCAAAAAGAAAAGATTTAGAGGTTCAGACATT AGGAACAAANTGTGGCCAGAGATACCACAGAGCCCTGAAGGGAAAGGCCTCACT
WI-21249	155	T	C	---	TTCTGGCATTCAAATGTACATGTAAAATCCAATTTAACAGATCAAAATTGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAATCACAATTGTATCTAAGTTTCACTTTTAAGAAACATTATAAAGGTAATT AAAACTCTAGGTGTATACTTA[T/C]ATGGAACTAGTTTATTTCCNATTAACTACTGTTCATTGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTGTTTTAAGGAATTATAAAACATTGAGA
WI-21504	147	C	T	---	TGACACAGCATCAATTTCATGAATACTTTGAAAGGGCCATTAGAAAAAAATAAAGAGCCAATTTGGGTC ATTTGAGAAAACATTTTCAGCACAATTACAGTGGGGGCACGGGCCGTTCGGCCTCCAGCTGGGTTTCCC AGATGCAACAAT[C/T]GCGGTTCTCGGCTTCTCGGCTGTTTTAAGGAATTATAAAACATTGAGA AAGTATGTTGTCCCAATTTTCAGCTGTGTTTTAAGGAATTATAAAACATTGAGA CAGGG
WI-21242	115	G	A	---	CTGCACCAGGGAGGACGAGCTGCTGGCAGGGACTAATAAACCTTCCACCTGGCCATGGTGGTGGTGTT CTCTATGGACCGAGCCCTGAAACGCGGGCAGGAGGGGCAGGGAGGAAC[G/A]CACTAGCTTGGGGGTG GGCACCAGCTTCAGACCCTT
WI-21475c	181	A	G	---	TAGCCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCCAGGCTTCTCACTTGCTTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGCAGTGCGTCTTTGGAGAAGGCCA[A/G]AAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCTTCCCGTTCTCCACCCTATTTCCCTGAAG

ID	Pos			Sequence
WI-21475b	117	A	T	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTC[A/T]CTTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGGACCTGGGCAGTGCGTGCGTTCTCCACCCTATTCCTCCCTGAAG ACTTAGGAGCAAGACCCTTCCCGTTCTCCACCCTATTCCTCCCTGAAG
WI-20893d	207	A	G	TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCGTGTGCAGGCTTGCTGCAGGG CTGTCTTCGGCGGTTTAAAGTGCTACTGAGGAATACAATCATTGTCACGTAAGTTCATCACCGCACTCC AGCGTCAGGCGCCAAACCTTTCCGTGGACCTGGGNAAACCTGCCATTTCTTCTCTTTTTTACAATGCAGT TTC[A/G]ACATAACATTGGTAGAGTAAACAACAAACCACAACCTAAATG
WI-20893c	179	T	C	TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCGTGTGCAGGCTTGCTGCAGGG CTGTCTTCGGCGGTTTAAAGTGCTACTGAGGAATACAATCATTGTCACGTAAGTTCATCACCGCACTCC AGCGTCAGGCGCCAAACCTTTCCGTGGACCTGGGNAAACCTGCCA[T/C]TTCTTCTCTTTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAAACAACAAACCACAAGCCTAAATG
WI-19941c	71	C	G	GAGCTCAAGGGAAGACCCTTACCCAGATAGGGACTAACTGGAGGGGTGGAAGGAAACAAGGTGAAA GGTAT[C/G]GGTCCTGGTGAGACAAAAGCAGCAGGGGCCTGAGAACACAGAGCAAGGTGGGGTTGGAG GGAGCACAGCAGGGTGCAGGAAGGGAGAGATGGGGAGAACCAAAGGACAGAGAGACAAAGCG AAACTGGGTACAGGAGGCATTNTGGAGGAGAAGGAGAA
WI-21552b	166	C	A	TGGGTACATGGACAGATGTATATGTTTATGGGTTATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCCTTCACCTCAAGCATTTATCCATAGTGTTACAAAGAA TCCAAGTATACTCTTGATTATTTAAAAATGTA[C/A]AATTAAATTTATTATTGAATTTAGTTACCCCC ATTGTGCTATCAAATATTCAATCTTATTCATTCTTTGTAACTATTTATTTGTA
WI-21552a	66	G	A	TGGGTACACTGGACAGATGTATATGTTTATGGGTTATATGGTTATATGATACAGATACACAATGT[G /A]TAATAATTACTTCAGAGTAAATGCGATCTCCTTCAAGCATTATCCATAGTGTTACAAAG AATCCAAGTATACTCTTGATTATTTAAAAATGTACAATTAAATTTATTATTGAATTTAGTTACCCCA TTTGTGCTATCAAATATTCAATCTTATTCATTCTTTGTAACTATTTATTTGTA
WI-21512	54	C	G	TCCTCGTACTTCATGCTCCCTCCCTGCCCCCAGAACCTTACAAAAATATTCTGT[C/G]TAGAGAGGGA AAGAGCTGGTGGTGCCTGCTCTGGAGGCAACGTCCAGGTCCGGGAAAGGCACTCGTCGTGTGATCTGTC TCAGTGATGGGAGGTCTCCACTCGCCCCCACGCGCCTCGGGGGCCAGAGCCTCGGGGATGAGAATATGCTGTAA TCCAGTACAGGGGGCTGCGTCGGTGGGGTCGCCCAACAGCCTCCTTCTTTGGGGG
WI-21513b	192	G	A	CACATAGTTTCTCAAGAAGAGGATGAACTGAAAACTCCTCTAAGGCAGGACAAAGCAACTTTCCATT AATTCTTAGTTTAGACCAGAATCTTTAATTTTATATTCTCCTTTAATAACTGTCAAAATACACCAAATA CTTAGAGGAGAAATATTCACAGTATACCAAAACATTTTAAGATAAAGAGGCAGTGTAA[G/A]AGTAG TATTCTCTACACACAGTATACAAATGATGCCTTCCTGCGAGTTTAGGAAC

ID	Pos			Sequence
WI-21514b	133	C	T	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAGTATCTCAACATTACAAACCCCCAATCTTCAAGGAAAGGAGCACATTACCATGGAGC[C /T]ACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANTTTAAGGCTCAGATGGGGTTAAGGGTGATTTGTCAAGGGTCATAAGGAACT
WI-21514a	100	A	G	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAGTATCTCAACATTACAAAACCCCCA[A/G]TCTTCAAGGAAAGGAGCACATTACCATGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANTTTAAGGCTCAGATGGGGTTAAGGGTGATTTGTCAAGGGTCATAAGGAACT
WI-22020	27	C	G	ATGAAACATGTTGCAGTGCGGATGAAT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGTATCATTCTACCTGTATGAGGGTACTT
WI-19576a	113	A	G	TTCATCGGTTCTTAATACAGTACAATCCTTTGTTGAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATTC[A/G]TCTAGTTCAGTGATTAGT CACAGAANTTAAACATCTGCCCAGATGTACACATTTGGTAAAAACTACAGCTTCTCTCCACGGGGA G
WI-21695a	141	A	C	ATACACAGGCCACAATTGCAGGATGGAAAGGCAGTGGGCACTTGGAAGTGACTACACATGGCAATA AGCAGCCTATCTTCTTTACCAACCAGAGTTTCTTGGGCATGTGATGTAGGCCAGACCCTTTCCAA GGGAATA[A/C]TACTACACTAAGCCTACACTGTGTGTTCAGANTTCTCAAGGCCCAGCAT AGTGGGAGGAAATGTGATGACTTCACTGTGTTATTATGAGGAACTCACTATACTAGGAAGCAACTTATGAGTG
WI-21574a	235	C	T	AAACCCAGAATTTTAGGTACTTTTGTATTATGAGGAACTCACTGATCCTGCAGGTGACAGCGC TGTAAATATTTGATCTAGCAGCAACTTCCACTGATCCTGCAGGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT TCATCACCTAAAGTGAAGCTGTGTCTATTCTCATTGTAATGTCTCC[C/T]GTCTGTCTGTCAGGTGGGA GGGCAGGCCAGGGAACTTACTGCCTACTTCCCT
WI-21644c	151	T	A	TGACTGCCAAGATTTAGGCCCCAACTTAGGACGCAAGGGTCACCTCTAACCTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTCACCATANTATTTAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGGA[T/A]TTCAATCAAGATCCATGGAATGATGCAGTTAACATGGTCAGCAAGTC TTGCCTACTGACCACCTTCCTTTCTAAATATGGCAACACAGCAAGTC
WI-21614b	55	G	A	TGTCTTTAACCTCAAAAGTCCAAATAAACATATAGACATTTGANTATAGCTATC[G/A]TTTAACA AACCTCATTATGATCACTGTTGCAATTTCAGTCAGTTGGGGACTGAACATTAAACCATACGTGTATTTCTAAGGTACTAGGGAGTT TTTACTGTGTGTGGGTTTGTTGGGACTGAACATTAAACCATACGTGTATTTCTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGGTCAATGGTATTTGGGCAGTTGGCTGTGTGTGGG
WI-21615b	151	C	T	GACCGAGAAAAACTGCAAGGCATATGATGTTTGTCGAAGTATCACATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAAGTACAAAGATGGCTATTTTAAATTTCATACATATTAAGATAAGGATGGACT CTTTCACTGAGTTATATC[C/T]AGGACACAATCGACGGATGTAATCTATTTGANTTATACCATAGGCCC TATTCTATATTGGGCCAAAGGGAAAAGGTAGGATGGTGGTACTGCTGTGTGGAAACGGA

Marker	Pos.	Allele 1	Allele 2	Sequence
WI-21981	61	T	A	TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTCTTGAGAGAAAAAAA[T/A]GTCTCCCTTATGGGTACTGTGTGATTTCAATAGGGTGTGGGAATTACAGGAACAATAAAAGGATATAATGGATGGGTTCACTCTGTTCTCTCACAGATCCGTGCTTGGGAATCTAGTTGTGAGGCGTTTAAGTTAAATTTGGATTACTTTTTACATGTGGAC
WI-21660	120	C	T	TCCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGTGTAACACGCCCTCTCCACTGCTTACTGTGTGTACCAAGAAGGCAGAAAGCAGCTCACCCAAGCCTAACCTGGCC[C/T]TGTCTTTTTCAGGCTTCTCAGGATGCCCAGCAGCACATACTGGGAACTGGGATGCAGGGAGAAGCCAGGGTCGTGTCTTCAGGAGGGGTCACAGC
WI-19105c	211	C	T	TGGAAAGTAGCCCTTCTGGACAGAAAGAATATTTGTGGTCCATGTGGTTTGAGTCTGTTAAGAAGGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATCAGACACGGGGTGAGCTCATGGTGGAACTCCTCCTTGTCTGTAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAATNTTGGGGGTCCCAGTGGATCTCCCCACAACTTC[C/T]TTCCAGGGGCAGGATTTCCACCCAGGGCCCAGGGTGCCCG
WI-19105a	33	T	C	TGGAAAGTAGCCCTTCTGGACAGAAAGAATATT[T/C]GTGGTCCATGTGGTTTGAGTCTGTTAAGAAGGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGGTGAGCTCATGGTGGAACTCCTCCTTGTCTGTAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAATNTTGGGGGTCCCAGTGGATCTCCCCACAACTTCCTTCCAGGGGCAGGATTTCCACCCAGGGCCCAGGGTGCCCG
WI-21760c	81	C	A	CAAACCTAGTCACTCTACTGATGCAAATGATTGGCAAATGATTGG[C/A]CCTCTGACTGCA[C/A]CCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35	A	G	CAAACCTAGTCACTCTACTGATGCAAATGATTGG[A/G]GGTGTCTTCCTAGCTTTACAATAAGNGGAGGGACCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198	T	C	TCTGCCCATATTGTTCCCAGCACCACTATTACTGTTATTATTCTCTTGAGGAAAACCAGGNATTAAGAAATCTGGTTGAATTTCCATGATGCCTAACTCTATGGTTAAAAATCCTTTCCTTACCAAAAGGAACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTGCAGAAATTTATCTCTAC[T/C]AGAGACAAATTCATAGTTCATAATCTTTCAGGGTTGTGCTTTACTTGGGGGGC
WI-21569b				CCAACATGCAACATAGTCTTCATTCTTAAAAAGTACATAGTAAAAGGTATGAAAAACATTTGTATTCAGAGAA[T/G]TCTAAGACAAATGGTCAAATATTCAAATGGCCTGGCACTAGTGGTAATTCCAGCAGACAAACAGCATGAGAAAAGGCCGGGAGACAGTAATAAATACGTGCCCATTGCAATGAGTTACCCAATCAAGCCCTTTACCTCCTTAAGGATGGCAGATTAGAAGAGACCCTNTCCCCAGGAGA
WI-20934a	72	T	G	TTTCCATTTATTCAGCCGGGCCATCAGAACAATAGCATCTATACCTTCGAAACC[T/G]CCTCTTAACCTCTCCCAGGCAAAGAAGAAGAAAGAGTGATCATATTGAATTCCTCAGAATGGTGGGATCTCAAGACTTTTTAGAAAGTGCTTATTAAGTATAAGAGAGGCTTGAAATATAAGATGATAAATGGTAGCCTTTCTGGAAATAATTTTTGTGTAATCTGTTTAAAAAGATTTTTGGATGCATTGTCCCCA
WI-21561	55	T	G	

ID	Pos				Sequence
WI-21961c	200	T	G	⋮	AGCTTTGCTTGAAAAATTTGGTACTTACTACCTTTGCAATTCTCTTTATTATTATTATTACTTTTATTTTTCCGTAAGTTATTGGGGTACAGGAGGTATTGGTTATATAAGTTCTTAGTGGCGATTGTGTGATTTTGGTGCACCCATTACCCAAGGAGTATACACTGCACCATACTCGGTCTTTTATCCCTCGCCCCT[T/G]CTCCCACTTTCCCCTCAAGTCCCAAAAGTCCATTGTATCATTCTTATGC
WI-21961b	73	G	A	⋮	AGCTTTGCTTGAAAAATTTGGTACTTACTACCTTTGCAATTCTCTTTATTATTATTATTACTTTTATTTTTCC[G/A]TAAGTTATTGGGGTACAGGAGGTATTGGTTATATAAGTTCTTAGTGGCGATTGTGTGATTTTGGTGCACCCATTACCCAAGGAGTATACACTGCACCATACTCGGTCTTTTATCCCTCGCCCCTCTCCCACTTTCCCCTCAAGTCCCAAAAGTCCATTGTATCATTCTTATGC
WI-21956	26	T	G	⋮	CCCACTTGGGGTCTCTTTCAAGTGAATT[T/G]TTCCTTTCGTTCCTGTTCCTTCTAAAGCCTTTAAAATGAACTTCCATTCCTGTTCTGAAACTTGCCTTAGTCTGTTTTCTGCTTCATGCCCCCTCAGTGCCCCTCAGTTGCCTTCTTCTGAGGGCGCAAGGACTGAAGTTGCTGTGGACCTGTAGGGGTTGCGACCGCCGGTAACTCAGGGTAACTCCTATCTCTTCCACCGGTAACACGGGTAACATTATGGGGGTCCAGGTT
WI-21966	148	G	A	⋮	CAAACATACATTATGGCTGCCTTTATTTAAGAAATGTTTACTGAGAATCTGTACTGTAACAACATATTTTGTTAGAAGCATGAGTGAGTGTGTGTGTGTGCGCGCGGCACGGCATGGCACTGGAGGGGATTGCAATGGG[G/A]AACAGGATAAAAAGGTATAAAAACTTGGTCCGAAATCTTTGCTTATTAACCTTGGCCCCTGCTCCTCACAATGTTTCTACACTTAATTCATAGAGAGGTAGA
WI-21930c	146	G	C	⋮	TATACTGGTTTTTGGTTACATGGATGAATTGTCTAATGGTGAAGTCTGAGATTTTAGTGTACCCATCACCTGAGTAGTGTACATTGTACCCAACTTGTAGGCTTTTATCCTTACCTTACCTTCCACCCTCCCCCATTTTGAGTCT[G/C]CATAGTCCATTATATCACTCGTATGCCTTTGCATACCCATAGCTTAACTCCC
WI-21139a	165	T	C	⋮	GCTCTAGTGAAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGTCAGTCCCTGTTCTGCCACTTACTAACTGCATGACCTTGAGCAAGCCACTTAATTCTCTAATTTCTCTGTGAAATGGGTACAATGTGGGTCAGCAGTAAAGGAACTAATACA[T/C]GTACAGCACTCAGCACAAGCCTGGGCACACAG
WI-20317b	217	G	T	⋮	CACTGCCATGGAAATACACAGGTAACACATTTTAAACAGTGGGGACAAAATTTAAGTACGTGGCCAGCTGTTGGTTGTCTGTGGTCATTAAAGACAAATGTTAAGANTCAGGAGTACTTAAGTGCTAGTGGTTACAAATTTTGTTCTTCTTCAGTTTTCATTAAGTAAATTCTAATAGATGATATACATATTACTGCAGATAAAACCATCATCAGAAA[G/T]TATTAAAATTAATTGCATATTTTGAGGCTACTCT
WI-22082e	179	G	A	⋮	CAGGACTTGGTTGCTGTGTCCCAACTGCACATAAATGTCCCTTTTTGTTTGAGTTATTGGTTGTGTGCGTTTTCCTTTTTGCATAAGAAAATATGTCCATTTAGTCCAGAGGCGTCTTGCTTATCCGGATGACGGAGGGTACACGGGGCGGTCCGCTCAGTTCCGCCGAAGGACGTATTC[G/A]CTGAACTGGGACGAGTCTACTCCTCCCCCACAGGAGCCCACGATTTCAAATCCTCTTTGCTGCAACCTCT

WI-22082b	67	C	T	CAGGACTTGGTTGTCGTCCCAACTGCACATAAATGTCCCTTTTTGTTGAGTTATTGGTTGTGTG[C /T]GTTTTCCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG AGGGTACACGGGGCGTCCGCTCAGTTCCCGCCGAAGACGTATTCGCTGAACTGGGACGAGTCTACTC CTCCCCACAGGAGCCCACGATTTCAAATCCTCTTTGCTGCAACCTCT
WI-20993	139	A	G	AACACAAACTCCATGCTCTTCAAGATTCCCACACCAGATACTAAGACATATTAAAATTTACAGCAAT TAAAACAGTGTAGTTTGGTACAATAACACATATAGCAATGATACAAATTAGGGGAAAAAACCCTGG GCTTCT[A/G]TAACAAGTGAGTATACATTAAAGACAGTATTGCAGAATGGCTTCAGGATTAATTTGA TTAATTTAGAGAGAGAGCCTATTTCAGGTCTTCCTAGCTCATCCACACACATCACC
WI-21723b	125	A	G	AAGCGATTTTATTAAATTGATTGGACATACTGTAGGTCAAATAATAATATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTCCCCA[A/G]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82	G	A	AAGCGATTTTATTAAATTGATTGGACATACTGTAGGTCAAATAATAATATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTC[G/A]ACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTCCCCACAACAA CGCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99	T	G	CAACAGATGCTTGAGCCAAAAAGCAAACATAGGCAGAAATACAATTGAGAAATATCTTCATGTTTC AACCTTTAATCTGACTTGCCTTTACTATCCTT[T/G]CCCCATTCTTCTTCTAATCTCTTTTGCCTTACAA TATATTACCTTCTAGGTATCACCTCATCCTATAGGAATGCCTTCTAGTTTAATGTCCTGCCCCAAACA ATACTAACCCATTGAAGGATAACTATGAAACCTTTAAATGGGACAGTGGG
WI-21006a	106	A	G	TGACAGATCACACCACATTTGTTTGTTGTAACTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACACATGTGCACACAC[A/G]AGAGGCAAGTACAAAAATGTAACC CCACCAAAGTGCATGTGAATGAAAGTGCAAAAAAGGCTTCATTTGCAAACTCTGAGGATCATTCTCT CTGCTTCAGGAAAATAAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138	C	G	CTGAGGCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCCTGGCTTGGAAATAACTGAAAAGATTCAT TTTCTCTTTGTGTACAAAGGATTCAAAATATTTCACATCTTCCTCTGCGAAGGCTGCCGTGG CTC[C/G]CAATACACACCAAAGCCAAAGCGTAACTTGGCTGCTCAGGAAGGCTGGGGAAGTGCCAG ATGGTA
WI-21079c	166	G	A	AATGAAAAATGCCACCCAGAGGGTTAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTTGATTCCTCCATGAAATTAAAGCTGTGTTGCTCACTTGTTTACATAA CTCAGGCGCCACCCTGAAATATCTGCTTGTGGG[G/A]AATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACACATCTGCCAAGTCCTGCCAGGGTAATAGGCATGGGCAAAT

WI-21079a	50	G A	---	AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGT[G/A]CGCAAAATCAAGT TGTTTTAATACCAGTGTGCAGCTTTGATTCCTCCATGAAATTAAAGCTGTGTTGCTCACTTGTTACA TAACTCAGGCACCCTGAAATATCTGCTAGTGGGGAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTCACCTGCCAGGGTAATAGGCATGGGCAAAT
WI-22129a	45	T G	---	TCTGTAGATTTTAGCCATGCCATATATTAACTTTAAGGAAAAG[T/G]TTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTCAATAAGTTAGCTCTAACAGTTAACATTGAAGTCTTATACCTTATATTA AATGTTTAGCAATCTCTACTACATTTCAAATATAAATAATTGGTTGCAAATTCCAGNAAAGGGCA TTAACCAAACATGGGACTGATCCTCGGGGGCTTCCCACCTGACTAAGGTTTTA
WI-21941	79	A G	---	TGGAGTTAAGTGGGGCTCTGCTATTCCCCAGAAGAAGGACTCGGAAGATGTTGATTCCAGGGCAGAGT GAGGGGCAGGAGAC[A/G]GGATGAGGCTCTTCTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGGACTGGCCAGGTTGGGGAGCCTCACCCAGAAGAGCCTCATTGACCCCACCACCACTCACC CAGCACACAGGCACACGCAGGGCACGCACACGNTGCACTCACCAGC
WI-18916b	42	C T	---	AATGGCATCCCTGTCGATACCAAACATCTTCAGCAGCTCAGC[C/T]GGCTTCCCACTTCTTGGTACCC GGTTAACTGCCAGGNGGGTGACAGTGATGCCAGGCCTCGCGCCCCACTACTGCACTGGACACAGCCTCACC AATGCCACCTTCATA
WI-18916a	35	G C	---	AATGGCATCCCTGTCGATACCAAACATCTTCAGCA[G/C]CTCAGCGGCTCGCCCCACTTCTTGGTACCC GGTTAACTGCCAGGNGGGTGACAGTGATGCCAGGCCTCGCGCCCCACTACTGCACTGGACACAGCCTCACC AATGCCACCTTCATA
WI-19828c	200	A G	---	TTCCCTTCTCCCCAAGAAGTGGGCAGAAAAGCTTGTTAACCTCCTTTTACAGATGAAGAAAAACAA GATCAGAGAGGTGCTAAGTGCTGTAGCCTAGTCCCAATCTTCTGGCCCCAATTCTGGGTTCTCCCCAAG CCCATGCTTCTTCCCACTTTCTCCACAATCTTTACTTCTTCTCTGACCCTCCACCACCCACCAAATT[A/G] [CTTTTAATTCTGGAAAAGAAACCCAGCTGCACACTGCCCTGCCCCT[C/T]AGCTGCATGCATGCCACCCTC
WI-21863b	47	C T	---	CACAAGAGTCTGTACAACCTTAGGGACCACCCCTGCCCCGAGCACCCCAGCCTCCCTGCCTCTGGTTGAAGTATTTT ATATCCCACCCACCCATCCCCAGCCTCCCTGCCCCGACCACCCCAGCCTCCCTGCCTCTGGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCCTTGATCCAACCCAGCATCT
WI-19860	51	C G	---	TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCCAAAGATG[C/G]CTGCATCAGTAT CTCCCACCCACATAAATTCTGTTTGATTTGCCATTCACCCATAAAATGGTGGGATCTACCTCCCCT CCTTGCAAATTTGAGCTGGNCCTCTGATCCTGTCTGTCTTCTAAGGATCTGAAGCC
WI-19889b	80	C T	---	ACCCAGCTCCTCTTACCCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAAACTGCAGGGCAAG AGGAGTGAGGGG[C/T]TACAGCATTTATTTCCCGTTCACTCCCTGTTAGCTTTGGTAGTGGCTGTGTAT TTCTCTACTGATAGTTCCTTGCCCACAGTCAACTATTGC

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WI-19891c	172	C	G	TGTTGGTCTGAGAATTCACAGCTTACTACAAGGAAGCTGAGAATTGCTTGGTGCCCCTCCCCCCCCG ACTCCTCTGTCCTGGGAAACGTGCCTTTGNCTCCCAGACACGTGTCCAGACGTCTCCTCAGCGGG AGCTCCCGATCCCTCAATTGCCATCTGTCTGACTC[C/G]CGTCTTCCCGGGGCGTGGGGCGTGCTTGT CAGGCAGGCGGCGGGGGGGAGGAAGGAGGAGAGATCCAGGGTCTGTCTG
WI-20155a	81	C	T	GCACCTGTAGGGGTGTAGCTTCCATGGTTCTCCAAGCACGGGCTGTACATTACCCTTAGGCTGACCAT TCCCTTGCGGGGGG[C/T]GCAAAACTGCTTGAGGAAATNTCCCAGGAGGAATAAACTAGAAGACGC ACCTGCTATTTCACCATACTATGGAGAATACAGCTAATGAAGTGGTGGCAGAAGCTTGGCCGTGTGA GTGCCCCAGGGTAAAAGTCTCTCTCTCGTCCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91	T	G	AGCCATACAATGCATTGCAAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGCGTCAGTGTACAAT ACATTCATGTCCAGGATAAGGAGGCA[T/G]ACACCAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTCCATCTATATAAATACACAGCTGGGGTGGGGAAGGATGCT GGGTGATCTTGTTCCCCCGCAGAGGGCCTGGGAGGCAGGGNGGGTGGTGGGAA
WI-20270a	53	G	A	AGCCATACAATGCATTGCAAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGC[G/A]TCAGTGTAC AATACATTCATGTCCAGGATAAGGAGGCATACACCAGGATTTATACACAGCTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTCCATCTATATAAATACACAGCTGGGGTGGGGAAGGATGCT GGGTGATCTTGTTCCCCCGCAGAGGGCCTGGGAGGCAGGGNGGGTGGTGGGAA
WI-20622	130	T	C	CCACTTTCAATATTTTACAAAATGCTCACGCAGCAAATATGAAAAGCTTCAACACTTTCCCTTGTA ACTTGCTGCAATAAATGCAACTTAACAAACATACAAATTTCTCTGTATCTTAAAGTTGAA[T/C] TACTAATTTTATGATGTTACTCATATTTTATTCATATACTTTAATGACATCATTGCCAATACATA CATTATTTTCTNTAACTTATTTATTTTACAATAAGCCAACATCGTCATCGTCATGCAG
WI-20768b	190	C	T	TTCCCACTCAAAACTCCCACCCCAACCTTCCTGGAAGGCAGGCTAACAGGACCTCCTGCCTGCCTGC TCACGACTGATTACTTCAATCCCAGCTGCAAACTGAAACTCATTCTGTATATCACCACTCTA CAGGAGAGAGGTCTATTTCTGGGGCACCCAGAAGNTCAGCACACATACTGCTGGGA[C/T]CAGGGACTC GTAATTCGCCTTGGTCCAACTCCTTCTATGGGGTTTAGCTGCCCTCATTCC
WI-20768a	71	C	T	TTCCCACTCAAAACTCCCACCCCAACCTTCCTGGAAGGCAGGCTAACAGGACCTCCTGCCTGCCTGC TCA[C/T]GACTGATTACTTCAATCCCAGCTGCAAACTGAAACTCATTCTGTATATCACCACT CTACAGGAGAGAGGTCTATTTCTGGGGCACCCAGAAGNTCAGCACACATACTGCTGGGACCAGGGACTC GTAATTCGCCTTGGTCCAACTCCTTCTATGGGGTTTAGCTGCCCTCATTCC
WI-21909	153	A	T	TGTTTGCTTTGTGCCAGGTACTCTACTGCTTTACATAAATTATCTCATTCTGTCACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAAATAAGGATATTGGTCATCTTTAAAGAAA TGTCTTAACATACCAAAG[A/T]AGTGGAATCAATGAATAAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCCACTAAATTTATATTTCTATGTGTATGGAAAG

ID	Pos				Sequence
WI-22202	128	A	G	---	TGTTGCTTGGTTGTTGCTTTCTGGAAACATATTGGAACACTTGTTTTCATAAGCTGTCCTGACAGTGGCACAAATCCCATCCATTCTTCAGGCCTTTAATAAGGTCATTATGAAATCTGAATTTCT[A/G]TTAATACTCGGTGCATTCATCTGCAAAAGCAACTGGCACAACCACTCCTTGCCGGTGCAGCTCTCGGAGAACATCTAATATTGAGTCTAGTTCTGTGCGGAACTTCTCCAGCTCAC
WI-22189	70	C	T	---	CCAAGGATGAAATTTCCACATTTATTTNCTTTATGTGAATAGAAAATGGCAGTGAAGTGTCCTATGAA[C/T]GAGGCGGAGGAATGGGCATGCGGCTGCGGTACCAGCGTTGTGCTTCCAAAGTACACTATGTGTGGTGGGAGACAAAGGGT
WI-22283	109	T	C	---	GGGGAGGCATCATAGAAAAAAACCCTCAGCCAGAAGTTAGGACACATTGTGATTCTCAGCCACTAACGAGCTGTATGACCTTGGTCACTAGGCCTCTGCGAGGCTCTGGTTG[T/C]TTCATTTGCAAAATAAAACCCAGACCGGGTCATCTTTCAGTTCCCTTCCCAGCTCTCATTATTTATGATTTGCTCTTAGTCTTTATGAGCCATGTATGATTTATCAGTCTCCCTGATGCACTCCAACTCAACTCAATGATGCAAAAG
WI-22290a	136	C	T	---	GACGTCATCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGGTTTATGGGCCTCTAAGCACCGGCCAGTAGTGGGGAATGCCACATGCAATGGGTGAGTGGGTGGGATCTCGGGGGGGGTCAGGGACCTTGCTTTT[C/T]TTCCAATCTCTCCTTCTTAGCCAGAACTTTGCGAGAGCCCTTNATTTCTCTCCTCTATTCCCCTCCTTTCCCCAAATGTCTAAGGTCCAATTCCCAGACCCCTCCCAG
WI-22292	53	A	G	---	CCAGTGGAAGGGTTTACAGCCATAGTGAGGTTCCCCCATTGCTCAGTACCAGA[A/G]GTTTGGAGTACGGTCGTTTAAAAAATACTTATCTGACCACAGTGGAA
WI-22387	186	C	T	---	ACCTTGCACACCTGCCATCCGGTGCCATCTCCTGGCTGGCACATCTATACCCACTCTGGCTCTGAAAGGCTTGTCAACCAAAAATGGGCAGCTGGGGCTAAGGCATATTTAAACAAAGGCTCCAAAGGACCCCTTTCACTTGGGTCTAGCATCCAGCCTCTCTCTCAGCAAAGGCAGGATTGTGGT[C/T]CCTTGTGTTTTCTGAACAGGGCCCAGGCAGCCAAGGCATGCCATCACTGCAGCACTCAACCCT
WI-22395b	127	A	G	---	GCCGTTCCAGTATTGATAATAATTGTGTTTAATTTCTATACAGAAATGGTTCTTTCTTGAATATTTGTAGGGATGGGATGAATTGAAAGTGAATTAAAGTCAAGATAAAGGGGCAACTCTTTAAT[A/G]AAGGAAATGTTACCAAATCCATAGTGAAGAGTAGAGAATAGAAAGTCCCCAGGCTCCT
WI-22405	90	A	C	---	TTTATGGCTCCTGAGTGCCTTCACCCAGCTACACTTTACCTTGTATCTATAAAAGTGTAATTTAGAGTAAATACATTGGCTGTAAAGTCG[A/C]GATCAGGTGCTCTCCACCAAAAGCAAAACAAAAACTGCTGAAATGTGGCAAGGTTTCTCAGTG
WI-22419b	67	T	C	---	CCCTTCTGGACAGTTGCTTTATGTGTTCAGACAATCAAGGNTCGCCTTCCAGGCACAGCCCAGTGC[T/C]CTGGAATGGCATCAGCATCCAGCGGCTCCCCGGCCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59	T	C	---	ATTTTCCCTTTCTGTGTTCGTATTTCCCCTTTTGTCAGTAAATNAGCAATACACTGA[T/C]TGGAAATCTGCATGCATGAATTAAATAACATTAACAGTTCATAAACACACCCCATATCAGAGTATAAAGCAAGAGGTTGAAAAATATCCCCTAACCGAATGCAAATTAGGTATCCCCAAAATTGCACATTCCTCCTCTAGTTT

Clone	Position	Allele			Sequence
WI-21763b	154	A	G	---	CATACCCTTTAGGTGCCCACACATTGATCTTAGTTAACAGTCTTGTGTAGTTCCCTCTTTAGGCTTCAAGATAATTGTGATTTCATCGCACCCCAGATACTTCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCACTGCTCTCCCACAGCTGATT[A/G]CAGACATTGCCTGCTGTGTCTTCTAGTGCACTTGA
WI-21763a	135	T	C	---	CATACCCTTTAGGTGCCCACATTGATCTTAGTTAACAGTCTTGTAGTTCCCTCTTTAGGCTTCAAGATAATTGTGATTTCATCGCACCCCAGATACTTCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCAC[T/C]GCTCTCCCACAGCTGATTACAGACATTGCCTGCTGTGTCTTCTACCCCAGCAGCTGTCTAGTGCACTTGA
WI-22440	64	A	C	---	CAGTCCCATTGAGTCCCCAGTCGGAGGGTGCCCAGTCGGAGGGTGCATTCTTCCTTTATCTTGCTTAAGCCACTTGGGTA[A/C]TCCATTCCAGCTCTGCCACCTTCTCCCAGTTTCTCATGTCAGAAGTCCCTGGAGGGAGGAGGCTTTCTGGAAAT
WI-22449	74	T	C	---	CAATGAATGTTGTGGCATATGATTTNCCATTGTGTGACAATTTATTAGCTGGCATCCGAATACAGTACTTCTTT[T/C]GAAAAATACACAATGGGAACTGACA
WI-21965a	112	A	G	---	CAGGTTCCACCAGAGGCTTTATTTCAGCCACTCAGGACCCTGGCTTTCTGCTCCAAGGCACTGAACACAGTCAGGCTCTTCTAAACACTGGCAGGACCTCCCCCACAGCC[A/G]CCCCCACAGGGTTCTGTTTCCCAAGTCCTGATGGATTCAGGCAAGCAAGACCTTCACCACTACCTGCTGGAGGAGGGTCATGAGGCAGCAGCCTGTGGTGCCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115	C	G	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCAAACCACATGGTTCCTAGTCAGAAAGTCTCATGGACTTTCCTAAG[C/G]TGTTCTCATGATCAGACCACCTCCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG
WI-22374a	149	T	C	---	AGCTTTTACAACAAAGCGAGGGGTTTAAGGAGCCTGAGGAGAATTTCACAACTATTGACTACTACAGAGTCTTCAATTCCAAAAACAGTTAATAGTAACTTGGTGGCACATACAACACATGCATTGAATACTCTGTATTATTCAGTAACTAAA[T/C]AGGNTCCTGCATCCATTCCTTCACA
WI-22250b	132	C	T	---	ACTTGTCTCAGGCAGGCATTTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCACTTTGAGGAATGTGCATTCACTGTCTGTGTATTATGGGGTTATTATGGGGTCTCTGCCTCCTGGCTGTTATG[C/T]GGANCCAGGAGGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
WI-22250a	89	G	A	---	ACTTGTCTCAGGCAGGCATTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCACTTTGAGGAATGTGCATTCACT[G/A]TAGTGGGTTATTATGGGGTCTCTGCCTCCTGGCTGTTATGCGGANCCAGGAGGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192	G	C	---	GCAGCCATCCTCCTCTCCAACACCTCCCAGCCACCCTGGGGCCACCTCATGCCCAGCAGCACCTACGTGGCCCGAGTACGGACCCGGCCTGGCCCTGGCTCTCCAGGACGTCCCAGCAAGTGGAGCCCCAGAGGTTGCTGTGGACTCCAGCACCTCCAGCCCCCAGCCGGATGAGGCCCCAGAACCTG[G/C]AGTGCTTCTTTGACGGCGGGGCCCGCGGTGCTCCTGGGAGGTGAGGAAGGAGGT

UTR-04932-2a	149	C	T	...	GCAGCCATCCTCCTCTCCAACACCTCCCAGGCCACCCTGGGGCCAGAGCACCTCATGCCCAGCAGCAC CTACGTGGCCCGAGTACGGACCGGCCGGCTGCCCCAGGTTCTCGCGTTCTCCAGGACGTCCCAGCAAGTGGA GCCCAGAGAGGTTTG[C/T]TGGGACTCCCAGCCAGCAGGGGATGAGGCCCAGAACCTGGAGTGCTTC TTTGACGGGGCGCCGGTGCTCAGCTGCTCCTGGGAGGTGAGGAAGGAGGT
stFIBBb	412	G	C	...	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGGGAGCATGAGCCCTTTCCCCACGGCCCTTGCCACTGTCTCCTGGCCCTCTCCTGATCATGCCAGG TTTGCACCAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAGATGCAGCCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCCTTAGAACCTTCCATGGTT
stFIBBa	341	T	C	...	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGGGAGCATGAGCCCTTTCCCCACGGCCCTTGCCACTGTCTCCTGGCCCTCTCCTGATCATGCCAGG TTTGCACCAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAGATGCAGCCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCCTTAGAACCTTCCATGGTT
stIGLV2	61	T	C	...	GTCACAAGAGGGCAGCGCTCTCGGGACGTCTCCACCATGGCCTGGGCTCTGCTGCTCCTCAC[T/C]CTC CTCACTCAGGACACAGGTGACGCCCTCCAGGGAAGGGGTCTTGGGGACCTCTGGGCTCTGATCCTTGGTC TCCTGCTCCTCAGGCTGCCAGCCACCGGGGCCCAGCCACTGACTCACTGGCCATGT
stSG10017c	70	T	C	...	GTTCAGGCTCATCTTGAACTCCTGGTGTCAAGCGATCCTCCCACCTCCGACCTCCCAGGGTGCTGGGAT TA[T/C]AGGCATGAGCCCCACCACCTGACACAAAATACATTATTATACTCTAAAGTATAGGATTACT TTAAGAGAAACTAAAAGTATGATGGCTTACTTTCTAATCC
stSG10017a	33	G	A	...	GTTCAGGCTCATCTTGAACTCCTGGTGTCAAGC[G/A]ATCCTCCCACCTCCGACCTCCCAGGGTGCTGG GATTATAGGCATGAGCCCCACCACCTGACACAAAATACATTATTATACTCTAAAGTATAGGATTACT TTAAGAGAAACTAAAAGTATGATGGCTTACTTTCTAATCC
stSG10023	63	A	T	...	TAATGATAATTAGGGCATTCTTCCCACACGAAGATGACACAATTGACCCAATATCATTGAGGC[A/T] AACAGTTTGGGCTGTTTTTCCAGTAGTAGTATGACAGTGA
stSG10096	36	G	C	...	GTGGAGAAAGATCGTCTTTCCTCCCCCATGACC[G/C]GGCTTCCCGCGGGCACCTGTGCGTTTCC ACCCCGGAGACGGCCCTTGTAGGGACCCACTGCGCCACTCCGCTGTGCGCTGGGTTCCGCCTCCTAG GGCTCGAGTGTTTAAG
stSG10118	107	C	A	...	TAGGCTTAAACCTGGAATCTACAAGCCAAAAGTCCCTCCCTGCCTGAGGGCAGTACCCTCCATTGGGC ACAGTCCAGACCAAGTCAAAGATGCCCATTCCTTGCG[C/A]CTCAGCCCTCAGTTCCTTCATTTCC ACCAGGCCGTGCCCTTGTTGAGTTTTTGTTTCCCCAGTGAG
stSG10120	89	T	C	...	TAGTAGGTAAGAAAAGCAAAGGAGGATTGCTTATGCGATGACTGTTTACAGTGGTGTCAGACTATGC CGTGTTCACGAACACTTTAATA[T/C]GTTGTTGTTAATCTGATTTATCCTCGTCTTACAAATG
stSG10178	42	C	T	...	TTGAAGCAATATTGTCTAGCACTCTGCTGACAGTCCG[C/T]GGGAGGAGAAGTGAACAGGAA TCGATTCTTTGTCTTTAACTGCCCTTAGTTAGGAGAGATGTTAAAATACTTGGC

ID	Pos				Sequence
stSG1019 3	136	G	A	---	GGAACAATACTACCTAAGGACAAAAATACTATTATTAAAAAAAAGTCTTCTAGTGTATATTGTTAACACATTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTGAGTGCCATCTATACAAACTTTTACTT[G/A]TTTGAAAACTGAGATTTAAGTTGCAAACT
stSG1020 2c	143	G	T	---	AAGCTAACTTAGGTGAATGGTGCCACTCAAAGGTCTTCCGAGGAAGCTCAGTCCTGGCTTGCGAGAGTCAGCCTTGGTCACCTCATAACGGGGCTCCAAGCTAAGGGCGTCAAGGAAGCAGTCCCACTGCTTCTCGCTGTCA[G/T]CAAGACCACAAGGCAGATGCCCACTCTGCTGCTCCTCTTTCCTTGTCTACTTTCT
stSG1020 9b	75	A	G	---	TCTTTTCTCTTTCACTCTCCAGTCACCATGCATGATTCAAATAAACTAATTCTCCCTTAAGATCCCACTTTAT[A/G]TCCAATAAATGTAATTATTATCAGCTGCTGAATT
stSG1020 9a	34	C	T	---	TCTTTTCTCTTTCCACTCTCCAGTCACCATGCATGATT[C/T]AAATAAACTAATTCTCCTTAAGATCCCACTTTATTTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1021 8	29	T	C	---	TACTAGACATGCAAAATGAGAAGATTACA[T/C]GTGAATATTTAAAGAAGTTATATTTGTTGACATAATATGCATTGTACCCGGGCATAATAAAGTTAAAAGCCAGTTATTCTGA
stSG1025 2	108	A	C	---	ATAGGTTTCAGGAACAAAATCATTAAAATGGAAAAAATGAGAAGAATTCTTTATTTTGGACCAATTTTAGGCACTTAAGAGTTTCTTTCTTTCCCTTCCTTGATCA[A/C]AGTGAAGATATGATAGGGAATTCAGAAATTTCTCTTCTTG
EST10915 0	123	A	C	---	CTGTATTAATTAAGAAGGCACTATTAATGAGGGGACGGAAAAATCTACCTGTACACAAAATTCTGTACTTTAACAGCATCTTCAAATAAACCTTTAAAAGGATAATAATGGTTTACGATCATTTTAAG[A/C]ATTTTAAGAACTGAGTTATTTGGAC
EST11023 1	166	T	A	---	TTTTTTGTTAAACCAACCACCACCCTGAAAGTTTCCACATGTGAAATATAGATACAACAGTGAACAAAATATGGTGGCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACCAGTAAAAACAGCAGGCAATTAGTCAATTAAAAAAAAATAGTACATGTTA[T/A]GTGTAATAAAATTACAAAGGCTTTCCCACTCGTGGATTGATTCCTTTTTGGAGGAGGAGTAATCCTGG
EST14096 8	71	G	C	---	GGGGATGTATATTACAGATAACAACAACTCACAAATACCACTCCACAAAATCTAAGGCCATTCTGTGA[G/C]TTATTTTAAAACTTGGTGTTTGCACATAATGATCTTAAAAAAAAATGAATTACCAAAACCAAGATTCTCTTCTAAAATGAAAATTTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATCTGAAG
EST22113 6c	125	C	A	---	TGCAAATTGTGAGAAGGCAGCAGCAGGGGCCAACCCCTGGGACCTCATCTCTGTCTAGAATGTGAGGTCGCAGGGATGGCTTAAGTCTTCCTCTGGCAGAGACCCGAGGTGCAGAGAGATGATTCTTCTCA[C/A]CCCTTCTCTCAGGGTCGTGGAG
EST22555 7	60	G	A	---	TCAAGCATGTGTAAGGCACTGCCCCGCCCAGACCCTTCTAACTTCTGCACACTGGAAGGT[G/A]AAACCTGGAGAGGAAGAAGACACTCCCCTCCTAGCTTCGGGCACCCTCCAAAGATGAGCATTCATCTTGGAGACCAAAAATAAAAAGGACAAAGACCAGGGCTCAGAG

ID	Pos				Sequence
EST22917 6	74	C	T	---	GTAAACCTTGCAAACGCCATGCTCAAATGAAGCCTGACTGACCAGGGGCTCTTGGGCCTCTCAATGCA ATAGAAA[C/T]TGACATGGGCGCCAAAAGACTTCCCAGACACAAAGCACGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65	A	G	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACTTAACCCTCAGGCTGTCCTACTCA[A/ G]TGTGGTTGCTAGCCTCACTCGCACACAGGAAGCTTGGAATTTGGAGGCTCCAAGTCACTCTCCA
EST36745 3	56	A	G	---	GAGGGGGAACTTCAACAGGATTCCAACAGTGAAGCAGAATCATGGGGCAAAAGTC[A/G]CTATGG GGCCAGACTGAGGTTGGACCACACAAGCACTCCAAGCTGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCACGGAGTAGCCAT
STS-R37410c	201	A	T	---	TGTGACCATACCAAACCTATGCAATAAAAGAAAAAATCCTCACTTAAAAAAACAAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTTGGA ATTTATTGGTTTGAATAAAATACAAAATGTGTATCCTCCTGAGACACATTTATAAACATTCTGGT T[A/T]TATTGTGAGTGGTGCTCTCAGTGGCCAAT
STS-R37410b	139	G	T	---	TGTGACCATACCAAACCTATGCAATAAAAGAAAAAATCCTCA[C/T]TTAAAAAAACAA AAAACCTTTGCAATGCTCATCATTTTTCAGGTGTGAATAAAAGTTCATAGCATTTTGGA GGAATTTATGTTTGAATAAAATACAAAATGTGTCCTGAGACACATTTATAAACATTCTGGT ATGTATATTGTGAGTGGTGCTCTCAGTGGCCAAT
STS-R37410a	48	C	T	---	TATCGTGGGAAGTTCCAACCTCATACTTATGCTGCTTTCTACTTGCTAATATTGGATGCTTCTTGCCA GGCTC[C/T]TTAAATTGTGCTGTAACCTGGGAAGAAACCTTCCTACTCTCCACAAACCCTGAA
STS-R42778	74	C	T	---	CAATCTGAAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGGAGGTGGGGACTGAGGAGCG ACTGCTAATCAGTATGGGGTTTCCTCCCGGATGGTGAAAATGTTCCGGACCTAGATA[C/G]TGACGA AGGTAGCACGACACTGTGAGTGCACTAA
UTR-04350	125	C	G	---	GAAATAAACTAAAACTGCAAAGCAAATCACTGTTAATAAGAATTGTTCTTCTTGT[T/C]GACAGTTG AAGTGGGTGTGAGATGGCATAGCAATGAACAGTGGGAGCCAATGAGGTCCTCAGAATGCGGGCAAA CTCCTCTGTGAAAATGTAT
stSG1026 6	55	T	C	---	GTATAATTCAGCATAAGCCAAAGCCTTTTAAAATAACCATACTATCATTTTATGAAATCTTTACA AGA[T/G]AAGCACAGTAGTACAATATTTAAGCATCTCCAAGTCTCCATTTGACTATC
stSG1028 2	70	T	G	---	CACTTTAGATATGGAGGAAAATGGTTTAATGGACAAAAGAGAGTCACAAAGGTCAGCCACGTTGGAACCAACATAG TTTCATCACCACGTTGAAACCATGTGTTGATATGCAAATAACAGCAAATAATTTTCACT[C/A]TTG TCAATGCCAATGCATTGAAAGGCCCAGAAATGAGAAAAGGATAACAAACTTTGATAAAAGGTA
stSG1031 0	128	C	A	---	AGAATTTCTGTGTG

ID	Pos			Sequence
stSG1033 1b	116	T	C	---	TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTTCGG GCTCCAACCTGTCCTAGGAAGGCCTAGACCTCAAACACCCAACACCTCCA[T/C]GCATTCCTCTTGG CTACTATGTCTTTCCCTGACTTCTGCCTCTGCCTCTCTGGGCTGCTGCTTCCACCTGTTCATCTGA CTTAGGACCCTCC
stSG1033 1a	107	A	T	---	TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTTCGG GCTCCAACCTGTCCTAGGAAGGCCTAGACCTCAAACACCA[A/T]CACCTCCATGCATTCCTCTCTTGG CTACTATGTCTTTCCCTGACTTCTGCCTCTGCCTCTCTGGGCTGCTGCTTCCACCTGTTCATCTGA CTTAGGACCCTCC
stSG1243 b	225	G	A	---	ATTGGCAAATGGGAAAATGACACCAATCATTTGATTACAGAAAATGGTTTATAAATCCTCCTCTTG AAATTATGTTCAGGCCCCAGCCTAGCTTATGCCTGCAATCCAGCACTTCGGGAGGCCAAGGAGA AGGATGCGCTTGAGCCGAGTTCGACACCAGCCTGGCAACATAGTAAGACCCCATCTCTGTTTTTT TTTAAAAAAAGAAATTCTGTTC[G/A]AAAGTATTTCAGACCAAAAGGAGGT
stSG1345 b	60	G	A	---	AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAATTGAACTAGTTTGCTTCATAAATGGGGCAA TCACATTTTAGCATGGGCCAAAAATTCAGGAGATGCCATGTCCATAAATGTCCATAAATGGGGCAA
stSG1345 a	54	T	G	---	AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAATTGAACTAGTTTGCT[T/G]CTTACGCGCT TCACATTTTAGCATGGGCCAAAAATTCAGGAGATGCCATGTCCATAAATGTCCATAAATGGGGCAA
stSG1385 b	117	T	G	---	TTAATGTCATCCAGGGAGGGGCCAGGGGATGGAGGGGGTTGAGGAGGCAGTTATTT TGGGTGGGATTCACCACTTTCCCATGAAGAGGGGAGACTTGGTATTTTGT[T/G]TCAATCATTAAGAA GACAAAGGGGTTGTTGAACTGACCTCGGGGGGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTTCTCGTCG
stSG139	69	T	C	---	TCGTCTCCTTTCCAGTGCTTCTGCCAGAAGCATCCCCATGATGTTGTGACCGCACAGCACTTTGTGTCT [T/C]GCTTGAGCACTGCCACTCTGGCTGCTGCCACTGATTGTGTACTGTCTTGCTGCCC GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTTGTCAATCCCT TGGCTCCTCCACTTCCAGTTTGGCTTCTCTGTCTCCAT[T/C]GAGTCTCTCCATGTGGCAAACAAGATGGC TACTGGTGGTCCCAGGTTCAGCTCCTCTCAGCTTGGAAATCCAGCAGCAAGAAGAGATGTCTCACTCCCA AGTCCATAAACTCAATCCTGGGAAG
stSG1427	103	T	C	---	CCCTGGAGTTTCTGAACATAGGAAGGAAGAGAATGCAAGTCATGTGTTAGGTCC[A/G]CTCCCTTGCATGA AATGTGGGAGAGGGAAATAAAGTTAGGCAACATTTAGGCAACAACCCCTTCCCTATCCTACC GCA
stSG1471	50	A	G	---	CAAAACCAAAATCCTTCCCACGATATATTACTATTTAGTCTAAG[T/C]TTTAATTCAAAGGTTGAGA ATGACGAATTCAAGAATTCTTCATACATAAATTGCTTCCTTAGTTCTGCAGATGGGTA
stSG1483	44	T	C	---	CACACCCACAAGTTGTGGAGGATGTCTTGTTGCAGCTGTCGTAGTTACTAATGCTGAAAGAGGAA [C/G]AATGTGGAGGATTGTCTTGTTGCAGCTGTCGTAGTTACTAATGCTGAAAGAGGAA AATGCCTGA
stSG1696	67	C	G	---	

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stSG1847 b	95	G	A	---	TTGCAGACAACAATGGAAGCTTTAAAACCTCTTCAACACAAATGTACCCCTAAAATGAAAGAATTTAGAGGTTAAATAAAACAAGTGAGAGAACC[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAATCATATCTGAATGACTGACTTGTTCCAATGTGAAAACCAAATTAAAAATAACTTGATCACTGTGCTTCAAACACAACTG
stSG1847 a	49	C	A	---	TTGCAGACAACAATGGAAGCTTTAAAACCTCTTCAACACAAATGCTACC[C/A]CTAAAATGAAAGAATTTAGAGGTTAAATAAAACAAGTGAGAGAACCGTTTACTTACATCAGTTCGGTTTATAGACATTGAATCATATCTGAATGACTGACTTGTTCCAATGTGAAAACCAAATTAAAAATAACTTGATCACTGTGCTTCAAACACAACTG
stSG1897 a	83	A	G	---	CTTAATGCCCCTTCCTCCTTCTGCACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGGAGGAGGACACAGGACT[A/G]GCCCACCACCTTCCTCCCGGTCTCCCAAGATGACT
stSG2022 a	86	T	C	---	TGTCTTGAGGTTTCAAATCTGAGATATCTATGGCAAGTTATAAAAAGTACATTGATCAAGGTACAATTTTAACATTAATATACA[T/C]ATTCCATAATCTCATCTATTAACACAGGCCTTTGTTGTTGTTATTTTTTCTCCCTACAATATTCCTGACTCTGTAGGGACAGTGGGCCTCAGTTGGGGGGTTGGGGGTGACT
stSG2076 a	104	C	G	---	AAACGTTGTCCCAAAATTGTGTTCAGTTCACAAGTATAAAATAGACTTCTGAAAAAAGTTTACAATTAGTTATAAAACACTTAAGAATATATTTGACATT[C/G]ACATCACAGTGGGGCATTTT
stSG2108 c	71	A	G	---	TTGAGCAAACAATGATTCGCGAATTGGGCAGCTCCAACCAAAAAATGATTGAGGGGCTCCACAGAGAGGAGC[A/G]TAAGGGGAAGACTTTATAGGACAACTGTAGAGAGTAGAACAAAGCAAAGCAGACGTTTGATTGGTTACAGTTACACAGTTGTCTTATCTTATTGGTCTATCTTATTGGGAAAGTCTGTAGTTATTGTAATTGTAAGTTTGTTGGGCGTGTCTGA
stSG2108 a	49	T	C	---	TTGAGCAAACAATGATTCGCGAATTGGGCAGCTCCAACCAAAAAATGAT[T/C]GAGGGGCTCCACAGAGAGAGAGCATAAGGGGAAGACTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGACGTTTGATTGGTTACAGTTACACAGTTGTCTTATCTTATTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAGTTTGTTGGGCGTGTCTGA
stSG2141 b	173	A	G	---	TTATTCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTATTTAAACAAATGACTGCCTGTACTGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCCACCACTGGCATGGCGATGGTGCAGGTGGGTGCAGTTCCCGTGGTCTCCTATTATTTTAAGGCGCAGTTCCCTGTGGTCTCCTATTATTTTAAGGC[A/G]AAGTTCCCTATTATTTTAAGGC
stSG2141 a	113	C	T	---	TTATTCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTATTTTAAACAAATGACTGCCTGTACTGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCCACCACTGG[C/T]ATGGCGATGGTGCAGGTGGGTGCAGTTCCCTATTATTTTAAGGCAGTTTTCAGAGCACTGGCATTCTGTTGCTCTG

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stSG2148	50	A	G	---	TGGGAAACAACCGGCTATAGTCTGAGTCATATTTTTAGACCGTGATTTC[A/G]AAAGAAACAATAAATGTGGATTAGAAAGGAAACCATCCATTACTGTATTTCGATACTTGTGATGTTCCACAGACGAGCTCATCAC
stSG2175	68	C	T	---	CTCAATGAGGACTCCATCAGCCAAGCGGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGTGCT[C/T]GCCGCGTGACTCAGCTAATGCTACCGGGGTTGGAGCGCCACACCGAGCCCAGCCACCTTTCCATACCTGGGCACGAGGGAAGGGAGTGGAAGGACCA
stSG2189	41	C	T	---	CAAGTGGTGAAAGCTGGGATTTGAGCCTGATATTCACACTA[C/T]CTACATTCCCTCCAGTATAATAGGAACTCATCGCTAACTTTGAGCACTTAGTGTTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTCCAGCTTTGCGAAC
stSG2200	49	T	C	---	TGTTGATGACCATAGAGGATGCAAAGCTCCGGGCTGGTTCTGTATGATGT[C/T]TTATATTTATGTATAATGTCTTACCTGATGATACCCAACATATTACTACTGTATAGATGAGGATGGCAGCTTGGCTGGTCAAT
stSG2243	85	G	T	---	CATTTTCTGCCTCCTGCTTCCCAGTACTACCCCGTCCAGCAACTGCCTCTCGTATAAATAAGTATCAAGATGGTCAGTAGAAAAG[G/T]AGAGCCATCCTCCTCAGCCCTGGAAGACAGTGTGGGAGCTTCAGCT
stSG2257	65	A	C	---	TCAGTGATTGTAGGAGCTGGCTAAGTCATCATCTAAACTCTGTGAGCGCTATCAGAAGGGCAG[A/C]CTGTCAGGAACTCTCGCCAAGCACTGGGCTGTCCTCAGGCAGAATTCTTCCT
stSG2306	67	A	G	---	GTCATCAGCGTAGAGGTCACTGTGTATAAAACAAACAGTAGCTATATGATATTTGGGAACTATTTACA[A/G]TATGTCTCCCATTGGGTTTTCCAAACTGATACAACCATGAGGTGAACACTTTCACTGTTTCACAGTTCCTCCAGAGA
stSG2334	70	T	G	---	GAAAACTACCCACAGCACATCATGTTAAAAGAAGAGAGGATGAAAGAAAAAATCCCGCAAAAAACAAAAAA[T/G]TGCAGTGGAGGGGGCTGTGTGGGAGGGGTGAATG
stSG2339	63	T	C	---	AGAGCAGAATGGTGAATCAACAAGACCTCAAATTGTCTTGACTGCAGAAGTAACTGCTGTCAC[T/C]GTTCTCAGAGTCACCATTACGGTGACTGTGTCTATTCTGGCTGTTCCTATTCATCA
stSG2465	76	C	T	---	CAAGACTAAGAAGCCGCACCCGAGTGGTCCCACTCAAAAAAGAGATTTCTGATTCTACCTCAAAATGCAGAAAACCA[C/T]TACAGATTAAAAGAGAAAACACACACACACTTGAGAAACTCGCCCCTCCCTCATCTTCAAAAGTGTGGGGTATGCA
stSG2549	140	T	C	---	TTGCAGGCTTGTATTCCACAATAACAAAGTCATGTATAGAGAATGTGAAATGATACTTGAAAACCAAGATATATAAAATATTGAAGTCATTTATGCCTTTTGATGACTGGGTTAAATATGCAAAGCAGCTAAAGGAATAT[T/C]TACACCACCCACCCCTTTTAACT
stSG2577 b	123	T	G	---	AATTGCCAAATGGAAAATTCCCAGAGGATTTTTAGACCAACTTTGCCCTGTTGCATTCCCAGTTTGGTCCCAATATAGGCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAACGAC[T/G]GAACAATCCCGGCGCCCAGATTAATTATT

stSG2577 a	121	C T	---	AATTGCCAAATGGAAAATTCCCAGAGGAGGATTTTTAGACCAACTTTGCCCTGTTGCATTCCCAGTTTGGT CCCAATATAGGCCTTCTGCAAGAAGAGAGATCAATGCCGAACCGAACTGTGAAAG[C/T]ATGAACAATC CCGGCCCAGATTAATTATT
stSG2700	58	G A	---	ATCTCCTGACTGCTTAGTGGGGAAAGGAATCAATTATTTATGAACTGTCCGGCCCC[G/A]AGTCAC TCAGCGTTTGCGGGAAAATAAACCACTGGTCCCAGAGCAGAGGAAGGCTACTTGAGCGGCGGACACCA
stSG2724 b	101	T G	---	AAACAAGCTTTGTCATTTCCACTACATTTGTTGTGCTTTATATTAATAATTGCAAATGCTATAAT TTAATACTTATATTCCAATTGCTTGCATAATCA[T/G]TTTTTTTAATCCTGGGGTGTTGAAAGAAC
stSG2776 a	65	G A	---	GTGGCCGATCTTTACTTTTCCAGAAAAGGCGGTAAATAAAAACCTGTAGAAAAGTCTGAATATGC[G/ A]TATTGGCCCTTTGGAGTTAGGCCCAGGAACTTCAAACAAGGGGACACTGCTGGCCAACCACAAAA ATATCCACTAATTCCCGAATATAGTAACCCTGTCTTGTCCGAATG
stSG2791 b	109	G T	---	AAGGAAAGGTGGAGGGGAAGAAGGGAAGAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTC TATTATACTTCTGAACGGTAAACTAGCAATTTAATAAATATT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2791 a	100	A G	---	AAGGAAAGGTGGAGGGGAAGAAGGGAAGAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTC TATTATACTTCTGAACGGTAAACTAGCAATTTA[A/G]TAAATATTGGGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2826	85	C T	---	CCGCCAATTTCAACACACATTCTATGAAAACTAAGGGTGGATCATGTACAAACAAAAACAAGC TCCCTCCCTCCAAAACAAA[C/T]GAACAAAATAAAGAAGAAATAAAGTGCCCAGGTTTA ATTTTTTCC
stSG2850	88	G A	---	ATGGGTGCATTGTAAAAGGCAAATTAAATACTTTTCAGGCAGGGCGTGGCAAATTAATGAGCTGA TGTGTCCCAAGGGAGACGGCCG[G/A]GGCTCACACACATCCCATCAAATACTCCTCCCAT
stSG3031	71	T C	---	ATACTCACGGGGCTGAAGGCAATGTGAAGGAGTGACTGCAAGTCCTGGCCATTTCTGTGGTGTCAGC AAA[T/C]CGCCCCTTTATTTAAATGATTCCAGACATCTGGGCAGCATAGCT
stSG3058	81	G A	---	GTCCCAACTCCTCTCCTCTTAGAGAAAAACTGTGATTACCTCAACTTGAATATGAAACTGTGATTG AAAAAGTCAAAAC[G/A]TGAAGAAGCATCAAAGGCAAAACTGGCTGAGGC
stSG3092	94	T G	---	CAGCATCTTCCAGAACATTCCTAGAACTGAACCATTCTTGTCACTATTGAAAAACAAAGCCAAGTTC CAAATCCAAAATAATAAATGAACGTGC[T/G]GATAAACATTCTTCTTATGGTTCCAGCCCTACTTT AGTT
stSG3230	95	A G	---	AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTTAGTCAATTGTCAGTGGAGTC[A/G]GTGGGGTGCTAAGTGTTCTGAACTGAAGTAG
stSG3245	160	G C	---	ACATCTCATACCCAGTAAGATGCAAGAAAGAAATATCTGAGAGCAGCCCTGCTCCAGGGGCCC CAGGTATGTGTAGAGGCCCAGTGGGGTGGCCCACTGGTGTTCTACCACCCCTGCCATCCAGTCTG GCCCCAGTACCTACCTGGGGAGGTTG[G/C]TTGTACTTGGCTTAAGTACTTCATGCTTTAT

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stSG3265	42	T	C	---	AGGTGAAAATGAGTTACTAAATGTAGCATTATTATTATAAGGAAT[T/C]GCATTGTGAATAGTTTCTCAG TTTTCATTATGGAAAGATGATGATTCAGCCCACATTCAGTGTATGTTTCTAAATAACACAATCGAC AGGACTGTCTGTTCAGCTGAATTCTTGGGCTTTATGTGGCAGTGTGGTAAAAA
stSG3269 b	141	C	T	---	TGTACTTACTGTGTCATCCTATCCATTCCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGGACT AGTGAAGGGAGGAGGAGTCCTCCCAAAGTACCCTTTAAGCTTGATAATTAGCTCCATAGCCCATGCT GCATGA[C/T]TGTAGATCCCCAAGTCCCTGACACATTTTCTTCTAAGAAACT
stSG3269 a	24	A	G	---	TGTACTTACTGTGTCATCCTATCC[A/G]TTCCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGGACT AGGAGTGAAGGGAGGAGGAGTCCTCCCAAAGTCCCTGACACATTTTCTTCTAAGAAACT AAAGCATGACTGTAGATCCCCAAGTCCCTGACACATTTTCTTCTAAGAAACT
stSG3284	130	C	T	---	TTAACTCAAGAACTTTCAGTTACAGGAAGAGATTTATCTAATATTAAAATGACTAAATTACAAAAAGC ATAAAAATGTTTGAAGCCATTTTAAAGTTGTTTGAAATCCATATTAGCACTCAGACTTCCCCA[C/T] TCCCTAACTTTTGTTAATTGCTGTAATGGGACATTTGTTGTTTGATCTACCC
stSG3292	99	A	T	---	GTCTCAAGTGAAATCTGTAAATACATTTTAAGTCTGACTTCAAATCGGTACATGAGGCTTAGACATA CACATCATTGGACAAGTGACTTAAATATCTAA[A/T]TACAAATCAAATAGCATTTCCTAACTTTCAA
stSG3323	26	C	A	---	TAAATGTCATATCTTAGCTCTCACT[C/A]CCAGTGTATCCATTTTCCCCAGCCGTAGAGCTTTTCTG TTTCTGTAGATTGCCTGTCCTGGACATTTGATATAAATGGAGTTGCTATCATGTTCGACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATCATCCATGCTTCATTCCTTTTTAA
stSG3369	69	C	T	---	GATCCCCAGTAGTATTATTTTCTAAATTGAAACTTGTTTGTGGAAATAAAAATCTGAGGACCACTCAGAG GG[C/T]ATAAGGGAACCCTCTTTGTCTTTGTTGTTCATTAGGACTTTCT
stSG3398	125	G	T	---	CAAGACTGTAAGAAACGTAGGCCTTGTGAGAGTGAAGGAAGGATGCTCGAACTTGCCCAGGACTCAGG CTTCAGCTTCACAACTCCCGAGGAAAGGAAATGACACATTTCCAAACTGTCCACCTTTGTAGC[G/T]CTGGGT CAAAGTCTAAAGAGAGGACAAATAAATAGAGACT
stSG3416 a	43	A	G	---	TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG[A/G]CTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTTCCACCTCAGCCAACTGAGTAGCTGGCCTGCAGGACAAGTCACCATGCCTA CCTAAGTTTTTGTAGAGACAG
stSG3424	173	T	A	---	GTAAAGACAAGGTTTTGCTATGTTGACCAGGCTGGTCTTGAACTCCTTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTGCTGGGATTACAGGTGTGAGCCACTGCGCCCGGCGACTTTTAAACTGAAT GTTGAAAATCATTCTGCTCTTTGCTGGGTAACACTGA[T/A]CAAGTTGCTTAACCTTTGTGAAACCAC TTTCCTTATCTGTAACAAAATGGACAAAACAGAACTTTTTCCTTTTCCTCTC
stSG3436	88	T	A	---	GTTCATGTTAAAGATTAGGAAGAGCTGTGATGTGAGGGGTCAGGTGATGTGATGGAGGCCTCACAGA ATGAGTGGCAGAGAGGGCCCC[T/A]GAAATAGCTTACTCTGTTTCCTATC

stSG3463	103	C T	---	GATACAGAAGATAGTGTTGGTATGGATGGATAGTAGTATGAAGGACAAATAATACAAATATATTTATTG AAATAAACAAAAATGCATACACAGCTCAATGGGTCAC[C/T]TGGAACAAACTTGCTTGACTATATTA CTGA
stSG3491 b	71	G A	---	CAAGATACTTCATTGTCTCTAAGTAGTGCAGTGCTGGCAAATATTTCTCACGAACAAGGACGATTTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTAGCAGTCTGA ACAATCTTCTAATCTTTTACTGGCACCTGTGGATTTCTATTAAACTCATTTATACTATTTTCTGTGATG ACAGAAAATAAGTTAAC
stSG3523	33	C T	---	TAGCCATCTTACTCTAGTTCTTTTGGGTTTTA[C/T]GCATATATGTGTGTACAAACACACACACACC CCTAATTCCTCAAATGCTCTTGGCATAAGTTTTATCTCTTACTGGTCTC
stSG3536	213	A G	---	AGTACAAACACAGATTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTAGCCTACACACAGCTGCTACAAAAACCAAAATACAGAATGGCTTC TGTGATACTGGCCTTGCTGAAACGCATCTCACTGTCATCTTATTGTTATATTGTTAAAATGAGCTTG TGCACCATTAG[A/G]TCCTGCTGGGTGTTCTCAGTCCTTGCCATGAAGTATG
stSG3583	112	G A	---	GAAAAAGCTTAACATACGATCCATGTGCAAACCCAAAACAGGATCTACGAACTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586 a	60	G C	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAAATCAGGTGTGGTGGTG[G/C]ACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACTCCAGCTTGAGACTGTTTCAAAAA
stSG3589	101	T C	---	ATATAGTGCTGGTAGCATTATAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAGGCAAAAAAGT GTATATACCACCCTGGCACACAAAAAACCCCAATGA[T/C]CCTATTTCCAAGAATGTATCCAGATGAAA GTATCCAACAACAAAAGCTATATACAC
stSG3590 a	70	A T	---	GAGAGATGAGCTATTTATTCTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTTCTAAAAAAAA AAA[A/T]TTTCTCTGATGTCTCTTGACCCTGTAGGAAGAAACACATTCAGTTTCTACACT
stSG3619	78	A C	---	CAGTGAGACTTCTCATTTTATAGCAAATACATTTTGCAGCTTAAATTTTCTTGAATTCATATACGCT TCTGTCATTT[A/C]AACAAACTTCCAGAGAAAACTGGGCTCTATATTTAAG
stSG3644	40	T C	---	ACATATGTAACTGCCATTAGTAGCCATATTAGGATGAGA[T/C]GGATTGAGAGAGGCATGAACCAAGG ATGCGTAATAATCATTATGAAATAATAAGTTATCTGGGGAAACGGCCATTTGTCCAACATTTACTAA GTGCCTACTA
stSG3646 c	70	G A	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAATATGTCTTACT GGT[G/A]ATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55	A	G	:::	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAAGAATATATGATGATAACAATA[A/G]TATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTCTCCATTGTAGAGTCATT CTTCTCTTGTA
stSG3646 a	43	A	T	:::	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG[A/T]TGATAACAATAATATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTCTCCATTGTAGAGTCATT CTTCTCTTGTA
stSG3693 b	85	A	C	:::	ATTGTTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAACCCTGGACTCACCT GAAATATCCTACGAGGC[A/C]TCGCCCTCCGAGACTGACGATTATTAACCACCCACACGGAAAAAGG
stSG3693 a	30	C	T	:::	ATTGTTTCCCTGAACATTCCCGTGGTCTCC[C/T]TCTGAAAGCCGATGACCATCCAACCCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAACCACCCACACGGAAAAAGG
stSG3698 b	145	G	A	:::	TCTTGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCAATCCCCAGGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]AGAATACCACCACCTTCCCTCACTGCAGA
stSG3698 a	51	C	G	:::	TCTTGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCAATCCCCAGGGTTG[C/G]TCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGAATACCACCACCTTCCCTCACTGCAGA
stSG3724	107	C	T	:::	ACCAGCCTCATGTGCAGAGGGTCTCCTGCTGGATCCCCAACTGGAGCCATCCCTGGGCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGCTCAGTGTCTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104	G	A	:::	GCCAAAACAAAAGATCTTTGGGAGTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAATATATTATTACCAGCCAACAGCAAACAGCCC[G/A]AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAAATAACGGCACATTTA
stSG3751	128	G	A	:::	CGGAAGAAGAAACACAAATCCACAGGAACAATCTATGGTTCATACCTTTTTAGAAAGATGATTTTG AGGGCTTCAGTGTATTTAAAGGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGGTCCC[G/A]TT GCTGACTCCATGTGTTGCAAGAG
stSG3787	49	T	A	:::	TTCTGTGCAAAGAATCCACATCATTGTTTGGTAGCAGAGAGGATCTCTTA[T/A]AAAGTTCCCTAAGA CACTGAGGGCATAAAACCAAACAAAATAAAATAAAGGAGTGATAGGCTAAAGCAGTATCTTCCCCT
stSG3880 b	115	G	C	:::	GACAAGAGGGAAGAGAGATGCGCCAGAGACCAGGGCTGGGCGGCTCCTGAGTGCCAGGCGC CACCACACGTCCTGTGGGTCAAGGCCCCTCCTCGTGGGAGGCAGGTCTA[G/C]GGCCACGGAGGATGCAG GGCTGGGAGGGGACCCCACCCTCGGGGGACCCAAAAGGAGTCCATTCTGCCCT

stSG3880 a	36	G C	---	GACAAGAGGGAAGAGAGATGCGCCAGAGACCAGGGCTG[G/C]GGCAGCTGGGGGTCCTGAGTGCCAGG CGCCACCACACGTCCTGTGGGTCAAGGCCCTCCTCTGGGGAGCAGCAGTGTCTAGGCAGCAGGGATGCAG GGCTGGGAGGGGGACCCCACCTCGGGGACCCAAAAGGAGTCCATTTCTGCCT
stSG3895	44	A G	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTTAGTGTT[A/G]TTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTTATCACCATGGAACAAGATGCTGATTCGTCAACTG AAAAT
stSG3902	104	T C	---	TCTGTTGAGACTGGAGAGAGACCAGGTACCAAGCACCGACTCTGGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTCACCTCAAATGTGAACTGCTTTCTTTC[T/C]TCAGCTCAATAGCTTAACATCTAATTC ATGTTTGCTCCCTTGCTGGACAAT
stSG3935	50	G A	---	GGGTGTCTGACGGACAGGCCACACCCAGCAGTTCAACAAGCAATTTGTCC[G/A]CTAGTGTGCAGGC TCCTCCCCAGTTCCCACAGGCTGAGTACTATGGGGTCACAACCTTCCTGGACGT
stSG40	25	A G	---	GAGGAAGAGGTTGAAGAAGTGCTGA[A/G]AAATATATTAAGATTTCCTTGGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTTAGAATAAGGAACAAAATAAACCCTTGTGTATGTATCA CCCAA
stSG4009	32	A G	---	GTGTGGGCTGTCTGATGATGAATGGCGCGCCTC[A/G]TACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATTCTCTGATGGGCTTTAAGGGCTGAACCATATCTGAAGGTTTTCCCACACTGCTTACA
stSG4033	123	T C	---	AGAAGCCCTTGGGGACAATGGCAGTGCCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTAACCAAAGAACCTAATGTTTTCAAGCATAAAGGTACTTT[T/C]TGTGAAC AGGTGGGCAACAC
stSG4038 a	29	G A	---	GCTGAGAGCACGTGTACAGCCCACGCCTGT[G/A]CGCAGGCCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCCTCACTCAGTCAGGGCTCAGGCTCCCGGAGAGCACCTGAGGGTTCCATCACT
stSG406	53	T C	---	ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAAACGAACAAAA[T/C]GGTTTTAGTT TTGCTGAAGACTGGCCTTATTAATGGACAGCCTTTCCTAACAAGAGATTATTAACTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55	G T	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGCTAGATGTATTAG[G/T]ATAAAAAA GTTGCTTCTGTGTAATACTTTAAAGCTTGCTTATCTGTAAACCTATGTGTCTTGAGAATCAAG CCTTTGGACTAACCCCAGGGCATTGCCCTTCATCCTGG
stSG4095 a	27	A C	---	ATCTGGGCTGAATTAGTCAAGCAGGTC[A/C]GATACTATTGTCTGCTAGATGTATTAGGATAAAAAA GTTTGCTTCTGTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTTGAGAATCAAG CCTTTGGACTAACCCCAGGGCATTGCCCTTCATCCTGG
stSG4120	65	G A	---	TGCATGTTCCACATCTTTCATAACAGCAAAATGTATAATAAAACTTACGTACTTATGGATAATCAC[G/ A]CTTTTCCCCTCAGAGCCCACAGTTAAACACGTTCCAGCACCATTAATCCACCGAGCT

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stSG4128	54	A	G	...	CTTGGCAGATAAGGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTTCTA[A/G]TATATTATTT TACTTCTTCTGAAAATGCCACATAATTTGCAATAAATGATTCACTCCTTAGCTCCAAAAGCAAGTCC TTTATCAAAATGCAAATGTTCCAGAGGG
stSG4209 b	128	G	A	...	CACGAAACAGATGCAGCCTACACAGTGCTGTAGGACGGCTCACAAACATCCACATGGCACAAGC AGGGGCCGGCCACTCCAGCAAACGAAGCAGCCACCCCCGAACCTTGCAGAGGCCGCACTCCCTC[G/A]GC AGGGGGGACCACGAGGCGACAGGTGCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65	G	A	...	CACGAAACAGATGCAGCCTACACAGTGCTGTAGGACGGCTCACAAACATCCACATGGCACAA[G /A]CAGGGGCCGGCCACTCCAGGCAAACGAAGCAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTCGGC AGGGGGGACCACGAGGCGACAGGTGCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31	G	A	...	CATTACCCAGAACGCCCATGGAGGACCAGAGC[G/A]CCACGGCCGCGGGACTCCCGCGATGGCTGGGGGG GCTATGGCCTCTGACAAGAGGGATGAGCGGAGGGAGGGTGCCTGCCTCCTCCCCCCCAGGGGGGCAGAGACGTGAC TGGGGGGACCATGCGCCGAAGAGAGGATGACCGGTCATG
stSG4301	81	T	G	...	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGAGGGTAGTGGCTCCCACACTTTCCAT TTAAGCAAATAAAT[T/G]AGCTTCTGAGTAGTTGTTCCCAGTTCACCCAACATTTG
stSG4331 b	71	T	G	...	CTCACAAAGGCCAACACAGAAAAAGATACAAATACATTCATCCAGCTAATATTTAGTTTTATGACAC AGAG[T/G]TTTCAAACAAGTTAAGTGTCACCTGAAGAGCATGTTAAAAGTTAAGTTATCACTT GGAGAGCAGATTTCTTGGCCTCGCCCTTGTGATTCTGTTCTGTTTGAGGGGTGTGC
stSG4340	76	G	A	...	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/A]TAAGTGGGAGATAAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109	A	C	...	TTCCCAACCATTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGGCAC AAGTTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGC[A/C]CCTTCACAACTAGAAACGACTC AGCGACTTTTTCTGTGAGCAAATGTCGAGG
stSG4361 a	24	T	C	...	TTCCCAACCATTGAGTGACAGAGC[T/C]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGG CACAAGTTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGCACCTTCACAACTAGAAACGACTC AGCGACTTTTTCTGTGAGCAAATGTCGAGG
stSG4376	73	A	G	...	TTTCACTGCTACTGGTTCGGTGTCTGAGTCCTCAAACTCTGCTTTGCAAGTGCTTCTCCAAGGGGAG AACAG[A/G]CTGGAACTGCGGCTCTGCGAGAGAAATGACAACATACGATTTCTT[T/C]TCAGTCTTGTAGT ATCCACAGTAGTGATGTCTGTCCATGTACAAGTGTCTGTCCAGAACACCCATTAAATTCCATGCC
stSG4381	50	T	C	...	GAAGGCCACAAAACACTCCATAGCCAGAGAATGACAACATACGATT...
stSG4410	79	A	G	...	ACCAATGGTTCTGCTATGTGCATCCGATATTTTTGCCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAAACACCGC[A/G]TGACAACGAACCCAGTGACTGTGAAACTCAGGCTGCAGGAGGTGGCTTGT CAGCTGGGT

Name	Position	Alleles		Sequence
stSG443	65	C/T	---	AGCAGATCAGTCAGCCCACTTGTCTCTCTCTCTCTTTAGGGAGAGAGGCTAGGCAGTGAACACATCA[C/T]GTATGCAATGAGAAAATAACCAACTGGTAGGATGGGGAGGGGAGGGGAGGGGAGGGGAGGCAGGGAATAGGCAC AAATGGAATTCTATCCTGGCTGTCGTCCTTCTCTCTCAGGTC
stSG4430 a	54	A/G	---	ATGCACATTAAATGAATGGCCTAACTACTGGGAACTTTAGTAGTTCTATAAGGT[A/G]ATTAACATA GGTTAGGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATGAGGCATCAAGAGGGCCATTTT
stSG4448	99	G/A	---	CCTCCCTTCCCTTCCCTTCCCTTCCAGTCTTTTCCATACTGTTCCCCCTCCCGCCCCCCAGGCTCT CGCCTAGCCCCTGCCCTCTGGGGTCACTGC[G/A]TGGGGTTAGGCCCCCAAAAA
stSG4449	92	T/C	---	ATTAGCCATTCATCTTGCAACAATTGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT TAACTTTGGACAACTTAAAACTTA[T/C]TAGTGACATTGCTGTCTAATAATCAAATACTTCATCATA GGCTGAACATAATTATTAAAAGAGCAAAGTTACCCCTCCC
stSG4467	42	C/A	---	CAGACATGAGGGGATGGCCCGTCTCTCTCTGGGACAGAGCCTCA[C/A]AGATGATGTCCATGTTTTGTGT GAATGAAACTCAAACACTCTTCAGTTTTTAGAGTCATTTTCTGGTATCGAGCGACCACCACCGAGGAG CACACCCTGCTTCCAAGGCTGCTGCCTTCTGCACAGT
stSG4475	21	A/C	---	ACATGTCATTTCCTGACCAGG[A/C]TATTAAATAGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGA TTAAGAGACACAAACTGGACTTTTGTTTCTTTTACTGTAGCACCCAGGTTTCATG
stSG4477	32	A/G	---	GTAACATTCTGGGGTGGGGGTGAGACAAACA[A/G]ATGAACCAATAATTAATTACAATTATACATT TCAAGGAGACTTTTAATCTAGGTAATGTGAAACGCAGCCATCAATGGTTTGTCAGGAAAAGGGAGA TGAAGTCTTGCTCTGGGCAACGTTTGGCCTCATTGCAGTCAGACTTGGC
stSG4531	79	C/T	---	TGAACTCAGAGCTGGGTGGGGAGCTGCAGCGGAGCTGGGGCGCGGCGGCCGGGGA CAGCGAGCCGTCG[C/T]GCCACGTCCTGGCGTTGGTAGAGAGGACATAGGCTGCCTTGGACTCGATCT GATTCTCATTGACAGGGGAGACGCGTGTTGTCATCAA
stSG4550 b	86	G/A	---	TGCATTAAGGAATGATACGGCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT AAAAGAGACAGTGGGCACC[G/A]CAATTGGAGGGGAAGGGGAGGCAGGGTTTTAGAGAAC
stSG4550 a	85	C/G	---	TGCATTAAGGAATGATACGGCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT AAAAGAGACAGTGGGCCAC[C/G]CAATTGGAGGGGAAGGCGGGGGAACAGGGTTTTAGAGAAC
stSG4590	47	A/G	---	AATCAGGCACAAGCTCGGGAGAGGAGAAGCCAACAAAAGCTCTCTGCAC[A/G]ATGGGAGGGGAGGAGACAC CATTGAAAAAGGCATCGTTCCTTCCTTCCATGCCAAGCGAGGCCTGGCTCCCACAGGCATGGTCTCCTTG
stSG4623	22	T/C	---	AATCTGTATCACCCAGCCGCTGG[T/C]CAATGTACTAGTAGCTTTCCACAGGGATTTTTTATACTATTC CTATAAGGTTTTATCATGAATAAAAAAGCTCACAACTCTTTCAGCCATTGCAGATTCACATTTATCT TAATATTCCTGTTCAAGATGCTCTGGAG
stSG4843	102	A/C	---	TAAAAAAAAACAACCCCCCAAAAAAAACACCCAGAAGTTTTGAGTTTTATGTTTTCAGATTTAAAG GTATTTCTTCTTTAGCTTCTAAATTTTGAGTCAT[A/C]ATCAGAAGAGTCTTCCCTACTCCAAGGTGA GAAAGGA

Marker	Pos				Sequence
stSG4850 a	38	C	T	---	GGAATCTAAACTGGGAATGGCCGAGGAGGAGAGGGGCTC[C/T]GTGCACTTGCAGGCCACGTCAGGAG AGCCAGCGGTGCCTGTCGGGGGAGGTTTCCAAGGTGCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTCCC
stSG4879	86	A	G	---	AACTCTGAAGGGGGTGACCTCAACCCAGCACCCTTGTTTCTGTGAGGTCCTGCTTTTGCAGAATGGCCTG CCCCTGGGGACTGGAGCAG[A/G]CTTGGGTGAGCTCTAGGTGGGAGGGGTGGTGGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104	G	A	---	ACTGGACTGGCTCGCTTGCTGAGCGGCGTGAGCGGCCGTGCGGCTGACCACCTCGCCTCTTCCAG AGACTCGCCCGCCGGTGACCACGACTACGCTCTGCC[G/A]GTGGGAAAGCAGAAGCAGGACC
stSG4896	112	C	T	---	AAACAAATCAAACCCAATCCCAGCAGTCTATGTACAGGGCCACTCCCTCGCCTCTCTGCCATAGAGA GGTTGGGGGCAGTGAGGAGTGGTGGGGGCTGGCCACCTTTCT[C/T]CAGCCACCAGGCCCCCTGAGG AATTAATTGACTG
stSG4932	22	G	A	---	ACAGTGCCGATGGTTACACAAT[G/A]TTGTAAATGTATTTAATCCCACTTACGAATGATTAAAATGA TAAATCTTATGTTTATTTCATCACTACCAAAAGGCTGTGGGTGCAGGGGTGCTGGTTTCTGGTCCT
stSG4950	24	A	G	---	TCATGACTCCCAGGAAAAGGTCCT[A/G]TCTTAGCTTCCTCCTCCCTACTTCCTCCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136	G	A	---	AGATACGGGCAAAACACTGGGATGGCCTTCCTGACAACTTAAGAGGTCTCCGAGTTATATTCTGGGTT GGGAAACAACTGACCCAGCCCTTATTCCTTCAAGGACTACTCAGTCATTGGCAAGGAGGATTCATGAGCC CC[G/A]GTGACACAGATGGGGGCCCTGCTCTATATTCAAC
stSG4961	91	C	T	---	GAAGGTGCTCTGAGGAGGTGTGACTCTCCCGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAAGGAAAAGTA[C/T]AGAGAGGGCATTCAGGCCAAGTCAGCAACACAGACAA
stSG4967	72	A	G	---	ACTGGTGCCTCTCAGCAGATTCAGGGGTCGTGCAGGGCTGGTTACCACAAACTCAGTAGGAGTGCAA GGGCCT[A/G]TACCCCCGGAGCTAGACACGCCTGGGTTTGAATCTCAACTTCTCCCCTTTTCTTGCTGTGC AACCTTG
stSG4997	22	T	C	---	CAAAGGAGGAGTAGGAGCCCCAA[T/C]TTTTAATGGTTTCCTCTCCCCCTCATGCTATTTGATCCAAAAA CTATATACAATTTTGTAGCAGTCTCTGTGTATAGTTATTACACATGTTTAGAAGGGAGGGGAGGCAAGAA GGGGATAGGGGAGAATGGTGATCCAAAT
stSG6312	37	C	T	---	ACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA[C/T]TATGCCATGCGGGAAATAAAATGCTT ATCCAGTGGAGCGGCTCCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107	G	A	---	GCTCTGGTCAAGCAAATTCTCCAGGACAGAAGCAACAAGGACAGTAAACACACATGTATGACCCTTA CAAGTGCTTTAAGATTTTAAAAAATGTGATGTTTGTCCAC[G/A]ATAGTTCAGGCAATTAAGAATAT GCAAACCAGAGAATTTCTGTGAAAAACATTTGCTCTTTGGCCTGGTGGTGGACAGAAAGGGTGGCCAA ATGGATTGAGTGATGAGCAGACATG

ID	Pos				Sequence
stSG6362	88	G	C	---	TGTGAAATGTACACTCAGGTCTAACAAATACCTATTATTTCTCTGGTTAAGAAGGTTTAGCAGGAGCCTCCAATGAGCACTGTATGTA[G/C]AGAAAAGGGAGGAGGAGCAGGAGGAGGAACAGAGATCTGCACAGAAT
stSG8010	62	G	T	---	CACATCTGTGTTTCTGGAGCAAAGGGAAACCACAGAAGGCCAGGAGTTGGGTGTGCACTGG[G/T]TGTCTTTCAAACTGGGTGGAACCAAACTGAGTCCTTGAAGTCTCGCTCCTGAGGCTGCAGAAGAATAGATGGCTT
stSG8022	53	G	A	---	AGCTCCTGACTCCCTGTTCAGTGACGTCATGTTGGTAGCCTGAAATGGACCAC[G/A]GTGGGAGTTATTTACACCATGGAAAACTGGAAAACTCTACAAATCAATGCGTTTATTTCTTATTTCAGAGGGCAGGTTTATCAGCACACGCTGTATCTCC
stSG8032	67	G	C	---	TGATTGTTAGGGATAAGTGGGCATTGTGTTTACAAATTACTTCCAAAGAATTCAGAAAATTGTGTGT[G/C]TGGGAGGCAGGGTAGCAAGATAAAAAGAGGGAGGACAGCTGGGGTTGGTAAAA
stSG8064 b	46	C	A	---	AGCTGGCTCTCTTCCTTCTGTGTTCGGGGAGGCTTCACGTCCTCG[C/A]CCGGTGGTCCCTGGGTGGCCTGCAGGACCAGGGGGTGGGAAACAATGCCAGGAGAATTCCTGTCACATCAAACAGGGAACA
stSG8064 a	23	G	C	---	AGCTGGCTCTCTTCCTTCTGTGCGTTG[G/C]TTCGGGGAGGCTTCACGTCCTCGCCCCGGTGGTCCCTGGGTGGCCTGCAGGACCAGGGGGTGGGAAACAATGCCAGGAGAATTCCTGTCACATCAAACAGGGAACA
stSG8072	59	A	G	---	CACCATCATCACATCGAGTAGGCCGAGTATTAGTGGCCGCAGTTCAAGCCTGTGTTCAAAAGAGGGCAGAAGGAAGTCCGAGTATTAGTGGCCGCAGTTCAAGCCTGTGTTCAAAAATACACCCACACCACCCCACTCAACCTTGTATCCAAATTCCA[A/G]AAGTGTAACTAAAGTATAAGAATATCATGACTAGTTAAAAGATAGCAAATACCATAAGGTACAAGTCAAGTTCAAGTATATAACAAGTATCTGAGTAACAAATGTCCTTGGAAATGGG
stSG8100	40	A	G	---	AAGGCTCCTTGAAAGCATGTTTATTTGTTCCATTAACTTGTTCTCAGCTATACTGAAGTATGATTGACAAATAAAACTTGCATATTTGAGATGTACAGTGTGATGATACATGTGTATACAATGTGAAATGA[T/C]TGTCATAATCATCATTCAATAATTGGTATATTGGTTAGGAAATGTGATGGT
stSG8102	138	T	C	---	CAGTGGTTCTCAAACTCCAGCGTACACGAGGATGGTGTCTTGTGCTTGTTGTAATACACAGATGACTAGGCCCACCTGCGCGGAGTTCCTGTTGGAGTCCTGAGAATATTC[A/G]TTTCTAACAAGTTCCCAGGTGACCCTGAGGCTCTTGGACTGGGGAACATGCTTTGAG
stSG8105	110	A	G	---	GTGTGTACATCATTGGGAATGGAGGGGAATAAATGACTGGATGGTCGCTGCTGCTTTTTAAGTTTCAAATTGACATTCCAGACAAGCGGTCCTGAGCCT[T/C]GTGCCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8130 b	96	T	C	---	GTGTGTACATCATTGGGAATGGAGGGGAAATAAATGA[C/G]TGGATGGTCGCTGCTTTTCAAGTTTTCAAGTTTCAAGAGCCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8130 a	36	C	G	---	TTGTGGGACTTCAAATTCTTCCTTCAGATTTAAAATGACATTATGCATGTACATATTTTAAAATTTAGAGAACAACATTTAGAGAACAACAAATCTAAGAAATGAATGAGATGTT[T/A]CTGAAATCTGATTCAAACACTTATCTTAAAACTGACTTCTGTCATCCTCTGTCCTGTGTAAGG
stSG8145 b	124	T	A	---	

ID	Pos				Sequence
stSG8145a	97	C	T	--	TTGTGGACTTCAAATTCTTCCTTCAGATTTTAAAATGACATTATGCATGTACATATTTTAAAATTTAGACACATTTTAGAGAAGAACACAATTGTGAAA|C/T|ACAAATCTAAGAAATGAATGAGATGTTCTGAAATCTGATTCAAACACTTATCTTAAACTGACTTCTGTCAATCCTCTGTCCTGTGAAGG
stSG8150	36	A	G	--	ATTGTTCTTGCAATTGCTTGGATTTTTCAGAATAGT[A/G]ATAAAATAATAACGGAATCCTAGGCATTCGTGTTTTTCTATGTTTTTAACAGGATTTTCTCTAATGTTTCGCTATTAAATACCATGCAGGAAATTGGGAAAT
stSG8340	30	C	T	--	AGAGGATTATGGAGAGAGCTGGGCAGGATC[C/T]CAACATTATGACCCTGAACCTCCAGAACTGGATTCACTAGAAGGAGAGGAGAAAAACGGCTCATCAAAA
stSG8466	111	G	A	--	TGTGTATTGGGTGACTGTAGCCTAAGGATAAATGAAATAAATGACAGCAATGTTATAAGCAGTGGGAGGAGTGAACTGGGAATACTTGGTTACAAGGTATTTGCACTACCT[G/A]TGAAGCAGCACAGCATTATTTGAAAG
ESTD-ACE	--			--	GATCAAGCAGTGCACACGGGTCACGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATACAGTACTACCTGCCAGTACAAGGATCTGCCCGTCTCCCTGCGTCGGGGGCCAACCCCGGCTTCCATGAGGCCATTGGGGACGTGCTGCCGGCTCTCGGGGCCTCTGAACATCTGCACAAAATCGGGCCTGC
ESTD-ADA	--			--	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTCCCCAGCTCCACCCAGAGGCCCCTGGGGAATTCCAGGGTCACTGTTCCTTCCTGTCTCCCTGTGGGAATCAAGCCAGCTCCAGGCCAGAAGTGGGACTGTGAGGACATGGGAGGCCTCGGGCACTGAGCTGCAGACCCGCAGACCAACTGCTCTGAGCTTTCTGGGCCTCTGAGTCTTCCTC
ESTD-AK-168	--			--	GGGGAGTGACAGCTAGAGCACCAAGGGGGGCCTCTACAGCTGTGTTCTCATGGAGGACAGGCTTCTGCTCATTCTGG
ESTD-ALB	--			--	AATCCCAGCCACTTTAGGAGGCTGAGGCAGGCCATATCACCAGAGGTCAGGAGTTTGAGACCAGTCTGACCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTGGTGCATGCCTGTAATCCCAGCAGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCGGAGGTTGTGGTGAGCCGAGATGGCACCATTGCACTCCAGCCTGGGCAACAAGAGTAAAACTCTGTCTTC
ESTD-ANT1	--			--	TCTCCTGTCATTCCTACTCCATTAGTTCAAGGTCAAGGTGAAGAACTGGGGCAATTAACCAAGTAATTCATGGACTGCCCAACTGCGAAACAAGAAGGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTTTTTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD-APOA2	--			--	CCAGGTGTTGTGGCCACGTGCCTGTAATCCCAGCTACTCGGGGAGACTACTGAGGCATGAGAATCTTTTGAACCGGGGAGGCGGAGGTTGCAGTGAGCTGAGATGACAGAGCAAGGGCCAGTGGACACACCATGGCACAAAGCCTCACTGCCACTGCCACTGCCACTGCCACTGCCAGCCTAGGTGACAGCAAGACTCC
ESTD-ARSB	--			--	GGAAGAAAATGGAGCCTGTGTGGGAAGGAGAGGCGTCCGAGGGGGTGGGCTTTGTTGGCCAAGCCCCTTGCTGAAGCAGAAGGGCGTGAAGAACCGGGAGCTCATCCACACTCTCTGACTGGGCTGCCCAACACTCATGAAGCTGGCCAGGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTTCGACGTGGTGAAACCATCAGTGAAGGAAGCCCCATCCCCCAGAATTGACCCAAAC

ESTD-AT3a	AGACCTCAGTTCCTCTTCTGTGTAAAGGGAAGTTTGTTCTTGGATCTCCATGGGCCCAGCCAGCACTG GTGCCCTGTGTGAGTCTGTATCAGGTGATGGGACCAGGTGGAGAGGAATTTGAAAGGGCATTG GAATTCAGAGACAAAGAGACAGATATTAAGAGCTGGGGAAATGTGG
ESTD-B3AR	GGCTGCCAGGGGTTCCGTGGGAGGCGGCCCTAGCCGGGGCCCCTGCTGGCGGTGCTGGCCACC GTGGGGAGGCAACCTGCTGGTCATCGTGGCCATCGCCCGGACTCCAGACTCCAGATGACCAACGT GTTCGTGGACTTCGCTGGCCCCAGCCGACCTGGTGATGGGACCTCGGTGGTGCGCGGCCGCCACCTT GGGGC
ESTD-BA511	GGGCAACATAGTGAAACCCCATCTCTACAAAAAATTACAAAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAG TGAGCCAAGATGGTGCCACTGCA
ESTD-BCL2	AGCTGGATTATAACTCCTCTCTTCTTCTCTCGGGGGCCGTGGGGGTGGGGGCGAGCTGGGCGAGAGGTGCCGTT GGCCCCCGTTGCTTTCTCTGGAAGGATGGCGGCCACGCTGGGAGGAACAGGGTACGACAACCGGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTGTCGGCAGAGGGGCTACGAGTGGGGAGGATGTGG GCGCGCGCGCCCCGGGGGCGGCCGCCACCGGGCCATCTTCTCCTCCCA
ESTD-BCR	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCATCTGCGCAAGA GACCAAAAGAGGTCAGCTTCGTTGTCCCGGGAAAGGGAGGCAGGTGACAAGCTAACTCTGCTTCAAA ATCAACCATCCGGTGGACACTGTGTGGCGTGCCATCTGCCTGGCACA
ESTD-BRCA1a	AAGAGAGAAACTAGAAACACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAA CCAAATAAAT
ESTD-BRCA1b	ACTAAATGTAAGAGAAAAATCTGCTAGAGGGAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAA ATGGGAAATGAGAAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAATGTT TTTAAAGAAGCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD-BRCA1c	ATGCATCTCAGGTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAAATAAAGGAAGATAC TAGTTTTTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAGGCGTCCAGAAAGGAGGAG CTTAGCAGGAGTCCTAGCCCTTTCACCCCATACACATTGGCTCAGGGTTACCGAAGAGAGGGGCCAAGA AATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAGGATGAGAGCTTCCC
ESTD-C1R	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCCTCCCCTAATTTGCTCGGGAAGCACATTCATCAA
ESTD-C6	CCCAGTCAGTTTGGGGGACAGCCATGCACTGCAGCCTCGGTAGCCTTTCAACCATGCATTCCATCTAA GCTCTGCAAAAT

ESTD-C7	--	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	--	GGCAAGTTTTTATTGATAGAGAGGAAATCAAATAATGGCAATGAGGAGACATCACCTGAATGTTAG GCAGTGCCTAACTGGGGATGGCACAGACAATGGCAGTGCCAACCCATAGGGCGGATACAAAAGAC AGGCAAGGAAGGGGTAGAACCATCAAAGAGGAATAGGCTGGTGACCCAAAGCAAGGAGGACCTAG TAACATAATTGTGCTTCATTATGGTCGTTCCCGGCCTTCTCTCTCACACAC
ESTD-CB23	--	TAGAACCATCAAAGAGGAATAGGCTGGTGACCCAAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCGTTCCCGGCCTTCTCTCTCACACATACACAGAGCCCCTACCAGGACCAGACAGCT CTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTTCCAGAGGACCTGAAAAACGTGTTCCCACCCGA GGTCGCTGTGTTGTTTGAGCCATCAGAAGCAGAGATCTCCCACACCCAAAA
ESTD-CB24	--	ACCAGGACCAGAGCTCTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTTCCAGAGGACCTGAA AAACGTGTTCCCACCCGAGGTCGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCCACACCCAAAAG GCCACACTGGTATGCCTGGCCACAGGCTTCTACCCGACCACGTGGAGCTGAGCTGGTGGGTGAATGG GAAGGAGGTGCACAGTGGGGTCAGCACAGACCCGCAGCCCCTCAAGGAG
ESTD-CB25	--	GTTTTCTTCAGACTGTGGCTTCACCTCCGGTAAGTGAGTCTCTCCTTTTCTCTCTATCTTTCGCCGTC TCTGCTCTCGAACCAGGGCATGGAGAAATCCACGGGACACAGGGCGTGAGGGAGGCCAGAGCCACCTG TGCACAGGTACCTACACTGTCTGTCTTGTCAACAGAGTCTTACCAGCAGGGGTCCTGTCTGCCACC ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGTATGCCGTG
ESTD-CB27	--	TTTTCTGTTCCCTGAAGATTGAGCTCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGGGCCTGGTTGCATTTCAGGAGTTCTGCTCATCACTGACCTATCTTCTGA TTTAGGGAAAGCAGCAGCATTCCCTTGGACATCTGAAGTGACAGCCCCTCTTTCTCTCCACCCAATGCTGCT TTCTCCTGTTCATCCTGATGGAAGTCCTCAAACACCATTCCATACC
ESTD-COL2A1c	--	AGAATGTATATAGTCCTCAAACTGGCCATCTCCATTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTCCTGTCACTTTCAGGGTGTTCAAGGTGGAAAGGT GAACAGGGTCCCGCTGGTCCTCCGTCCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCTTTG GTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD-COL2A1d	--	TGAGAGAACACCTAGTCCTCCATCCTTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGCTGGGACCTGGAACACTGACTTCTTCTACTGCAGCAGACAAGACTTACCC AAGAGAGATTAATGGCAAAGATATACAATACAATTTTATTTGACCAAACACTATCATGGAACAGC ATT
ESTD-CPT2	--	GCCGCAATGCCCGGGAGTTTCTCCAATGTGTGGAGAAGGCCTTAGAAGACATGTTTGATGCCTTAGAA GGCAAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCCTTCCTCATGAAAAC TGGGAGGCCGGGCCATAGTGCTCATGCCTGTAATCCCAGCATTTGAGAGGCTGAGGCGGGTGGATCAC TTGAGGTTCAGGAGTTTGAGACCAACCTGGCCAACAT

ESTD-CTLA-4	--	ATGGCCTTGCCTTGGATTCAGCGGGCACAAGGCTCAGCTGAACCTGGCTACCAGGACCTGGCCTACCGCAC TCTCCTGTTTTTTCTTCTTCATCCCTGTCTTCTGCAAAGCAATGCACGTGGCCCAGCCTGCTGTGGT ACTGGCCAGCAGCCGAGGCATCGCCAGCTTGTGTGTGTGAGTATGCATCTCCAGGCAAAGCCAC
ESTD-CYP2D6	--	CAGGCCAGCGGTGGTCGAGGTGGTCACCATCCCGGCAGGAGAACAGGTCAGCCACCACTATGCACAGGT TCTCATCATTGGAAGCTGCTCTCAGGGTTCCCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD-D11S1873	--	AAAAAAACATTTTAAACACCTTTCAATCATATACACCATAAATTTCCATTTTCACATAAGTCAGTT TGAGCTGAGTTTTCCAATTACTTGCAATCTAAAATGTCATAACTGATTAATGCAAGTTCAACAGACA ACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTATGCCCATAT CTGCATGTC
ESTD-D17S33	--	CATCCCCAAGCCCATCCTCTTAGCCACTGGCATTTTTTGCCGCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCCAGGGGGCGCCCTACCCTTTGTAGTCCATGGGAAAGGCTCCTCTGGGGCGGGTG GGGTTGTGTGGCTATGTGGTCTTGTGTAGACGGGGGCTTTGGTTTCAGTTGCACTATTGCGTTATT GCAGATTGCTTGTCTTCTTCCCACCTGAGCGAGCCTC
ESTD-D18S8	--	TTTGAGACCACCCTGGCCAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGGGTACACCTGGCCTATCGTAATCCCAGCTACACTCGGGAGGCTGAGGCAGGAGAATTGCTTGAACCCA GGAGGCAGAGCTTGCAGTGAGCCAAGATCACCACCACTGCACTTACAGCCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD-D3S11	--	AACTGATTAGAAACCTGAAAATACATATTTTATCTGAAAAAAGTGAGTTATTGGCTCATCACATTGG AATTTTTTGCATCATCATTAAAAAAATCCAATAAAGTACACTGTAATAAAGAATTCAACAGAATATCATTGT TTATTCAAACTATTTATCACTTATTTATTGGTAAGCCATACTAAATTCTAAAGCATGTTTCTGAAAG TTTA
ESTD-D3S12	--	AGGTTCCACATTATTGCTGATGTTTGCTGATGTTTCCAGGAGCCTTGATGTCATTCTGTATCTCCTCAG GTATCCCACCTTGAGACGTACTTTTCAAAAACTCTCTACAGCCGTTGTGTTGTTATTAATTCAAGGTTGA ACATAAAGTA
ESTD-D3S2	--	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCCTGC TGAGTCTTATTCAAAAACTGACACGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCC AGAAGTGAAACATACTGCTCCTAGAAGCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGDATGG CAGGTATGAAATATAATAATCTGTCCTTTATTTGGAAGGATGCCGGTATGT
ESTD-D4S338	--	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCTATATATGGCAGGTATATGAAATGTATTT CTTAAACAATAAACTTGAAAGTCCAAAATTACTCCTTGATCCATGGACTGCAGAATAAATGTTATTT TAGCTGTCGAGAAAACAATACTAATCTTGCATATGTTCATCAGAGCCCTTGGGTGACCAGGTGTATT GCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTTCAATGCAGTAG
ESTD-D4S95	--	CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAATTTTGAGAAGAGCAAAACAACTTTCAAGG ATAATGGGGCAATCACTCACTTTCTTTCTTCTTTTAGAGTCTACCGG

ESTD-D7S399	::	::	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCCTTCACAAACATTTTCATCCATGGACTCCATACTAG AATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DM	::	::	GTGGGGACACCGAGGGCTCCAGGCTGGGCGGCTGCACGTGTGGCTCAAGCAGCTGCTCGGCCTCCACT TCCATGGGTGTGGGGGCCTGGGACCTCACTGTGTCCTGGGGAGGAGGAGGAGGTGGGGAGGGGAGGACA GAATGCTGATTATCTGGTGGAGAACCAGAACTTCTGGCCTGTGGGTAGGGGCAGCTGCTTCCAAGACC TCCTGATTTGAGGAAGGGGAGCAGCAGCAGGAGAGCGAAGAGAACAGAGT
ESTD-DRD1	::	::	TCCCCAGCCCTATCGGTCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACCCATCAC ACAAAACGGTCAGCACCCAACCTGAACTCGCAGATGAATCCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAAGAAACTAAGGTAC
ESTD-DRD2	::	::	TCTGCCTTTGGTGCAGGAGGCTGCCCGGGGAGCCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCCACCCGAGAGGAGGACCCGGTACAGCGCCCATCCCACCCGCACCCAGCTGACTCTCCCCGGACCCG TCCCACCACGGTCTCCACAGCACTCCCGACAGCCCCGCCAAACCAGAGAAGAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAAGACCCATGCCCAATG
ESTD-DRD3	::	::	AAGACGATGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTGTGGGGGGCCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTCAGGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCCAGAGGAGGTGCGTGATGCCAAGGGGCTTCCTGTGTGAGGAGA
ESTD-ERBB2	::	::	TCTTTCAGGATCCGCATCTGCGCCCTGGTTGGGCATCGCTCCGCCTAGGTGTCAGCGGCTCCACCAGCTGG GGTGAGGGGGTGGTGGGCTCAGTGCCGGGGCCGGTGCAGACCCCCACGCGCGGGGCTGGGAGGACTTCACCC CGCCCTCACCTCCGTTTCCTGCGCAGTCTCCGCATCGTGTACT
ESTD-ETS2	::	::	ACTCACAGTGCTTTTAAGTGAAAATGGTCGAGAAAGAGGCACCAGGAAAGCCGTCCTGGCGCCTGGCA GTCCGTGGGGACGGGGATGGTTCTGGCTGTTTGAGATTCTCAAAGGAGGAGGAGCCGAGCCATGTCGTGGACACACAC AGACTATTTTAGATTTCTTTTGCCTTTGCAACCAGAACAGCAAATGCAAAAACTCTTTGAGAGG GTAGGAGGGGTGGGAAGGAAACAACCATGTCATTTCAGAAGTTAGTTTG
ESTD-F2	::	::	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCAACTGTGCATGCACGCTTAACCTCT GCACCAAATGGCCTCCAAGGCCCGTAGGGGAACTGGGGGATGGGGTGAGGAATGGCCC AGCCCAGTCCCGGCCGGTGCCTGGGTCCCAACAGAGGAGGCCCGTGGAGGAGGAGGAGGATGGGGC TGGATGAG
ESTD-F9	::	::	AGATCCTGATGATTTTTTCCTATTTTTTCTAAATGTTTTACAGTTTGAAGTTTTAGATTTATGCCCA TGCTCCATTTTGAGTTAATATTTGTGTAAAGTATGATGTTTAAGTCAAAACTTCATTTTTTTCCATA GGTATGTCCAATTTATCCAGCACAATTTGTTAAAACAAAAAC

Label		Sequence
ESTD-GCDH	::	CGCAGACCGGTCAGTGTGGGGTCGGGAGTGTGGAGGGAGGAGGAAGGAGGGAGGAACTGGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCGGCACCGTGGTTGTTCTGCTCGCTGCCCCTGTTCAGCTGTCTGTCCGCAGTCGA GTGTAAGGGGACCTCTGGTCGGCACCGTGGTGTTCTGCTGCTGCCCCTGTTCAGCTGTCTGTCCGCAGTCGA CTCTGTCCCGGAAATTCCGAGAGCT
ESTD-GCK	::	GTTTTATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGCTCACCATGAC AACCACAGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAATCCCCCACCCCACCCTGGCTGG AGCAGGAAATGCCGAGCGGCGCGCCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAAGCTGTCCCCAGGTCACAG
ESTD-GNAT2	::	GACCCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCACAGGCATCATTG AAACCAAGTTTTCCGTCAAAGACTTGAATTTCAGGTAAGTGCATGGTTCCCTAGG
ESTD-GPPK2L	::	AGTCTTCATCTGCGGGTGTCCAGGTAGATCCCTTTCACCGCGCGAGAACTGCTCGATATC
ESTD-HRAS	::	CTGGGCTCGCCCCGCAGCAGCTGCTGCGACCTGCGCGCGGCGCCAGGCTCACCTCTCTATAGTGGGGGTCG TATTCGGTCCACAAAATGCATCTGGATCAGCT
ESTD-HSD3B1	::	TTGGAAAGTTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCCTGGGCCCACATTCTGGCCTTG AGGGCCCTGCAGGACCCCCAAGAGAGGCCCCAAGCATCCGAGGACAGTTCTACTACTATATCTCAGATGACA CGCCTCACCAAAGCTATGATAACCTTAATTACACCCTGAGCAAAGAGTTCGGCCTCCGGCTTGATTCC AGATGGAGCTTTCCTTTATCCCTGATGTATTGGATTGGCTTCCTGCTG
ESTD-HT2	::	GGGCTAAAATTTCCGAGCAACTTTGCATAGACTGTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGGAGGAAGAGATGTGTTACAGTTTGTCAGAGAGAATAAAAGGATAAACCTGGGGTTTTCTGTGC TTTGCTTCTTCTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTTCAAAGAAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAAACAAGACACACCTT
ESTD-HT4	::	ACCAAACGAGAGCGCGGATACAGACACTCTTAAGTTTTGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTTGGGTGTGCCTTCTATCGGCAAGAATGCGTACTTATTTGAATAGTAGAGGTAA ACCACACGCCCCAAGAGTCACTGAGACTGGCAGGTTCTGCAGCAGGCGGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGGCGCCGAAGACATGCAGATGTGC
ESTD-HT5	::	AACACACAAGCCCCAGCGGAGAATTGAACTCGCGACCCCTGGTTTACAAGACACCAGTGCTCTAACCCCT GAGCTATGGAGCCCTCGTCTGCGTGTTGGTTTTTCTTCCTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTTAGCTTGAGTAAAATTCCAGGATATTCTCCTACAAAATGAAA ACATTTTCGTCGCTCGTGTAAATCCCTGAAAAGGTTCT
ESTD-IGFBP1	::	ACCCAGTGGAGCCCCGCTCATTGCACGGTCTTGGCAGGAGGGTGCCCTGGGAGGAGAAGGAAGAGATGTTC CAGGGCCACACATAGCTTAGTTGGGAGACTC

Label	Sequence
ESTD-IGHV4-6	TTTACTATTTCAATGGATACAGAATTGTGGGAGTCACTATATTCCTATGAACAAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCTACATTGTTGTGTGTGAGTGACGGGCAGTGGTGGATCCGAGAGTGTGGTGGG TGCACGGACAATAATGATTCAGAAAGCAATATGGAAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAAATACTTCACAAAATACTCACAAAATAAAACCCA
ESTD-IL1A	CAAAGTAAGCACCCAATAAATGTTAGCTATTACTACTATCATTATTATTTATTTTATTTTTTG AGATGGAGTCTGGCTCTGTCGTCCACCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CCTCCTGGGTTCATGCCAATCTCCTGCCCTCAGCCTCCCGAGTAGCTGGGAATACAGGCACCCGCCACT GTTCCCGGCTAATTTTTGTATTTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	CCACTTACAGATGGGATAAATGGGTACAATGAAAGGGCCAATAGCCCTCCCGTCTCTGTATTGAGGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCCTCAGGAGCTCTGTCTGTCAATTGCAGG
ESTD-KRT10	CCAAAGTTAAATAGTAGTATTGGAGTTATCTGAGAAATTTCCATGTGTCAGTGTTACCTTTTTGGCAATATT AAAGGAAGAAAAATGCATTTTAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAAATATTGCCATTACACTACAACTAACTATGTAGCTGCTTTTTAAATAGTCTC TGCCCAGATACATCTCCCCTATATAAGTTATAAACCAGTATTGATA
ESTD-KRT8	ACCCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
ESTD-LF79	GGGGTGATTTTGAGGCTCAGTTAATATTTCAAATTGTAACCGTAGCAAAACTGCATTGGTATTTAGA AAAATAAAAAATTTCCAATATGTAGTGCTGTTGTTTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCAGGAGGGCCTTCCCTTACCACCCAGA
ESTD-LMP2	TACACACTTTCCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCCAAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	TGTCAGTGTCCCCTAGGGGCACCTCACCACTCCAGCTTCTTCAGCTCTGCCTGCCTCTGCTGCCTGCA AGGGTTTGCTTAATTCTCAATTCAATGTCTCTTCATCTTTAGCAGCTGTGGGGTTTTGTTGTTGTTC TTCTGTTTTTGCTTAGTAGTATCTGACTACTTTTAATTATAAAAAGAGATGTATCTAAACAAAATAGAG ATTGTTATCAGAAGTTCACAACATTTATTAAAATTTTTCACCTG
ESTD-MCC	TTGTCAGGAGTGTGTGATGCTGCCTCCCCCAGCTCTGTCCCTAGCCGAACTTCAGGACAACGTGCAG
ESTD-METH	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAAACAGCATGCATCCCGAA TCTCAGGAAGTCTCTGTCTTTCCAAGGGTTTGGTCTAAGTTGCTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTCTAGAGCATCTGGTTCCTGTGTTTTTAGCATGG
ESTD-NF1	ATTATCCAGATGAATTTACAAAACTATACCAGATCCCACAGACTGATATGGCTGGT

ESTD-RDS	⋮	CCCGAGGAATCTGAGAGCGAGAGCGAGGGCTGGCTGCTGGAGAGAGCGTGCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAAGCTGGGCAAGGGCCAAGGGCAAGCCGAGGCGCGAGACGCAGG CCAGGCCCCAGAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCCTCCCGAAACACTGAGAAATAGTGCACT CCAAGAAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD-RYR1	⋮	CTTCGTGACGGGAGGTCACGTCCTCCGCCTCTTTCATGGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTGATGACCAGCGCAGACTTGTCTACTATGAGAGGGAGCTGTGTGCACTCATGCCCGC TCCCTCTGGAGGCTGGAGCCACTGAGAATCAGCTGGAGTGGGGAGCCACCTGCGCTGGGCGCCACT CCGAGTCCGGCCATGTCACTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-SPTB	⋮	TGAAACACCCTGTGGTCCGGAGCCAGGTTGTGTTTCTCCTGGGAGCCTGAGGAGTTTGTTGTCTGTGTG CAGTCCCCCGCGGCCACCTGCTGGTTGAGCCTGGACATACACCTTCACCTCCTTTGGCCCGGGAGAAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTTGTGCACACCCTCTGTGAAGACCCCAACCCCTGCCTCC CCCACCCAAGCCAGTTTCCTAGCAAGGGCAGGAC
ESTD-SSA1	⋮	TTCACTTTGTGGATTGTTCTTTGCTGTGTGCAGCCACCTTTCAACATGATGGATCCCATTTGTCCAAG TTTGCTTTGGCTGCCTGCTCTGTGTGGGATATTGAAAGAGATCTTTGCCAGTCCAATGTCCTAGAGAG TTTTCCCAATGTTTTCTTGTAATAGTTTCATAGTTTGAGGCCTTAGATTTAAGTCTTAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	⋮	AAATGGTCAGGACCCTGATCCACAAGAAGTGGTACCATTTCATCAGGGCCATCAGTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATCATCTTAAAATGACTTGTGGGACAGGATCA ATTTCCTCTCACCTAGAAACGTTGTTTGTTACAACTTTCTTCCCAGTATGGATGGGATTATGATGGGGG GAGAAGCAAATTTAAAATAGGACCCCATGAGACACATCA
ESTD-THRB	⋮	TGCGGCGCCTTTCCTCCGCGGCAGGGTAGACTTCTTACTTGGCTGTGTTGATTTCCAAGAGAGAAGAGTCCCAAG CACACGAAAAACAGAAGTTGCAGATCCCATGAGGCCCAGTCTCAAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCCCTGTAGATGGG
ESTD-TNFA	⋮	TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACACCAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGGTTCAGCCTCCAGGGTCCTACACACAAATCAGTCAGTG GCCCAGAAGAGACCCCCTCAGAATCGGAGCAGGGGAGGATGGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCCAACTTTCCAAATCCCCGCCCCCGCGGATGG
ESTD-TYR	⋮	TAGTGAAGTTTCATCTCCTGTCAGCTTCTGGATTTCTTGTTCCCACCGCAACAAGAGAGTCTATGC CAAGGCAGAAAAGCTGGTGCTTCATGGCAAAATCAATGTCTCTCCAGATTTCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCATAAATATTGATGTGTTAAACAT GGGTGTTGATCCATTTTCATTTTCATTTGGCCATAGGTCCCTATGGGGATGACA

ID	Sequence
ESTD-TYRP1	AGTAGTGGATGAAGCTAACCAGCCTCTCCTCCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATATAGATTGAGTTATTAACTGTATTTCTTTCACTTTATTACCTTCTTTCT AATACAAGCATATGTTAGAATTAAAGTTCTAGGCATACTT
ESTD-VB12	TTCCCAAGGCCTCAATACAAGTCTTTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACCAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGATGTCACCAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	AGGTAGGAAAAGCAAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCCTTGG TCCCCTAGAGTCTG
ESTD-WT1	AAGACCTACGTGAATGTTCACATGTGCTTAAAGCCTCCCTTCCTCTTCTACTCTCTGCCTGCAGGATGTG CGACGTGTGCCTGGAGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCCAGTGAGAAACGCCCCTT CATGTGTGCTTACCCAGGCTGCAA
ESTD-s14544	TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTCGCTGTGTGGGTTAGATGCAGGATTTATATGATCCGTTAACC TCT
EST717706	AGCACCACCTCTCAAGCTCAAGCCTCAGCCACCAGATGTGTTCTCTATAAGGATGACGTGCTGTTTTACAA CATCTCCTCCATGAAGAGCACAGAGAGTTATTTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAAGAGAAAACCACTGCAGAGTACCAGCTGTTGGTGGAAGG AGTGCCCCAGTCCCAGTCCCCAGGTGACACTGGACAAGAAAGAGGGCCATCCAAGG
EST524186	CAAATTACAGGGGTCAACTGCTATGATGTGTTTGGAGCCCAGTCACCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCGCGGGAGGAGTTGGGCGGGAGTACGGGGCTGCAGGCATACACTAAAGTGAAAACTGTGAGTGTGG
EST135863	CCCACTCTATTTGCCCAGCGCCCAGGGACAGAGCTGATCCTTGAACTCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGCTGCCTTATCGCCCCCAGCCCAGACCCTGCTGCAGACAT AAATAGGCCCCTGCAAGACCCTGGCTGCTTAGAGACTGCGAGAAGGAGGGTGCGTCCTGCCCTGCCCCG GTCACTC
EST519767	AGGCAGAAAACTGGGCGCCCCCATGCGGGGGACGTGGAAGGCCACTTGAGCTTCCTGGAGAAGGACCTGA GGGGACAAGGTCAACTCCTTCTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAGAACTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGGTGCAGATGCTGGCC CCTTTGGAGAGCTGAGCTGCCCCTGGTGC

EST	Sequence
EST114586	CCACTTTGGTAGTGCCAGTGTGACTCAGTGTGCTCATCCACAATGATTTCTCCAGTGTCGTCATCTTGTTCTCGAGTTTCTCTGCCAGTGTTGCTATTGCGAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTCCACAGTGGTCCCATTAAAAACATTCTATGAGCCAGGAGAAGAGATTACGTATTCCTGCAAGCCGGGCTATGTGTCCCGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTTCTG
EST398528	CGGTCTTCCTTCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAGGCATTTCTTGAGGTGAGTACACCTTCCCCACTCTCTTACGGTACAGAAAGGAGGATGAACAGCAGGAACACGTGGAAAAGGCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCTCCACAGGCTGCTATAATACAGCCCT
EST624480	ACCTGGTGTTGCTGGTGCTGTGGGTGAACCTGGTCCTCTTGGCATTGCGGCCCTCCTGGGGCCCGTGGTCCTCCTGGTCCTGTGTGGGGTAGTCCTGGAGTCCTGGGTGCTCCTAGTGAAGCTGGTGGTCGTGATGGCAACCCTGGGAACGGATGGTGTCCCCCAGGTCGCGCGGATGGTCAACCCGGTCAACCCGGACACAAGGGAGAGCGCGGTTACCCTGGCAATAT
EST360272	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGCCAACTATGCCTCTCAGAACATCAACTACCACTGCAAGAACAGCATTGCATACACTGGATGGGATGAGGAGACTGGAAACCTGAAAAAGGCTGTCATTCTTACAGGGCTCTAATGATGTTGAACTTGTTGCTGAGGGCAACAGCAGGTTCACTTACACTGTTCTTGTAGATGGCTGCTGCTCTAAAAAGACAAATGAATGGGGAAAGACAA
EST122740	CCCCCAGTTGACAGCCACTGCTCTAGACTAAGTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGTATTACATAAAGAAGTCAAGTGGTTTTACTCCTCATGACCAAATATTCTTCCCTCCTTAGGATGAGGTGATAGTAAATGACCGATGGGGTCAGAACTGTTCCTGTCACCATGGAGGATACTATAACTGTGAAGATAAATTCAAGCCACAGAGCTTGCCAGATC
EST768078	ATGCTAAGGGGATCGGACATGAAAGGACCCTGTGAGCCGATTGTCCTATCTCCAGCGGCCCTGTCATCCAGCTCACTCATCAATGGGGCCCAGTGGCCCAGGCCACTGGGCTCCGGAGGACTCACCACTGCGCCCCCTGCTGCCCATGTGTGGACTTGGTCTGCAAGTTGAGGACTTCTTG
EST444387	GCAGCCAGGAGCCGCGGTGCGACCTGCACCATGCGCCCCGGCATAGATGCGGGAACTCGACTTCAAGGACGTCCTGCTCCGGACCTAAGCGGAGCAGGCCTCAAGAGCCGGAGGTGGG
EST128393	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGGAGAGCAGAATATGGTCCTCTCTTTGCTCCTAACATCTATGTACTGGATTATCTAAAATGAAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGGCCATTGGCTATCTCAACACTGGTGAGTGAGTGATTACTTGAGTAAGGGAAACTTGAATGTTATTCAACTGGAATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
EST544198	CTTCTGCCTAATTTGAATGATGTAATTTGCTGTGGGACCTGAGCACTTTTATGGCACAAATGATCACTATTTTCTTGACCCCTACTTACAATCCTGGGAGATGTATTTGGGTTTAGCGGTGGTGTATGTTGTGTACTATAGTCCAAGTGAA

EST103982	--	TGCCTGGGGTGGCAAGGCTGCAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTCACTTGATGATGTTCACAATTGGGGCTTGACTTTCCAACACGGAGAAG CATTGTTTCTTCGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTTG
EST367517	--	CCAAGTCGTTCAATTTAGCTTTGCAGGTTTAACTCGATTACTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAAACTTAGTTTTTCTGATCTATGGTTTCAAGTTAAACAG
		CACGTGGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAATCTGTCCCAAACTTGTGGCTGAC TTTATGGGCTAAGAAGTTTCACTGGATGCATTAATAACAAATATTTACCTTTTGAAAAATAAATG AAGGATTTGACCTGCTTCGCTCTGGAAAGAGTATCCGTACCGTCCTGACGTTTTGAAACAATACAGAT GCCTTCCCTTGTAGCAGTTTTCAGCCCTCCTCTACCCTA
EST405622	--	GCTCTCTATACCCCTGTGGTCCTCCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTCATGCAGCGTGTGACAGGATGGAAGAACTGGCTCCCTGACGGGAGCCAGTGTGG ACAGCACCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAGGCAAACCTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST182883	--	TTCCCGCCAGCCCCCCATCCTTGGCACCCTGGTCCCCCTCAGGGGCCCACCCGCGGGCCACTCACCGCTCT CGCTCTCGGTAACATCGGCGGCGGGCCGTCCTTGAGCACACTAGCCTTGGACCGGTTCCGTATAGGAGG ACCGTGTAGGCCTTCCTGTCCCGGCCTTGCCAGGGCCCTGCAGAGAGAGGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCCACGTG
EST705233	--	CAGTGTATCTGGAAAGCCTACAGGACCACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATTCCGAGAGACCCTAGAAGATACACGAGACCGA ATGTATCAAATGGACATTCAGCAGGAACTTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATAGCA CACTTGTCACCTACATTTCTGATTGGTGGACTCTTGCTGCTAAGAACCTT
EST587077	--	AGACCATGAAGGAGTTGAAGGCCTACAAAATGGAAGCAACTGAGGAACAACTGACCCCGGTGGCGGAGG AGAGCGGGGCGCACGGCTGTCCAAGGAGCTGCAGGGGCGGGGCGCCGGCTGGGCGCGGACATGGAGGA CGTGCGCGGCCGCCTGGGTGCAGTACGCGGCGGAGGTGCAGCGCCATGCTCGGCGGCAAGCGGAGGAGC TGCGGGGTGCGGCCTCGCCTCGCCACCTGCGCAAGCTGCGGTAAGCGGCTCCTC
EST741676	--	CGCCTGGGTGCAGTACGCGGCGGAGGTGCAGCCATGCTCGGCCCAGAGCACCGAGGAGCTGCGGGGTGCG CCTCGCCTCCCACCTGCGCAAGCTGCGGTAAGCGGCTCCTCCCGCGATGCCGAGAAGCGCC TGGCAGTGTACCAGGCCGGCCGGGGCGGGGCGGGGCGCCGGCTGCAGCGGCCATCCGGAGGCCTG GGGCCCCCTGGTGGGAACAGGCCGCGGCGGGGCGGGGCGCCCACTGTGGGCTC
EST432118	--	TGTAGCCAAAGTCACCTGCATCATCATTTGGCTCTGCTGGCAGGCTTGGCCAGTTTGCCAGCTATAATCC ATCGAAATGTTATTTTTCATTGAGAACACCAATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCCTCCGATAGGGCTTGGCGTGACCAAAAATATACTGGGTTTCCTGTTTCCTTTTTCTGATCAT TCTTACAAGTTATACTCTTATTTGGAAGGCCCTAAAGAAGAGGCTTATG
EST367704	--	

ID		Sequence
EST260211	::	TAATGTAAGCTCATCCACCAAGAAGCCTGCCACCATGTTTTGAGGTTGAGTGACATGTTCGAAACCTGT CCATAAAGTAATTTTGTGAAGAAGGAGCAAGAGAACATTCCTCGCAGCAGCACTTCACTACCAAATGA GCATTAGCTACTTTTCAGAATTGAAGGAGAAAATGCATTATGTGACTGAACCGACTTTTCTAAAGC TCTGAACAAAGCTTTTCTTTCCTTTTGCAACAAGACAAAGCAAAGCC
EST512120	::	ATCCTGAGCTCGCCAATAAGCTTCTTGGTTCTACTCTCTTCTCCACAAGCCCCAATTTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCCTTGTGCTCCCACTCAATACAAAAGGCCCCTCTCT ACATCT
EST201182	::	GTTCCGAATCCTCCTCCTGAAAGTGGCCGGGGTTTAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGGCCTTGAAGCTGGGAGTGGGGTTTAGGGACGCGGGGTCTCTGCGTGCATCCTAAGCTCT GAGAGCAAACCTCCCTTGAAGCTGGGGAGTGGGGTTTAGGGACGCGGGGTCTCTGCGTGCATCCTAAGCT CTGAGA
EST530186	::	ACAATCCAGGTCACACATTCCAGAAGAGGAGGGGGTGGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGGAGGGCCACGAGGGATCGAAGTTAGTGAAGTC
EST687875	::	CTTCCTATGGGATTTGACTTTATTTTCTCCATTGTCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGCAGCTCATGACAATTGAAGCTGACAATTACACAAGAAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTCGAAACATTGAAAGTTGTTTTGGTGTCACCTTAATTACACAACCTAG CAGACGGAACTGAACTCAGGGTAAGAAT
EST340882	::	GTGGGGGCAACAGTGGGGAGAGAAGGGGCCAGGGTATAAAAGGGGCCCACAAGAGACACGGCTCAAGG ATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST373825	::	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCCTCTTTCTCTTCTCCCTTGGA CTTTGAGTCAAATTGGCCTGGACTTGAGTCCCTGAACCAGCAAAGAGAAAGAGGACCCCAGAAAT CACAGGTGGGCACGTGCGTCTACGCGCATCTCCCTTCCACGGGAATTTTCAGGGTAAACT
EST740822	--	TCCAGGGGTGGCTGGACCCCAGCTCTCGCAGCAGGAGGACGTGGCTGGGCTCGTGAAGCATG TGGGGGTGAGCCCAGGGCCCCAAGGCAGGGCACCTGGCCTCCTGCCCCTGCTGGGGTCTCAGCCCTGCCTGTCAC CCAGATCACTGTCCTTGCCCAGCGCGCAGCCCTGTGATGCGCCTCCTGCCCCCTGCTGCGGCCCTC TGGGGACCTGACCCAGCCCAGCCCTTTGTGAACCAACACCTGTGCG
EST453110	::	GCCCTCCTCTCTTCCAATTCTGTCCCAATTCTGTCCCTATAGTTTTCCTCTATTAAGTGAACTACATGCATTCTTTAGT GGATAGATGCACACAACACACAAGCCATTATGGGGAAGGATCCACGTGTGCCATATTGTAACA CATTTTTCTGCAAATCACCTCTTTCATTTAACAGCCCTTATTCAATGGCCTTTTCTTTTTCAGTAGTA CATACACAATCTGTGTCATTGTTGAAT

EST65258 8	--	TGCCCCATCACGCGGCCGAGACATGGCTTGCCACAGCTTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTCCACCCTGACTGGCACAGCCATGGCCGGCGGTGCTTCTCGGGGCTCGTCGGGGGG ACAGCTCCACTCTGACTGGCACAGTCTTGCATGGAGACTTGAGGAGGGAGGGCTTGAGGTTGGTGAG GTTAGGTGCGGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	--	ATGCAGGATGAAGGTGGACAGGGAGGGAGAGAGGGCCAACCTGTCATCCCAGGGCCTGCAGATGTCGCTG GACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	--	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTATTAGCATTGTTTGTTTAGCATTACCTAA TTTTTTCCTGCTCCAGACTGTTAGCTTTTACCTTAAATGCTTATTTTAAAATGACAGTGGAAG TTTTTTTTCCTCGAAGTGCCAGTATTCCCAGAGTTTTGGTTTTTGAACTAGCAATGCCTGTGAAAAA GAAACTGAATACCTAAGATTTCTGTCTGTGGGGTTTTTTGGTGCATGCA
EST35879 9	--	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGGCTGTACCCAATTAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCCTGGAAGACAGCAGGGGCAGGAGAAGAGCTGCCTGGATGAA
EST68308 5	--	GGAAAAGAGATTTAAGAAGCTTGATTTGGACAATTCTGGTTCTTGAGTGTGGAAGAGTTCATGTCTCT GCCTGAGTTACAACAGAATCCTTAGTACACGCGAGTAATAGATATATTCGACACAGATGGGAATGGA GAAGTAGAGACTTTAAAGGTAAGAAAGTAGTTATTTTTA
EST54045 6	--	GGAATATTAAAAATATTTAAAATACCTCCATTTTGCTTATCCTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATGTGTCATGTTGTGGCAATTGTTTCTTACAAAATCGGATGGGAAATCT GTTAAGTAAGTACTGTTTTGCCTTGGAATTGGATTTTTAATGTTGACTTTATCAT
EST52908 0	--	ATCACAGGTCTCTCTGGTCTCTGGCCCATCATTCCTGGGAGAGATGGATGTGGTCTGTCGCAAGCCCTTTGG CAATGTGAGAGATTTGATG
EST19590	--	AGGAGAAGCTGAGGAGGGGAAGAGAGAGACAAGAATGACATTGATGAGTGAAGAGTGTCGGCTCAGGAT GCCGGAAAATGAC
EST76136	--	TGAAGCTTCTGCCCAGCTTGCATTGTTTCTAGGAGAACCCGGCTCATACCTTTATCTATAGCCTTCCCC TAGGTCTT
EST58607 0	--	CTCTGGATGGGTTCACAGGTGGCAGGCACACAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGCCCACATGGCGCGGGATGGCCGGCGGGGAGTTCTGGT TGCGGGCCACGGCTGTGGCCCTCGTTGTGAACGGTAGCCTTTGCGGTTGCGGATGCCTAAACCTTTGTTTCT TGGCCAAGGAGGGGCGGGGGTGCGGGGGTGCCATGCCTGAGATGTAGATGCGGCC

Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence

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EQUIVALENTS

While this invention has been particularly shown and
described with references to preferred embodiments thereof,
it will be understood by those skilled in the art that
5   various changes in form and details may be made therein
without departing from the spirit and scope of the
invention as defined by the appended claims. Those skilled
in the art will recognize or be able to ascertain using no
more than routine experimentation, many equivalents to the
10   specific embodiments of the invention described
specifically herein. Such equivalents are intended to be
encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table, or a portion thereof which includes a polymorphic site, or the complement of the segment or portion thereof.

2. The nucleic acid segment of claim 1 that is DNA.

3. The nucleic acid segment of claim 1 that is RNA.

4. The segment of claim 1 that is less than 100 bases.

5. The segment of claim 1 that is less than 50 bases.

6. The segment of claim 1 that is less than 20 bases.

7. The segment of claim 1, wherein the polymorphic site is biallelic.

8. The segment of claim 1, wherein the polymorphic form occupying the polymorphic site is the reference base for the fragment listed in the Table, column 3.

9. The segment of claim 1, wherein the polymorphic form occupying the polymorphic site is an alternative form for the fragment listed in the Table, column 4.

10. An allele-specific oligonucleotide that hybridizes to a segment of a fragment shown in the Table, column 7 or its complement.

11. The allele-specific oligonucleotide of claim 10 that is a probe.

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12. The allele-specific oligonucleotide of claim 10, wherein a central position of the probe aligns with the polymorphic site of the fragment.

13. The allele-specific oligonucleotide of claim 10 that is a primer.

14. The allele-specific oligonucleotide of claim 13, wherein the 3' end of the primer aligns with the polymorphic site of the fragment.

15. The allele-specific oligonucleotide of Claim 10, which is selected from the group consisting of the nucleotide sequences of the Table, column 5.

16. The allele-specific oligonucleotide of Claim 10, which is selected from the group consisting of the nucleotide sequences of the Table, column 6.

17. An isolated nucleic acid comprising a sequence of the Table, column 7 or the complement thereof, wherein the polymorphic site within the sequence or complement is occupied by a base other than the reference base shown in the Table, column 3.

18. A method of analyzing a nucleic acid, comprising obtaining the nucleic acid from an individual; and determining a base occupying any one of the polymorphic sites shown in the Table.

19. The method of claim 18, wherein the determining comprises determining a set of bases occupying a set of the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.